

STUDY TITLE

Supplemental Information for Potential Allergenicity Assessment of AAD-12 Protein Expressed
in Soybean Event DAS-68416-4 by Bioinformatics Analysis (Update, March, 2010)

DATA REQUIREMENTS

N/A

AUTHOR(S)

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STUDY COMPLETED ON

23-April-2010

PERFORMING LABORATORY

Regulatory Sciences and Government Affairs—Indianapolis Lab
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Indianapolis, Indiana 46268-1054

LABORATORY STUDY ID

101572S

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W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-l2: 1 - 80 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

72      12      12:+AD0APQAg-
74      10      10:+AD0-+AD0AKg-
76      3       7:+AD0AKg-
78      4       6:+AD0AKg-
80      3       4:+ACo-
82      2       3:+ACo-
84      1       3:+ACo-
86      2       2:+ACo-
88      2       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.70320.00357+ADs- mu+AD0- 3.1488
0.185
mean+AF8-var+AD0-45.600412.910, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.189928
Kolmogorov-Smirnov statistic: 0.0668 (N+AD0-29) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
63 22.9      5.3
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
63 22.9      5.3
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
63 22.9      5.3
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.1      5.8
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.8      7.3
gi+AHw-51242679+AHw-gb+AHw-AAT99258.1+AHw- pectin-methyltransferas ( 362)
61 22.3      8.3

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 63 Z-score: 89.4 bits: 22.9 E(): 5.3

```

Smith-Waterman score: 63+ADs- 27.778+ACU- identity (55.556+ACU- similar)
in 54 aa overlap (1-54:218-270)

```

                                10      20      30
AAD-12                        MAQTTLQITPTGATLGATVTGVHLATLDDA
                                ... : .  .. ... . : : .  .
gi+AHw-598 CYIEGTVDLIFGEARSLYLNTELHVVPDPMAMITAHARKNADGVGG-YSFVHCKVTGTG
              190      200      210      220      230      240

```

```

                    40      50      60      70      80
AAD-12 GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISN
          : : :  .... : ...  ....
gi+AHw-598 GTALLGRAWFEEARVVFSYCNLSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKR
              250      260      270      280      290      300

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 63 Z-score: 89.4 bits: 22.9 E(): 5.3
Smith-Waterman score: 63+ADs- 27.778+ACU- identity (55.556+ACU- similar)
in 54 aa overlap (1-54:218-270)

```

                                10      20      30
AAD-12                        MAQTTLQITPTGATLGATVTGVHLATLDDA
                                ... : .  .. ... . : : .  .
gi+AHw-598 CYIEGTVDLIFGEARSLYLNTELHVVPDPMAMITAHARKNADGVGG-YSFVHCKVTGTG
              190      200      210      220      230      240

```

```

                    40      50      60      70      80
AAD-12 GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISN
          : : :  .... : ...  ....
gi+AHw-598 GTALLGRAWFEEARVVFSYCNLSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKR
              250      260      270      280      290      300

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 63 Z-score: 89.4 bits: 22.9 E(): 5.3
Smith-Waterman score: 63+ADs- 27.778+ACU- identity (55.556+ACU- similar)
in 54 aa overlap (1-54:218-270)

```

                                10      20      30
AAD-12                        MAQTTLQITPTGATLGATVTGVHLATLDDA
                                ... : .  .. ... . : : .  .
gi+AHw-225 CYIEGTVDLIFGEARSLYLNTELHVVPDPMAMITAHARKNADGVGG-YSFVHCKVTGTG
              190      200      210      220      230      240

```

```

                    40      50      60      70      80
AAD-12 GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISN
          : : :  .... : ...  ....
gi+AHw-225 GTALLGRAWFEEARVVFSYCNLSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKR
              250      260      270      280      290      300

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 88.7 bits: 22.1 E(): 5.8

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (47-78:133-160)

```
      20      30      40      50      60      70
AAD-12  ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
              :  ::  :::::  .  :  ....  ::::
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPPRRFQGQDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150
```

```
      80
AAD-12  AISN
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210
```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)

initn: 39 initl: 39 opt: 59 Z-score: 86.8 bits: 21.8 E(): 7.3
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (15-63:3-55)

```
      10      20      30      40      50
AAD-12  MAQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQ
              :  ::::  :: . . . . . :  ::  :  .::  .  :
gi+AHw-886      FALIAVVATSTIAQMETSCLPGLERFWQQQPLPPQQTLPFQQQPFPPQQ
              10      20      30      40
```

```
      60      70      80
AAD-12  QITFAKRFGAIERIGGGDIVAISN
      :  :...
gi+AHw-886 QPPFSQQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLFPQQSPFSQQQLVLPPQQQQQLP
      50      60      70      80      90      100
```

+AD4APg-gi+AHw-51242679+AHw-gb+AHw-AAT99258.1+AHw- pectin-
methyltransferase pr (362 aa)

initn: 59 initl: 59 opt: 61 Z-score: 85.9 bits: 22.3 E(): 8.3
Smith-Waterman score: 61+ADs- 27.778+ACU- identity (55.556+ACU- similar)
in 54 aa overlap (1-54:241-293)

```
      10      20      30
AAD-12      MAQTTLQITPTGATLGATVTGVHLATLDDA
              :  ::  .  ..  .::  .  .
gi+AHw-512 CYTEGTVDFIFGEARSLYLNTELHVVPGDPMAMITAHARKNADGVGG-YSFVHCKVTGTG
      220      230      240      250      260
```

```
      40      50      60      70      80
AAD-12  GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISN
      :  :  :  ::::  :  ::  ::::
gi+AHw-512 GTALLGRAWFDAARVVFSSYCNLSDAKPEGWSDNNKPEAQKTILFGEYKNTGPGAAPDKR
      270      280      290      300      310      320
```

80 residues in 1 query sequences

Total Scan time: 0.090 Total Display time: 0.000

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

60      66      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
62      90
40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
64      44      32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      28      25:+AD0APQA9AD0APQA9ACo-
68      21      20:+AD0APQA9AD0AKgA9-
70      33      16:+AD0APQA9ACoAPQA9AD0APQA9-
72      9       12:+AD0APQ-+ACo-
74      11      10:+AD0APQAq-
76      6       7:+AD0AKg-
78      1       6:+AD0AKg-
80      4       4:+ACo-
82      2       3:+ACo-
84      2       3:+ACo-
86      4       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.63820.00354+ADs- mu+AD0- 3.5421
0.183
mean+AF8-var+AD0-44.819412.556, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.191576
Kolmogorov-Smirnov statistic: 0.0662 (N+AD0-29) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.1 5.6
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.9 7.1
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.4 7.4
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.4 7.4
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.4 7.4

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.9 bits: 22.1 E(): 5.6
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (46-77:133-160)

```

      20      30      40      50      60      70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      :  ::  ::::  .  :  ....  ::
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      80
AAD-12 AISNV
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
 gluteni (229 aa)
 initn: 39 initl: 39 opt: 59 Z-score: 87.1 bits: 21.9 E(): 7.1
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (14-62:3-55)

```

      10      20      30      40      50
AAD-12 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQ
      :  ::.  .:  .  .  .  .  .  .  :  ::  :  .  ::  .  .  ::
gi+AHw-886 FALIAVVATSTIAQMETSCLPGLERPWQQQPLPPQQTLFPQQQPFPPQQQ
      10      20      30      40

```

```

      60      70      80
AAD-12 ITFAKRFGAIERIGGGDIVAISNV
      :...
gi+AHw-886 PPFSQQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPQQSPFSQQQLVLPQQQQQLPQ
      50      60      70      80      90      100

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.8 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (21-53:238-270)

```

      10      20      30      40      50
AAD-12 AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      :  :  .  .  :  :  :  ::::  :  .  .  .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNV
      :..
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```


+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.8 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (21-53:238-270)

```

                10         20         30         40         50
AAD-12          AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . . : : : : : : : : :
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
            210         220         230         240         250         260

```

```

                60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNV
            ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
            270         280         290         300         310         320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.8 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (21-53:238-270)

```

                10         20         30         40         50
AAD-12          AQTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . . : : : : : : : : .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
            210         220         230         240         250         260

```

```

                60         70         80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNV
            ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
            270         280         290         300         310         320

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:33 2010 done: Fri Feb 5 12:55:33 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 3 - 82 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

66      20      25:+AD0APQA9AD0APQA9AD0- +ACo-
68      21      20:+AD0APQA9AD0APQA9ACo-
70      32      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      11      12:+AD0APQA9ACo-
74      10      10:+AD0APQA9ACo-
76      6       7:+AD0APQAq-
78      2       6:+AD0AKg-
80      3       4:+AD0AKg-
82      1       3:+ACo-
84      2       3:+ACo-
86      4       2:+ACoAPQ-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.66860.00352+ADs- mu+AD0- 3.7091
0.182
mean+AF8-var+AD0-43.840912.063, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.193702
Kolmogorov-Smirnov statistic: 0.0573 (N+AD0-29) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
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219) 60 22.1 5.6
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.8 7.2
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3 7.5
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3 7.5
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3 7.5

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 88.9 bits: 22.1 E(): 5.6

```

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (45-76:133-160)

```

                20          30          40          50          60          70
AAD-12  ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                :  ::  :::::  .  :  ....  ::::
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150

```

```

                80
AAD-12  AISNVK
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
initn: 39 init1: 39 opt: 59 Z-score: 87.0 bits: 21.8 E(): 7.2
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (13-61:3-55)

```

                10          20          30          40          50
AAD-12  QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQI
                :  ::::  ::  .  .  .  .  .  :  ::  :  .  ::  .  .  ::
gi+AHw-886          FALIAVVATSTIAQMETSCLPGLERPWQQQPLPPQQTLPFPQQQPFPPQQQP
                10          20          30          40          50

```

```

                60          70          80
AAD-12  TFAKRFGAIERIGGGDIVAISNVK
                :...
gi+AHw-886 PFSQQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPQQSPFSQQQLVLPQQQQQLPQQ
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (20-52:238-270)

```

                10          20          30          40
AAD-12          QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :  :  .  .  :  :  :  ::::  :  :  :  .
gi+AHw-598 TELHVVPDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEARVVFVSYCN
                210          220          230          240          250          260

```

```

                50          60          70          80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVK
                :..
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270          280          290          300          310          320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5

Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (20-52:238-270)

```

                10      20      30      40
AAD-12          QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVK
                ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (20-52:238-270)

```

                10      20      30      40
AAD-12          QTTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVK
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:33 2010 done: Fri Feb 5 12:55:33 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 4 - 83 80 aa - 80 aa

```

opt      E ()
+ADw- 20    2     0:+AD0-
22       0     0:           one +AD0- represents 3 library sequences
24       1     0:+AD0-
26       1     0:+AD0-
28       3     0:+AD0-
30       5     2:+ACoAPQ-
32      14     8:+AD0APQAqAD0APQ-
34      26    21:+AD0APQA9AD0APQA9ACoAPQA9-
36      54    44:+AD0APQA9-+AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
38      52    72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
40      86
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ-   +ACo-
42     133
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
44     171
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA
9AD0APQA9-
46     121
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
48     102
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0-   +ACo-
50     101
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0-   +ACo-
52     66
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
54     88
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACo-
56     69
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
58     65
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60     80
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ
A9-
62     79
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9-
64     39     32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66     17     25:+AD0APQA9AD0APQA9-   +ACo-
68     23     20:+AD0APQA9AD0APQA9ACoAPQ-
70     34     16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
72     14     12:+AD0APQA9ACoAPQ-

```

```

74      6      10:+AD0APQ- +ACo-
76      6      7:+AD0APQAq-
78      2      6:+AD0AKg-
80      3      4:+AD0AKg-
82      2      3:+ACo-
84      1      3:+ACo-
86      4      2:+ACoAPQ-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.69180.00355+ADs- mu+AD0- 3.5856
0.184
mean+AF8-var+AD0-43.914412.062, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.193540
Kolmogorov-Smirnov statistic: 0.0525 (N+AD0-29) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.1      5.7
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.8      7.2
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.6
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3      7.6
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.6

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 88.8 bits: 22.1 E(): 5.7
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (44-75:133-160)

```

20

30

40

50

60

70

10 20 30 40


```

AAD-12          TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                  :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSYCN
                210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKA
      :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (19-51:238-270)

```

                  10      20      30      40
AAD-12          TTLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                  :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSYCN
                210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKA
      :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:35 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 5 - 84 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-

```

```

22      0      0: one +AD0- represents 3 library sequences
24      1      0:+AD0-
26      1      0:+AD0-
28      3      0:+AD0-
30      1      2:+ACo-
32     11      8:+AD0APQAqAD0-
34     34     21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
36     61
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
38     68
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
40     80
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9-   +ACo-
42    112
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
44    152
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
46    130
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
48    103    132:+AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0-   +ACo-
50    114
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
52     70
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
54     81
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9-   +ACo-
56     71
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
58     66
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60     73
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
62     84
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-
64     37     32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66     21     25:+AD0APQA9AD0APQA9AD0-   +ACo-
68     23     20:+AD0APQA9AD0APQA9ACoAPQ-
70     33     16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72     14     12:+AD0APQA9ACoAPQ-
74      8     10:+AD0APQA9ACo-
76      4      7:+AD0APQAq-
78      3      6:+AD0AKg-
80      2      4:+AD0AKq-

```

```

82      3      3:+ACo-
84      1      3:+ACo-
86      3      2:+ACo-
88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.80460.00358+ADs- mu+AD0- 2.7946
0.186
mean+AF8-var+AD0-45.908712.867, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.189290
Kolmogorov-Smirnov statistic: 0.0525 (N+AD0-29) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.100
The best scores are:      opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.0 6.1
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.7 7.7
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.2 8.2
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.2 8.2
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.2 8.2

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.3 bits: 22.0 E(): 6.1
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (43-74:133-160)

      20      30      40      50      60      70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIERIGGGDIV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK---VHRFDEGDLI
      110      120      130      140      150

```

80
 AAD-12 AISNVKAD
 :.
 gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
 160 170 180 190 200 210

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
 gluteni (229 aa)
 initn: 39 initl: 39 opt: 59 Z-score: 86.4 bits: 21.7 E(): 7.7
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (11-59:3-55)

10 20 30 40 50
 AAD-12 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITF
 : :. :. :. :. :. :. :. :. :. :.
 gi+AHw-886 FALIAVVATSTIAQMETSCLPGLERPWQQQPLPPQQTLFPQQQPPFQQQPPF
 10 20 30 40 50

60 70 80
 AAD-12 AKRFGAIERIGGGDIVAISNVKAD
 :.
 gi+AHw-886 SQQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPQQSPFSQQQLVLPQQQQQLPQQQI
 60 70 80 90 100 110

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.0 bits: 22.2 E(): 8.2
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (18-50:238-270)

10 20 30 40
 AAD-12 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
 :. :. :. :. :. :.
 gi+AHw-598 TELHVVPDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
 210 220 230 240 250 260

50 60 70 80
 AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 :.
 gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFGGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
 270 280 290 300 310 320

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.0 bits: 22.2 E(): 8.2
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (18-50:238-270)

10 20 30 40
 AAD-12 TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
 :. :. :. :. :. :.
 gi+AHw-225 TELHVVPDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
 210 220 230 240 250 260

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)
  initn: 61 initl: 61 opt: 61 Z-score: 86.0 bits: 22.2 E(): 8.2
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (18-50:238-270)

      10      20      30      40
AAD-12          TLQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSSYCN
      210      220      230      240      250      260

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:35 2010
 Total Scan time: 0.100 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 6 - 85 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	1	0:+AD0-	
26	1	0:+AD0-	
28	3	0:+AD0-	

[illegible]

```

 96      0      1:+ACo-      :+ACo-
 98      0      0:      +ACo-
100      0      0:      +ACo-
102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.94690.00361+ADs- mu+AD0- 2.2455
0.187
mean+AF8-var+AD0-46.955213.181, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.187168
Kolmogorov-Smirnov statistic: 0.0525 (N+AD0-28) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 21.9 6.7
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.6 8.5
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.1 9.1
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.1 9.1
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.1 9.1

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 87.5 bits: 21.9 E(): 6.7
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (42-73:133-160)

      20      30      40      50      60      70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : : : : : : : : : : : : : : : :
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

      80
AAD-12 AISNVKADG
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)

initn: 39 initl: 39 opt: 59 Z-score: 85.7 bits: 21.6 E(): 8.5
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (10-58:3-55)

```

      10      20      30      40      50
AAD-12 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFA
      : : : : . : . . . : : : : : : : : : : : : :
gi+AHw-886 FALIAVVATSTIAQMETSCLPGLERPWQQQPLPPQQTLFPQQQPFPPQQPPFS
      10      20      30      40      50

```

```

      60      70      80
AAD-12 KRFGAIERIGGGDIVAISNVKADG
      : :
gi+AHw-886 QQQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPPQQQQQLPQQQIS
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (17-49:238-270)

```

      10      20      30      40
AAD-12 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . : : : : : : : : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVSFCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADG
      : : :
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (17-49:238-270)

```

      10      20      30      40
AAD-12 LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . : : : : : : : : : :
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVSFCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADG
      : : :
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```


+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (17-49:238-270)

```

                10      20      30      40
AAD-12          LQITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... :...
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSSYCN
            210      220      230      240      250      260

            50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADG
            ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
            270      280      290      300      310      320

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:35 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 7 - 86 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      3      0:+AD0-
      30      3      2:+ACo-
      32      9      8:+AD0APQAq-
      34      38     21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
      36      58     44:+AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
      38      71
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-

```

```

40      81
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-+ACo-
42    119
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
44    148
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
46    126
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
48    106
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
50    105
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
52     73
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
54     83   91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
56     72
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
58     73
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
60     90
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
A9AD0APQA9-
62     56   40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
64     40   32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66     16   25:+AD0APQA9AD0APQA9- +ACo-
68     25   20:+AD0APQA9AD0APQA9ACoAPQA9-
70     35   16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
72     12   12:+AD0APQA9ACo-
74       5   10:+AD0APQ- +ACo-
76       5    7:+AD0APQAq-
78       4    6:+AD0AKg-
80       3    4:+AD0AKg-
82       3    3:+ACo-
84       1    3:+ACo-
86       4    2:+ACoAPQ-
88       0    2:+ACo- inset +AD0- represents 1 library sequences
90       0    1:+ACo-
92       0    1:+ACo- :+ACo-
94       0    1:+ACo- :+ACo-
96       0    1:+ACo- :+ACo-
98       0    0:          +ACo-
100      0    0:          +ACo-
102      0    0:          +ACo-
104      0    0:          +ACo-
106      0    0:          +ACo-
```

```

108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.92780.00359+ADs- mu+AD0- 2.3831
0.186
mean+AF8-var+AD0-46.847613.124, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.187383
Kolmogorov-Smirnov statistic: 0.0498 (N+AD0-28) at 56

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 21.9 6.7
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.6 8.5
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.1 9.1
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.1 9.1
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.1 9.1

```

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 87.5 bits: 21.9 E(): 6.7
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (41-72:133-160)

```

```

                20          30          40          50          60          70
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : :: :...: . : ...: :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSRPPRRFQGQDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150

                80
AAD-12 AISNVKADGT
                :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210

```

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
initn: 39 initl: 39 opt: 59 Z-score: 85.7 bits: 21.6 E(): 8.5
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (9-57:3-55)

```

```

      10      20      30      40      50
AAD-12 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAK
      : :. . . . . : : : : : : : : : : : :
gi+AHw-886 FALIAVVATSTIAQMETSCLPGLERPWQQQPLPPQQTLFPQQQPFPPQQQPFPSQ
      10      20      30      40      50

```

```

      60      70      80
AAD-12 RFGAIERIGGGDIVAISNVKADGT
      .
gi+AHw-886 QQPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPQQSPFSQQQLVLPPQQQQQLPQQQISI
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (16-48:238-270)

```

      10      20      30      40
AAD-12 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . . : : : : : : : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGT
      : : .
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (16-48:238-270)

```

      10      20      30      40
AAD-12 QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . . : : : : : : : : .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGT
      : : .
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (16-48:238-270)

```

                10      20      30      40
AAD-12          QITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
                210      220      230      240      250      260

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGT
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:35 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 8 - 87 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      3      0:+AD0-
      30      4      2:+ACoAPQ-
      32     10      8:+AD0APQAqAD0-
      34     32     21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      36     69
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
      38     77
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
-
      40     86    101:+AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      42    128
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-

```

```

44      118
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
46      133
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
48      102
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
50      97
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
QA9AD0APQA9AD0APQA9- +ACo-
52      86
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQ- +ACo-
54      91
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
56      61
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
58      72      62:+AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
60      102
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
62      46      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64      32      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      23      25:+AD0APQA9AD0APQA9AD0APQAq-
68      35      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      25      16:+AD0APQA9AD0APQAqAD0APQA9-
72      10      12:+AD0APQA9ACo-
74      6      10:+AD0APQ- +ACo-
76      4      7:+AD0APQAq-
78      5      6:+AD0AKg-
80      3      4:+AD0AKg-
82      2      3:+ACo-
84      3      3:+ACo-
86      2      2:+ACo-
88      0      2:+ACo- inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo- :+ACo-
94      0      1:+ACo- :+ACo-
96      0      1:+ACo- :+ACo-
98      0      0: +ACo-
100     0      0: +ACo-
102     0      0: +ACo-
104     0      0: +ACo-
106     0      0: +ACo-
108     0      0: +ACo-
110     0      0: +ACo-
112     0      0: +ACo-
114     0      0: +ACo-
116     0      0: +ACo-
118     0      0: +ACo-

```

```
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.87940.00357+ADs- mu+AD0- 2.8634
0.185
mean+AF8-var+AD0-46.540612.935, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.188000
Kolmogorov-Smirnov statistic: 0.0485 (N+AD0-28) at 56
```

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
```

```
join: 42, opt: 30, open/ext: -10/-2, width: 32
```

```
Scan time: 0.090
```

```
The best scores are: opt bits E(1471)
```

```
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 21.8 6.9
```

```
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.6 8.7
```

```
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.0 9.3
```

```
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.0 9.3
```

```
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.0 9.3
```

```
+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
```

```
initn: 43 initl: 43 opt: 60 Z-score: 87.3 bits: 21.8 E(): 6.9
```

```
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (40-71:133-160)
```

```
10      20      30      40      50      60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : :: :...: . : :... :...
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPPrRFQGGQDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150
```

```
70      80
AAD-12 AISNVKADGTV
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210
```

```
+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
```

```
initn: 39 initl: 39 opt: 59 Z-score: 85.5 bits: 21.6 E(): 8.7
```

```
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (8-56:3-55)
```

```
10      20      30      40      50
AAD-12 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKR
      : :... :. . . . :. : : : :... :. :... :...
gi+AHw-886 FALIAVVATSTIAQMETSCLPGLERPWWQQQPLPPQQTLFPQQQPFPPQQPPFSQQ
      10      20      30      40      50
```

60 70 80
AAD-12 FGAIERIGGGDIVAISNVKADGTV

gi+AHw-886 QPSFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPPQQQQQLPQQQISIV
60 70 80 90 100 110

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.0 bits: 22.0 E(): 9.3
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (15-47:238-270)

10 20 30 40
AAD-12 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . :: : : :: : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTV
:::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.0 bits: 22.0 E(): 9.3
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (15-47:238-270)

10 20 30 40
AAD-12 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . :: : : :: : : :
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTV
:::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.0 bits: 22.0 E(): 9.3
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (15-47:238-270)

10 20 30 40
AAD-12 ITPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . :: : : :: : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260


```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTV
      ...
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPTYTKQLTEADAKTFTTSLEYI
      270      280      290      300      310      320

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:35 2010 done: Fri Feb 5 12:55:36 2010
 Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 9 - 88 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      1      0:+AD0-          one +AD0- represents 3 library sequences
      24      0      0:
      26      1      0:+AD0-
      28      3      0:+AD0-
      30      4      2:+ACoAPQ-
      32      9      8:+AD0APQAq-
      34      32     21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      36      71
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
      38      75
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
      40      93
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
      42      105
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      44      133
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      46      137
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-

```

Lambda+AD0- 0.188791

Kolmogorov-Smirnov statistic: 0.0498 (N+AD0-28) at 56

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.9 6.6

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.6 8.4

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.1 9.1

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge (339) 61 22.1 9.1

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.1 9.1

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 87.6 bits: 21.9 E(): 6.6

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (39-70:133-160)

```

      10      20      30      40      50      60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : :: :...: . : :... :...
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      70      80
AAD-12 AISNVKADGTVR
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)

initn: 39 initl: 39 opt: 59 Z-score: 85.7 bits: 21.6 E(): 8.4

Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar) in 53 aa overlap (7-55:3-55)

```

      10      20      30      40      50
AAD-12 TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRF
      : :... :. . . . :. : : :... :. :... :...
gi+AHw-886 FALIAVVATSTIAQMETSCLPGLRPWQQQPLPPQQTLPQQQPFPPQQPPFSQQQ
      10      20      30      40      50

```

```

      60      70      80
AAD-12 GAIERIGGGDIVAISNVKADGTVR
      :.
gi+AHw-886 PSFSQQQPPFSQQQPILPEPPFSLQQQPVLPQQSPFSQQQLVLPQQQQQLPQQQISIVQ
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (14-46:238-270)

		10	20	30	40
AAD-12		TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH			
			::	.	:: : : : : : : : .
gi+AHw-598	TELHVVP	GDP	MAMIT	AHARK	NADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSYCN
	210	220	230	240	250 260

	50	60	70	80	
AAD-12	LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR				
	:::				
gi+AHw-598	LSDAVK	PEGW	SDNNK	PAAQKTIF	FGYKNTGPGAAADKRV
	270	280	290	300	310 320

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (14-46:238-270)

		10	20	30	40
AAD-12		TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH			
			::	.	:: : : : : : : : .
gi+AHw-225	TELHVVP	GDP	MAMIT	AHARK	NADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSYCN
	210	220	230	240	250 260

	50	60	70	80	
AAD-12	LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR				
	:::				
gi+AHw-225	LSDAVK	PEGW	SDNNK	PAAQKTIF	FGYKNTGPGAAADKRV
	270	280	290	300	310 320

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 85.2 bits: 22.1 E(): 9.1
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (14-46:238-270)

		10	20	30	40
AAD-12		TPTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH			
			::	.	:: : : : : : : : .
gi+AHw-598	TELHVVP	GDP	MAMIT	AHARK	NADGVGGYSFVHCKVTGTGGTALLGRAWFEAARVVFSYCN
	210	220	230	240	250 260

	50	60	70	80	
AAD-12	LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR				
	:::				
gi+AHw-598	LSDAVK	PEGW	SDNNK	PAAQKTIF	FGYKNTGPGAAADKRV
	270	280	290	300	310 320

[illegible]

52 67
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
54 99
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-+AD0APQAqAD0APQ-
56 78
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58 102
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9AD0APQA9AD0APQA9AD0-
60 53 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
62 57 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
64 33 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66 18 25:+AD0APQA9AD0APQA9- +ACo-
68 32 20:+AD0-+AD0APQA9AD0APQAqAD0APQA9AD0-
70 30 16:+AD0APQA9AD0APQAqAD0APQA9AD0-
72 11 12:+AD0APQA9ACo-
74 3 10:+AD0- +ACo-
76 5 7:+AD0APQAq-
78 4 6:+AD0AKg-
80 3 4:+AD0AKg-
82 3 3:+ACo-
84 3 3:+ACo-
86 4 2:+ACoAPQ-
88 0 2:+ACo- inset +AD0- represents 1 library sequences
90 0 1:+ACo-
92 0 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 0 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 0 0: +ACo-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.70890.00314+ADs- mu+AD0- 3.6476
0.162
mean+AF8-var+AD0-46.298212.950, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.188492
Kolmogorov-Smirnov statistic: 0.0496 (N+AD0-28) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.9 6.6
 gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.6 8.4
 gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.1 8.8
 gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge (339) 61 22.1 8.8
 gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.1 8.8
 gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhib (217) 58 21.3 9.6
 gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-S (221) 58 21.3 9.8

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 87.6 bits: 21.9 E(): 6.6
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (38-69:133-160)

	10	20	30	40	50	60
AAD-12	ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV					
				:	:	:
gi+AHw-221	FGLIFPGCPSTYEEPAQQGRRHQSQRP	RRFQGGDQSQQQQDSHQK----	VHRFDEGDLI			
	110	120	130	140	150	

	70	80
AAD-12	AINVKADGTVRQ	
	:	:
gi+AHw-221	AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR	
	160	170

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight gluteni (229 aa)

initn: 39 initl: 39 opt: 59 Z-score: 85.8 bits: 21.6 E(): 8.4
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (6-54:3-55)

	10	20	30	40	50
AAD-12	PTGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----	LIFPGQHLSNDQQITFAKRFG			
	:	:	:	:	:
gi+AHw-886	FALIAVVATSTIAQMETSCIPGLERPWQQQPLPPQQTLFPQQQPFPPQQPPFSQQQP				
	10	20	30	40	50

	60	70	80
AAD-12	AIERIGGGDIVAINVKADGTVRQ		
gi+AHw-886	SFSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPPQQQQQLPQQQISIVQP		
	60	70	80

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.4 bits: 22.1 E(): 8.8
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (13-45:238-270)

```

                                10      20      30      40
AAD-12                      PTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                        50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
                        :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 85.4 bits: 22.1 E(): 8.8
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (13-45:238-270)

```

                                10      20      30      40
AAD-12                      PTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                        50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
                        :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 85.4 bits: 22.1 E(): 8.8
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (13-45:238-270)

```

                                10      20      30      40
AAD-12                      PTGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

                        50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
                        :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4-+AD4-gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase
 inhibitor (217 aa)

initn: 37 initl: 37 opt: 58 Z-score: 84.7 bits: 21.3 E(): 9.6
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (4-80:134-215)

```

                                10          20          30
AAD-12          PTGATLGATV--TGVHLATLDDAGFAALHAAWL
                   :.:.:. . :.:. . :.:. . :.:. .
gi+AHw-214 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
              110          120          130          140          150          160

```

```

                   40          50          60          70          80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
          . :.:. : . :.:.:. : . :.:.:. : . :.:. : . :.:.
gi+AHw-214 GYNLLYCPVTSTMSCPFSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
              170          180          190          200          210

```

+AD4APg-gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName:
 Full+AD0-Serin (221 aa)
 initn: 37 initl: 37 opt: 58 Z-score: 84.6 bits: 21.3 E(): 9.8
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (4-80:138-219)

```

                                10          20          30
AAD-12          PTGATLGATV--TGVHLATLDDAGFAALHAAWL
                   :.:.:. . :.:. . :.:. . :.:. .
gi+AHw-201 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
              110          120          130          140          150          160

```

```

                   40          50          60          70          80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQ
          . :.:. : . :.:.:. : . :.:.:. : . :.:. : . :.:.
gi+AHw-201 GYNLLYCPVTSTMSCPFSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
              170          180          190          200          210          220

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:36 2010 done: Fri Feb 5 12:55:36 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

[illegible]

```

76      5      7:+AD0APQAq-
78      1      6:+AD0AKg-
80      4      4:+AD0AKg-
82      3      3:+ACo-
84      2      3:+ACo-
86      6      2:+ACoAPQ-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.74630.00326+ADs- mu+AD0- 3.0558
0.168
mean+AF8-var+AD0-43.781711.657, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.193833
Kolmogorov-Smirnov statistic: 0.0394 (N+AD0-29) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.2 5.4
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 21.9 6.9
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.4 7.2
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.4 7.2
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.4 7.2
gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhib ( 217)
58 21.6 7.8
gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-S
( 221) 58 21.6 8

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 89.3 bits: 22.2 E(): 5.4

```

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (37-68:133-160)

```

      10      20      30      40      50      60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : :: :...: . : :... :...
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      70      80
AAD-12 AISNVKADGTVRQH
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)
initn: 39 init1: 39 opt: 59 Z-score: 87.4 bits: 21.9 E(): 6.9
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (5-53:3-55)

```

      10      20      30      40      50
AAD-12 TGATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFGA
      : :... .: . . . . : : : :... : :... :...
gi+AHw-886 FALIAVVATSTIAQMETSCLPGLERPWQQQPLPPQQTLPFPQQQPFPPQQQPPFSQQQPS
      10      20      30      40      50

```

```

      60      70      80
AAD-12 IERIGGGDIVAISNVKADGTVRQH
gi+AHw-886 FSQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQPS
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 87.0 bits: 22.4 E(): 7.2
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (12-44:238-270)

```

      10      20      30      40
AAD-12 TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . : : : :... : :... .
gi+AHw-598 TELHVVPDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEARVVFSSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
      :..
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 87.0 bits: 22.4 E(): 7.2

Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (12-44:238-270)

```

                        10      20      30      40
AAD-12                TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                        :: . . : : : : : : : : :
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSYCN
                210      220      230      240      250      260

```

```

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
                ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 87.0 bits: 22.4 E(): 7.2
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (12-44:238-270)

```

                        10      20      30      40
AAD-12                TGATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                        :: . . : : : : : : : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSYCN
                210      220      230      240      250      260

```

```

                50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase
inhibitor (217 aa)

initn: 37 initl: 37 opt: 58 Z-score: 86.3 bits: 21.6 E(): 7.8
Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
in 84 aa overlap (3-79:134-215)

```

                        10      20      30
AAD-12                TGATLGATV--TGVHLATLDDAGFAALHAAWL
                        : : : . . : : . : : : :
gi+AHw-214 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLETGGTIGQADSSWFKIVKSSQF
                110      120      130      140      150      160

```

```

                40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
. : : : . : : : : : : : : : : : : : :
gi+AHw-214 GYNLLYCPVTSTMSCPFSSDDQ--FCLKVGVVHQNKGKRRLLVKDNPLDVSFKQVQ
                170      180      190      200      210

```

+AD4APg-gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName:
Full+AD0-Serin (221 aa)

initn: 37 initl: 37 opt: 58 Z-score: 86.2 bits: 21.6 E(): 8

Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
in 84 aa overlap (3-79:138-219)

```

                                10      20      30
AAD-12                        TGATLGATV--TGVHLATLDDAGFAALHAAWL
                                :.:. . :. . :. . :. . .
gi+AHw-201 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
                   110      120      130      140      150      160

                                40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQH
                   . :. : . :.:. : . :.:. : . . . : . . :
gi+AHw-201 GYNLLYCPVTSTMSCPFSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSKQVQ
                   170      180      190      200      210      220

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:36 2010 done: Fri Feb 5 12:55:36 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 12 - 91 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      2      0:+AD0-
      30      7      2:+ACoAPQA9-
      32     10      8:+AD0APQAqAD0-
      34     25     21:+AD0APQA9AD0APQA9ACoAPQA9-
      36     85
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQ-
      38     70
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
      40     85     101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-

```

[illegible]

```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.69370.00338+ADs- mu+AD0- 3.4584
0.175
mean+AF8-var+AD0-44.175411.947, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.192967
Kolmogorov-Smirnov statistic: 0.0380 (N+AD0-29) at 36

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.6

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 21.8 7.2

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.3 7.5

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.3 7.5

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.3 7.5

gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhib (217) 58 21.6 8.2

gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-S (221) 58 21.6 8.4

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 88.9 bits: 22.1 E(): 5.6
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (36-67:133-160)

```

          10          20          30          40          50          60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          : :: :...: . : :...: :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGQDQSQQQQDSHQK----VHRFDEGDLI
          110          120          130          140          150

          70          80
AAD-12 AISNVKADGTVRQHS
          :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)

initn: 39 init1: 39 opt: 59 Z-score: 87.0 bits: 21.8 E(): 7.2
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
in 53 aa overlap (4-52:3-55)


```

      10      20      30      40      50
AAD-12  GATLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFGAI
      : :..  .: . . . . : : : : : : : : : : : : : : : : : :
gi+AHw-886  FALIAVVATSTIAQMETSCLPGLERPWQQQLPFPQQTLFPQQQPFPPQQPPFSQQQPSF
      10      20      30      40      50

```

```

      60      70      80
AAD-12  ERIGGGDIVAISNVKADGTVRQHS

gi+AHw-886  SQQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPPQQQQQLPQQQISIVQPSV
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.3 E(): 7.5
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (11-43:238-270)

```

      10      20      30      40
AAD-12  GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . . : : : : : : : : : : : : :
gi+AHw-598  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
      : : .
gi+AHw-598  LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.3 E(): 7.5
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (11-43:238-270)

```

      10      20      30      40
AAD-12  GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
      : : . . : : : : : : : : : : : : .
gi+AHw-225  TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSYCN
      210      220      230      240      250      260

```

```

      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
      : : .
gi+AHw-225  LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.3 E(): 7.5
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (11-43:238-270)

```

                        10      20      30      40
AAD-12                GATLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                        :: . . : : : : : : : : .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
                210      220      230      240      250      260

```

```

                        50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
                : : .
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhibitor (217 aa)
 initn: 37 initl: 37 opt: 58 Z-score: 86.0 bits: 21.6 E(): 8.2
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (2-78:134-215)

```

                        10      20
AAD-12                GATLGATV--TGVHLATLDDAGFAALHAAWL
                        : : : . . : : . : : : .
gi+AHw-214 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
                110      120      130      140      150      160

```

```

                30      40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
                . : : : . : : : : : : : : : : : : :
gi+AHw-214 GYNLLYCPVTSTMSCPFSSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
                170      180      190      200      210

```

+AD4APg-gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName:
 Full+AD0-Serin (221 aa)
 initn: 37 initl: 37 opt: 58 Z-score: 85.8 bits: 21.6 E(): 8.4
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (2-78:138-219)

```

                        10      20
AAD-12                GATLGATV--TGVHLATLDDAGFAALHAAWL
                        : : : . . : : . : : : .
gi+AHw-201 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
                110      120      130      140      150      160

```

```

                30      40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHS
                . : : : . : : : : : : : : : : : : :
gi+AHw-201 GYNLLYCPVTSTMSCPFSSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFKQVQ
                170      180      190      200      210      220

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-

[illegible]

```

54 111 91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
56 69
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58 69
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60 64
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
62 51 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64 42 32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66 10 25:+AD0APQA9AD0- +ACo-
68 25 20:+AD0APQA9AD0APQA9ACoAPQA9-
70 27 16:+AD0APQA9AD0APQAqAD0APQA9-
72 7 12:+AD0APQA9ACo-
74 11 10:+AD0APQA9ACo-
76 4 7:+AD0APQAq-
78 2 6:+AD0AKg-
80 4 4:+AD0AKg-
82 2 3:+ACo-
84 3 3:+ACo-
86 3 2:+ACo-
88 4 2:+ACoAPQ- inset +AD0- represents 1 library

```

sequences

```

90 0 1:+ACo-
92 0 1:+ACo- :+ACo-
94 0 1:+ACo- :+ACo-
96 0 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 0 0: +ACo-
106 0 0: +ACo-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-

```

+AD4-120 0 0: +ACo-

331323 residues in 1471 sequences

Expectation+AF8-n fit: $\rho(\ln(x))+AD0-$ 5.43100.00331+ADs- $\mu+AD0-$ 4.9373
0.170

mean+AF8-var+AD0-42.130011.266, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43

Lambda+AD0- 0.197596

Kolmogorov-Smirnov statistic: 0.0453 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.3 5.1

gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229)
 59 22.0 6.5
 gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339)
 61 22.5 6.6
 gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339)
 61 22.5 6.6
 gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339)
 61 22.5 6.6
 gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhib (217)
 58 21.7 7.4
 gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName: Full+AD0-S
 (221) 58 21.7 7.6
 gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana (457)
 61 22.5 9.1
 gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen (480)
 61 22.5 9.6

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 89.7 bits: 22.3 E(): 5.1
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (35-66:133-160)

	10	20	30	40	50	60
AAD-12	ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV					
				:	:	:
gi+AHw-221	FGLIFPGCPSTYEEPAQQGRRHQSQRP	RRFQGGQDQSQQQQDSHQK----	VHRFDEGDLI			
	110	120	130	140	150	

	70	80
AAD-12	AINVKADGTVRQHSP	
	:	:
gi+AHw-221	AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR	
	160	170

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
 gluteni (229 aa)
 initn: 39 initl: 39 opt: 59 Z-score: 87.8 bits: 22.0 E(): 6.5
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (3-51:3-55)

	10	20	30	40	50
AAD-12	ATLGATVTGVHLATLDDAGFAALHAAWLQHAL---	LIFPGQHLSNDQQITFAKRFGAIE			
	:	:	:	:	:
gi+AHw-886	FALIAVVATSTIAQMETSCIPGLERPWWQQQLPPLPQQTLFPQQQPPFQQQPPFSQQQPSFS				
	10	20	30	40	50

	60	70	80
AAD-12	RIGGGDIVAISNVKADGTVRQHSP		
gi+AHw-886	QQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQPSVL		
	70	80	90

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (10-42:238-270)

```

                                10      20      30
AAD-12      ATL GATV TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
              210      220      230      240      250      260

              40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
              :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270      280      290      300      310      320
```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (10-42:238-270)

```

                                10      20      30
AAD-12      ATL GATV TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
              210      220      230      240      250      260

              40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
              :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270      280      290      300      310      320
```

+AD4-+AD4-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (10-42:238-270)

```

                                10      20      30
AAD-12      ATL GATV TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
              210      220      230      240      250      260

              40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
              :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270      280      290      300      310      320
```

+AD4APg-gi+AHw-21413+AHw-emb+AHw-CAA45723.1+AHw- aspartic proteinase inhibitor (217 aa)

initn: 37 initl: 37 opt: 58 Z-score: 86.7 bits: 21.7 E(): 7.4
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (1-77:134-215)

```

                                10      20
AAD-12                        ATL GATV--TGVHLATLDDAGFAALHAAWL
                                :.:. . :. . :. . :. . .
gi+AHw-214 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
              110      120      130      140      150      160

```

```

              30      40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
              . :. : . . :. :. : . . :. :. : . . :. :
gi+AHw-214 GYNLLYCPVTSTMSCPFSSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFQVQ
              170      180      190      200      210

```

+AD4APg-gi+AHw-20141714+AHw-sp+AHw-P30941.2+AHw-SPI7+AF8-SOLTU RecName:

Full+AD0-Serin (221 aa)

initn: 37 initl: 37 opt: 58 Z-score: 86.6 bits: 21.7 E(): 7.6
 Smith-Waterman score: 58+ADs- 21.429+ACU- identity (55.952+ACU- similar)
 in 84 aa overlap (1-77:138-219)

```

                                10      20
AAD-12                        ATL GATV--TGVHLATLDDAGFAALHAAWL
                                :.:. . :. . :. . :. . .
gi+AHw-201 FENELLNIQFAISTSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQF
              110      120      130      140      150      160

```

```

              30      40      50      60      70      80
AAD-12 QHALLIFP-----GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSP
              . :. : . . :. :. : . . :. :. : . . :. :
gi+AHw-201 GYNLLYCPVTSTMSCPFSSDDQ--FCLKVGVVHQNGKRRLALVKDNPLDVSFQVQ
              170      180      190      200      210      220

```

+AD4APg-gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana o 2 (457 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.1 bits: 22.5 E(): 9.1
 Smith-Waterman score: 61+ADs- 38.710+ACU- identity (58.065+ACU- similar)
 in 31 aa overlap (36-66:108-138)

```

              10      20      30      40      50      60
AAD-12 TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA
              : : . . : : :. . :. .
gi+AHw-259 YSNAPQLIYVVQGEGMTGISYPGCPETYQAPQQGRQQGQSGRFQDRHQKIRRFRRGDIIA
              80      90      100      110      120      130

```

```

              70      80
AAD-12 ISNVKADGTVRQHSP
              :
gi+AHw-259 IPAGVAHWCYNEGNSPVVTVTLLDVSNQNLDRTPRKFHLAGNPKDVFQQQQQHQSRRGR
              140      150      160      170      180      190

```

+AD4APg-gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen
 Der (480 aa)
 initn: 60 init1: 60 opt: 61 Z-score: 84.7 bits: 22.5 E(): 9.6
 Smith-Waterman score: 61+ADs- 32.692+ACU- identity (59.615+ACU- similar)
 in 52 aa overlap (13-60:83-134)

```

                                10      20      30      40
AAD-12      ATL GATV TGVHLATLDDAGFAALHAAWLQHALLIFPGQH--L
                                .: .: .: .: .: .: .: .: .: .:
gi+AHw-215  NPTGGH SKMESKPI LNHG YCHIHFWIGSESTKDEAGVAAIKSVELDDFLGGYPVQHREI
                   60      70      80      90     100     110

                   50      60      70      80
AAD-12  SNDQQITFAKRF--GAIERIGGGDIVAISNVKADGTVRQHSP
                   . . . . . : : : : :
gi+AHw-215  EEFE SRQFSSYFKNGI IY LKGGYESGFTKMI DELKPSLLHVKGKKRP I VYECAEISWKVM
                   120     130     140     150     160     170

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:36 2010 done: Fri Feb 5 12:55:36 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 14 - 93 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      1      0:+AD0-
      30      5      2:+ACoAPQ-
      32     16      8:+AD0APQAqAD0APQA9-
      34     29     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36     57     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
      38     74
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-

```


sequences

```

108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.37420.00333+ADs- mu+AD0- 5.2757
0.172
mean+AF8-var+AD0-42.213611.314, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.197400
Kolmogorov-Smirnov statistic: 0.0446 (N+AD0-29) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)   60 22.3      5.1
gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu ( 229)
59 22.0      6.5
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.5      6.7
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.5      6.7
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.5      6.7
gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana (
457)   61 22.5      9.2
gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen ( 480)
61 22.5      9.6

```

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 89.7 bits: 22.3 E(): 5.1
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (34-65:133-160)

```

```

          10          20          30          40          50          60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          : :: :...: . : :...: :...
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPPRRFQGQDQSQQQQDSHQK----VHRFDEGDLI
          110          120          130          140          150

          70          80
AAD-12 AISNVKADGTVRQHSPA
          :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
          160          170          180          190          200          210

```

```

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight
gluteni (229 aa)

```

initn: 39 init1: 39 opt: 59 Z-score: 87.7 bits: 22.0 E(): 6.5
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (2-50:3-55)

```

          10      20      30      40      50
AAD-12  TLGATVTGVHLATLDDAGFAALHAAWLQHAL----LIFPGQHLSNDQQITFAKRFGAIE
          : : : . . : . . . . : : : : : : : : : : : : : : : : : :
gi+AHw-886 FALIAVVATSTIAQMETSCLPGLERPWWQQPLPPQQTLFPQQQPPFPQQQPPFSQQQPSFS
          10      20      30      40      50      60

```

```

        60      70      80
AAD-12  RIGGGDIVAISNVKADGTVRQHSPA

```

```

gi+AHw-886 QQQPPFSQQQPILPEPPFSLQQQPVLPQQSPFSQQQLVLPPQQQQQLPQQQISIVQPSVL
          70      80      90      100      110      120

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (9-41:238-270)

```

          10      20      30
AAD-12  TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
          : : . . : : : : : : : : : : : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSYCN
          210      220      230      240      250      260

```

```

        40      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
          : : .
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
          270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (9-41:238-270)

```

          10      20      30
AAD-12  TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
          : : . . : : : : : : : : : : : : .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSYCN
          210      220      230      240      250      260

```

```

        40      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
          : : .
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
          270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 87.6 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (9-41:238-270)

```

                                10      20      30
AAD-12      TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: .  :: : :  :: : :  .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
                210      220      230      240      250      260

```

```

                40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
                ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen
 Ana o 2 (457 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.1 bits: 22.5 E(): 9.2
 Smith-Waterman score: 61+ADs- 38.710+ACU- identity (58.065+ACU- similar)
 in 31 aa overlap (35-65:108-138)

```

                10      20      30      40      50      60
AAD-12 TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA
                                : :  .. : .  : :  .... : : :
gi+AHw-259 YSNAPQLIYVVQGEGMTGISYPGCPETYQAPQQGRQQQSGRFQDRHQKIRRFRRGDIIA
                80      90      100      110      120      130

```

```

                70      80
AAD-12 ISNVKADGTVRQHSPA
                :
gi+AHw-259 IPAGVAHWCYNEGNSPVVTVTLLDVNSQNQLDRTPRKFHLAGNPKDVFQQQQHQSRGR
                140      150      160      170      180      190

```

+AD4APg-gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen
 Der (480 aa)

initn: 60 initl: 60 opt: 61 Z-score: 84.7 bits: 22.5 E(): 9.6
 Smith-Waterman score: 61+ADs- 32.692+ACU- identity (59.615+ACU- similar)
 in 52 aa overlap (12-59:83-134)

```

                                10      20      30
AAD-12      TLGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH--L
                                .: : : : : : : .  :  : : .
gi+AHw-215 NPTGGHSMESKPILNGHYCHIHFWIGSESTKDEAGVAAIKSVELDDFLGGYPVQHREI
                60      70      80      90      100      110

```

```

                40      50      60      70      80
AAD-12 SNDQQITFAKRF--GAIERIGGGDIVAISNVKADGTVRQHSPA
                . . .  : :  : :  : :
gi+AHw-215 EEFESRQFSSYFKNGIYLLKGGYESGFTKMIDELKPSLLHVKGKKRPVYECAEISWKVM
                120      130      140      150      160      170

```

[illegible]

```

52      56      106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
54      114
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
56      67      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
58      59
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60      78
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ
-
62      55      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
64      36      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
66      12      25:+AD0APQA9AD0- +ACo-
68      27      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      25      16:+AD0APQA9AD0APQAqAD0APQA9-
72      8       12:+AD0APQA9ACo-
74      11      10:+AD0APQA9ACo-
76      6       7:+AD0APQAq-
78      2       6:+AD0AKg-
80      4       4:+AD0AKg-
82      2       3:+ACo-
84      3       3:+ACo-
86      1       2:+ACo-
88      4       2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.36070.00333+ADs- mu+AD0- 5.3609
0.171
mean+AF8-var+AD0-42.341011.353, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.197103
Kolmogorov-Smirnov statistic: 0.0453 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090

```

The best scores are:

opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.3 5.2
 gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight glu (229) 59 22.0 6.6
 gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.5 6.7
 gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.5 6.7
 gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.5 6.7
 gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana (457) 61 22.5 9.2
 gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen (480) 61 22.5 9.7

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 89.6 bits: 22.3 E(): 5.2
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (33-64:133-160)

	10	20	30	40	50	60
AAD-12	ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV					
				:	:	:
gi+AHw-221	FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGGQDQSQQQQDSHQK----	VHRFDEGDLI				
	110	120	130	140	150	

	70	80
AAD-12	AINVKADGTVRQHSPA	
	:	:
gi+AHw-221	AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR	
	160	170

+AD4APg-gi+AHw-886963+AHw-emb+AHw-CAA59338.1+AHw- low molecular weight gluteni (229 aa)

initn: 39 initl: 39 opt: 59 Z-score: 87.7 bits: 22.0 E(): 6.6
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (56.604+ACU- similar)
 in 53 aa overlap (1-49:3-55)

	10	20	30	40	50
AAD-12	LGATVTGVHLATLDDAGFAALHAAWLQHAL---	LIFPGQHLSNDQQITFAKRFGAIE			
	:	:	:	:	:
gi+AHw-886	FALIAVVATSTIAQMETSCIPGLERPWQQPLPPQQTLPFPQQQPFPPQQPPFSQQQPSFS				
	10	20	30	40	50

	60	70	80
AAD-12	RIGGGDIVAINVKADGTVRQHSPA		
gi+AHw-886	QQQPPFSQQQPILPEPPFSLQQQPVLPQQSPFSQQQLVLPQQQQQLPQQQISIVQPSVL		
	70	80	90

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 87.5 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (8-40:238-270)

```

                                10      20      30
AAD-12                      LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
              210      220      230      240      250      260

              40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAE
              ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 87.5 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (8-40:238-270)

```

                                10      20      30
AAD-12                      LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
              210      220      230      240      250      260

              40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAE
              ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 87.5 bits: 22.5 E(): 6.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (8-40:238-270)

```

                                10      20      30
AAD-12                      LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
              210      220      230      240      250      260

              40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAE
              ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270      280      290      300      310      320

```

+AD4APg-gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen
 Ana o 2 (457 aa)

initn: 61 initl: 61 opt: 61 Z-score: 85.0 bits: 22.5 E(): 9.2
 Smith-Waterman score: 61+ADs- 38.710+ACU- identity (58.065+ACU- similar)
 in 31 aa overlap (34-64:108-138)

```

      10      20      30      40      50      60
AAD-12 TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA
      : : .. : : : : : :
gi+AHw-259 YSNAPQLIYVVQGEGMTGISYPGCPETYQAPQQGRQQGQSGRFGQDRHQKIRRFRRGGDIIA
      80      90      100      110      120      130

```

```

      70      80
AAD-12 ISNVKADGTVRQHSPA
      :
gi+AHw-259 IPAGVAHWCYNEGNSPVVTVTLLDVSNQNLDRTPRKFHLAGNPKDVFQQQQHQSRGR
      140      150      160      170      180      190

```

+AD4APg-gi+AHw-21591547+AHw-gb+AHw-AAM64112.1+AHw- gelsolin-like allergen
 Der (480 aa)

initn: 60 initl: 60 opt: 61 Z-score: 84.6 bits: 22.5 E(): 9.7
 Smith-Waterman score: 61+ADs- 32.692+ACU- identity (59.615+ACU- similar)
 in 52 aa overlap (11-58:83-134)

```

      10      20      30
AAD-12 LGATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH--L
      . : : : : : : : : : : :
gi+AHw-215 NPTGGHSMESKPIILNGHYCHIFWIGSESTKDEAGVAAIKSVELDDFLGGYPVQHREI
      60      70      80      90      100      110

```

```

      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA
      . . : : : : : :
gi+AHw-215 EEFESRQFSSYFKNGIYYLKGGYESGFTKMIDELKPSLLHVKGKKRPVYECAEISWKVM
      120      130      140      150      160      170

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 16 - 95 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      2      0:+AD0-
      30      6      2:+ACoAPQ-
      32     18      8:+AD0APQAqAD0APQA9-
      34     30     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36     54     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
      38     79
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
      40     89
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9- +ACo-
      42     142
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
      44     166
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA
9AD0APQ-
      46     104
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      48     121
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      50     77
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q- +ACo-
      52     73
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      54     106
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9-
      56     60     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      58     71
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
      60     73
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
      62     56     40:+AD0APQ-+AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
      64     29     32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
      66     15     25:+AD0APQA9AD0APQ- +ACo-
      68     23     20:+AD0APQA9AD0APQA9ACoAPQ-
      70     26     16:+AD0APQA9AD0APQAqAD0APQA9-
      72     14     12:+AD0APQA9ACoAPQ-
      74     11     10:+AD0APQA9ACo-

```

```

76      9      7:+AD0APQAq-
78      2      6:+AD0AKg-
80      3      4:+AD0AKg-
82      2      3:+ACo-
84      2      3:+ACo-
86      3      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120 0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.34590.00343+ADs- mu+AD0- 5.5817
0.176
mean+AF8-var+AD0-43.259511.506, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.195000
Kolmogorov-Smirnov statistic: 0.0555 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 22.1 5.6
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.4 7.3
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.4 7.3
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.4 7.3
gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen Ana (
457) 61 22.4 9.9

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.9 bits: 22.1 E(): 5.6
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (32-63:133-160)

10      20      30      40      50      60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIERIGGGDIV

```

gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK---VHRFDEGDLI
110 120 130 140 150

70 80
AAD-12 AISNVKADGTVRQHSPAEW

gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
160 170 180 190 200 210

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.9 bits: 22.4 E(): 7.3
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (7-39:238-270)

10 20 30
AAD-12 GATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . : : : : : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

40 50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEW
:::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.9 bits: 22.4 E(): 7.3
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (7-39:238-270)

10 20 30
AAD-12 GATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . : : : : : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

40 50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEW
:::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.9 bits: 22.4 E(): 7.3
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (7-39:238-270)

10 20 30
AAD-12 GATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH

```

:: . .: : : :... : ...
gi+AHw-225 TELHVVPDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
          210          220          230          240          250          260

```

```

          40          50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEW
:::

```

```

gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
          270          280          290          300          310          320

```

+AD4APg-gi+AHw-25991543+AHw-gb+AHw-AAN76862.1+AHw-AF453947+AF8-1 allergen
 Ana o 2 (457 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 84.5 bits: 22.4 E(): 9.9
 Smith-Waterman score: 61+ADs- 38.710+ACU- identity (58.065+ACU- similar)
 in 31 aa overlap (33-63:108-138)

```

          10          20          30          40          50          60
AAD-12 TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVA
:: .. : : :... :...
gi+AHw-259 YSNAPQLIYVVQGEGMTGISYPGCPETYQAPQQGRQQGQSGRFQDRHQKIRRFRRGDIIA
          80          90          100          110          120          130

```

```

          70          80
AAD-12 ISNVKADGTVRQHSPAEW
:
gi+AHw-259 IPAGVAHWCYNEGNSPVVTVTLDDVSNSQNQLDRTPRKFHLAGNPKDVFQQQQQHQSRRGR
          140          150          160          170          180          190

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 17 - 96 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:

```

one +AD0- represents 3 library sequences

```

24      0      0:
26      1      0:+AD0-
28      1      0:+AD0-
30      7      2:+ACoAPQA9-
32     19      8:+AD0APQAqAD0APQA9AD0-
34     30     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
36     59     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
38     78
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
-
 40     94
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ- +ACo-
 42    130
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
 44    173
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA
9AD0APQA9AD0-
 46    113
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
 48    104
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
 50     80
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9- +ACo-
 52     81
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9- +ACo-
 54    100     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
 56     56     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
 58     81
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9-
 60     60     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
 62     65
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
 64     25     32:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
 66     16     25:+AD0APQA9AD0APQA9- +ACo-
 68     25     20:+AD0APQA9AD0APQA9ACoAPQA9-
 70     23     16:+AD0APQA9AD0APQAqAD0APQ-
 72     20     12:+AD0APQA9ACoAPQA9AD0-
 74      5     10:+AD0APQ- +ACo-
 76     10      7:+AD0APQAqAD0-
 78      2      6:+AD0AKg-
 80      3      4:+AD0AKg-
 82      2      3:+ACo-
 84      2      3:+ACo-
 86      3      2:+ACo-

```

```

88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.38670.00341+ADs- mu+AD0- 5.4933
0.176
mean+AF8-var+AD0-43.426911.513, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.194623
Kolmogorov-Smirnov statistic: 0.0582 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.8

gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.3 7.5

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.3 7.5

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge (339) 61 22.3 7.5

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 88.7 bits: 22.1 E(): 5.8

Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar) in 32 aa overlap (31-62:133-160)

```

          10          20          30          40          50          60
AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          : :: :...: . : ...: :...
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI
          110          120          130          140          150

          70          80
AAD-12 AISNVKADGTVRQHSPAEDW
          :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR

```

160 170 180 190 200 210

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (6-38:238-270)

AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . .: : : :... :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
210 220 230 240 250 260

AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDW
:::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (6-38:238-270)

AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . .: : : :... :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
210 220 230 240 250 260

AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDW
:::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (6-38:238-270)

AAD-12 ATVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . .: : : :... :
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
210 220 230 240 250 260

AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDW
:::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI

270 280 290 300 310 320

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 18 - 97 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	1	0:+AD0-	
28	1	0:+AD0-	
30	6	2:+ACoAPQ-	
32	21	8:+AD0APQAqAD0APQA9AD0-	
34	23	21:+AD0APQA9AD0APQA9ACoAPQ-	
36	57	44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-	
38	85		
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ			
A9AD0APQ-			
40	86		
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQ- +ACo-			
42	135		
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-			
44	171		
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA			
9AD0APQA9-			
46	113		
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-			
48	106		
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-			

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

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The best scores are: opt bits E(1471)

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gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a (339) 61 22.4 7.4

gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a (339) 61 22.4 7.4

gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k l pollen allerge (339) 61 22.4 7.4

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 88.8 bits: 22.1 E(): 5.7
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (30-61:133-160)

```

                10      20      30      40      50
AAD-12  TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                : :  : : : :  :  :  :  :  :
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRPFRFQGGDQSQQQQDSHQK----VHRFDEGDLI
                110      120      130      140      150

```

```

        60      70      80
AAD-12  AISNVKADGTVRQHSPAEWDD
        :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
        160      170      180      190      200      210

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.4
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (5-37:238-270)

```

                10      20      30
AAD-12  TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                : :  .  : : :  : : :  :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
                210      220      230      240      250      260

```

```

        40      50      60      70      80
AAD-12  LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDD
        :..
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.4
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (5-37:238-270)

```

                                10      20      30
AAD-12      TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... :... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
              210      220      230      240      250      260

```

```

              40      50      60      70      80
AAD-12      LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDD
              ::.
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFGGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270      280      290      300      310      320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.4
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (5-37:238-270)

```

                                10      20      30
AAD-12      TVTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... :... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
              210      220      230      240      250      260

```

```

              40      50      60      70      80
AAD-12      LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDD
              ::.
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFGGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270      280      290      300      310      320

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
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Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 19 - 98 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()

```

+ADw- 20      2      0:+AD0-
22      0      0:          one +AD0- represents 3 library sequences
24      0      0:
26      1      0:+AD0-
28      1      0:+AD0-
30      5      2:+ACoAPQ-
32     18      8:+AD0APQAqAD0APQA9-
34     28     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
36     58     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
38     82
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0-
40     93
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
42    137    123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9A
D0APQA9-
44    161
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA
9-
46    106
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
48    111
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
50     86    121:+AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
52     82
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0- +ACo-
54    100
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0-
56     70
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
58     69
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60     57     50:+AD0APQA9AD0APQA9AD0-+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
62     60     40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64     25     32:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
66     20     25:+AD0APQA9AD0APQA9AD0- +ACo-
68     27     20:+AD0APQA9AD0APQA9ACoAPQA9-
70     21     16:+AD0APQA9AD0APQAqAD0-
72     18     12:+AD0APQA9ACoAPQA9-
74     11     10:+AD0APQA9ACo-
76     9       7:+AD0APQAq-
78     0       6: +ACo-
80     4       4:+AD0AKg-
82     2       3:+ACo-

```

```

84      2      3:+ACo-
86      4      2:+ACoAPQ-
88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.32380.00343+ADs- mu+AD0- 5.7987
0.177
mean+AF8-var+AD0-43.431211.6666, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.194614
Kolmogorov-Smirnov statistic: 0.0528 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
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219) 60 22.1 5.8
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.4 7.5
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.4 7.5
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.4 7.5
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 54 20.4 8

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.7 bits: 22.1 E(): 5.8
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (29-60:133-160)

10      20      30      40      50
AAD-12 VTGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      : :: :...: . : .... :...
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK---VHRFDEGDLI
      110      120      130      140      150

```

60 70 80
AAD-12 AISNVKADGTVRQHSPAEWDDM
::

gi+AHw-221 AVPTGVAFWMYNDHDTDVAVSLTDTNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
160 170 180 190 200 210

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (4-36:238-270)

10 20 30
AAD-12 VTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . : : : : : : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

40 50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDM
:::

gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (4-36:238-270)

10 20 30
AAD-12 VTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . : : : : : : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

40 50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDM
:::

gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.7 bits: 22.4 E(): 7.5
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (4-36:238-270)

10 20 30
AAD-12 VTGVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . : : : : : : : :
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

```

      40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDM
      ...
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTKQLTEADAKTFTSLEYI
      270      280      290      300      310      320

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 54 initl: 54 opt: 54 Z-score: 86.2 bits: 20.4 E(): 8
Smith-Waterman score: 54+ADs- 43.750+ACU- identity (68.750+ACU- similar)
in 16 aa overlap (65-80:30-45)

```

      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDM
      .. .:..: :.. :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAPK
      10      20      30      40      50
gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 20 - 99 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	1	0:+AD0-	
28	2	0:+AD0-	
30	3	2:+ACo-	
32	19	8:+AD0APQAqAD0APQA9AD0-	
34	25	21:+AD0APQA9AD0APQA9ACoAPQA9-	
36	56	44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-	


```

38      87
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQ-
   40    93
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
   42    132
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   44    163
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
   46    108
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
   48    113
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
   50     98
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9- +ACo-
   52     82
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0- +ACo-
   54     89
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACo-
   56     68
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
   58     69
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
   60     56    50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
   62     61
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
   64     24    32:+AD0APQA9AD0APQA9AD0APQ- +ACo-
   66     19    25:+AD0APQA9AD0APQA9AD0- +ACo-
   68     30    20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
   70     18    16:+AD0APQA9AD0APQAq-
   72     19    12:+AD0APQA9ACoAPQA9AD0-
   74     11    10:+AD0APQA9ACo-
   76      9     7:+AD0APQAq-
   78      0     6: +ACo-
   80      5     4:+AD0AKg-
   82      1     3:+ACo-
   84      2     3:+ACo-
   86      5     2:+ACoAPQ-
   88      1     2:+ACo- inset +AD0- represents 1 library sequences
   90      0     1:+ACo-
   92      0     1:+ACo- :+ACo-
   94      0     1:+ACo- :+ACo-
   96      0     1:+ACo- :+ACo-
   98      0      0: +ACo-
  100      0      0: +ACo-

```

```

102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.27690.00346+ADs- mu+AD0- 6.0403
0.178
mean+AF8-var+AD0-43.854411.795, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193672
Kolmogorov-Smirnov statistic: 0.0507 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)   60 22.1      5.9
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.6
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.6
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3      7.6
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)   56 21.0      7.7
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)   54 20.4      8.2

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 init1: 43 opt: 60 Z-score: 88.5 bits: 22.1 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (28-59:133-160)

          10          20          30          40          50
AAD-12      TGVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
              : :: :...: . : :... :...
gi+AHw-221  FGLIFPGCPSTYEPAQQGRRHQSRPFRRFQGDQSQQQQDSHQK----VHRFDEGDLI
          110          120          130          140          150

          60          70          80
AAD-12  AISNVKADGTVRQHSPA EWDDMM
      :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (3-35:238-270)

```

                                10      20      30
AAD-12                        TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
                210      220      230      240      250      260
```

```

                        40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320
```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (3-35:238-270)

```

                                10      20      30
AAD-12                        TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
                210      220      230      240      250      260
```

```

                        40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM
                :::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320
```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (3-35:238-270)

```

                                10      20      30
AAD-12                        TGVHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ... .
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSSYCN
                210      220      230      240      250      260
```

```

                        40      50      60      70      80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMM
                :::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
                270      280      290      300      310      320
```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 56 Z-score: 86.4 bits: 21.0 E(): 7.7
 Smith-Waterman score: 56+ADs- 26.866+ACU- identity (49.254+ACU- similar)
 in 67 aa overlap (19-80:33-99)

```

                        10      20      30      40
AAD-12      TGVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                        : .:. .: : : : . :. :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                10      20      30      40      50      60

                50      60      70      80
AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPAEDDMM
                . : .: .: .: .: .: .: .: .: .: .:
gi+AHw-273 KMLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
                70      80      90      100     110     120

gi+AHw-273 GATTLQHRRRR
                130

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 54 initl: 54 opt: 54 Z-score: 86.0 bits: 20.4 E(): 8.2
 Smith-Waterman score: 54+ADs- 43.750+ACU- identity (68.750+ACU- similar)
 in 16 aa overlap (64-79:30-45)

```

                40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMM
                        .. :... :.. :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAP
                10      20      30      40      50

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:37 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

72      19      12:+AD0APQA9ACoAPQA9AD0-
74      7      10:+AD0APQA9ACo-
76      7      7:+AD0APQAq-
78      0      6: +ACo-
80      8      4:+AD0AKgA9-
82      2      3:+ACo-
84      1      3:+ACo-
86      5      2:+ACoAPQ-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.33880.0036+ADs- mu+AD0- 5.7902
0.186
mean+AF8-var+AD0-43.734911.708, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193937
Kolmogorov-Smirnov statistic: 0.0480 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  59 21.8      3.1
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.0      5.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  55 20.7      6.7
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.7
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.7
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3      7.7
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)  56 21.0      7.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

```

initn: 59 initl: 59 opt: 59 Z-score: 93.5 bits: 21.8 E(): 3.1
 Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
 in 18 aa overlap (63-80:30-47)

```

          40          50          60          70          80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMK
              ..  ....  ...  :
gi+AHw-126  TKVDLTVEKGS DAKTLVLN IKYTRPGDTLAEVELRQH GSEEWEPMTKKGNLWEVKSAKP
              10          20          30          40          50

gi+AHw-126  LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
              60          70          80          90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.5 bits: 22.0 E(): 5.9
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (27-58:133-160)

```

          10          20          30          40          50
AAD-12  GVHLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
              :  :  ....  .  :  ....  ....
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSQRP RRFGQDQSQQQQDSHQK----VHRFDEGDLI
              110          120          130          140          150

          60          70          80
AAD-12  AISNVKADGTVRQHSPA EWDDMMK
              ..
gi+AHw-221  AVPTGVAFWMYNDHDTDVVA VSLTDTNNNDNQLDQFP RRFLAGNHEQEFLRYQQQSRRR
              160          170          180          190          200          210

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 55 Z-score: 87.6 bits: 20.7 E(): 6.7
 Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
 in 18 aa overlap (63-80:30-47)

```

          40          50          60          70          80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMK
              ..  ....  ...  :
gi+AHw-144  VKVTFKVEKGS DPKKLVL DIKYTRPGDTLAEVELRQH GSEEWEP LTKKGNLWEVKSSKP
              10          20          30          40          50

gi+AHw-144  LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGT TYTPEE
              60          70          80          90

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
 aller (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.5 bits: 22.3 E(): 7.7
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (2-34:238-270)

```

          10          20          30
AAD-12  GVHLATLDDAGFAALHAAWLQHALLIFPGQH

```

gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

40 50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK
:::

gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.5 bits: 22.3 E(): 7.7
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (2-34:238-270)

10 20 30
AAD-12 GVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . .: : : :
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

40 50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK
:::
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
allergen +AFs-S (339 aa)

initn: 61 initl: 61 opt: 61 Z-score: 86.5 bits: 22.3 E(): 7.7
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (2-34:238-270)

10 20 30
AAD-12 GVHLATLDDAGFAALHAAWLQHALLIFPGQH
:: . .: : : :
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
210 220 230 240 250 260

40 50 60 70 80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMK
:::
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFGHEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
270 280 290 300 310 320

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)

initn: 36 initl: 36 opt: 56 Z-score: 86.4 bits: 21.0 E(): 7.8
Smith-Waterman score: 56+ADs- 26.866+ACU- identity (49.254+ACU- similar)
in 67 aa overlap (18-79:33-99)

10 20 30 40
AAD-12 GVHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA


```

gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLKVGCG
      10      20      30      40      50      60
      50      60      70      80
AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPAEWDDMMK
      . :  :.  .:  .::  :.  :.  .  :.
gi+AHw-273 KMLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
      70      80      90      100      110      120
gi+AHw-273 GATTTLQHRRRR
      130

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:37 2010 done: Fri Feb 5 12:55:38 2010
Total Scan time: 0.090 Total Display time: 0.010

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-l2: 22 - 101 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

    42      124  

123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-  

   44     161  

136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-  

   46     106  

138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   48     113                                     +ACo-  

132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   50     100                                       +ACo-  

121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   52       85                                         +ACo-  

106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   54       86                                           +ACo-  

91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   56       62                                           +ACo-  

76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   58       68                                               +ACo-  

62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-  

   60       54        50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-  

   62       67  

40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   64       29         32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   66       17         25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   68       30         20:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   70       19         16:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   72       16         12:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   74       10         10:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   76        4          7:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  

   78        0          6: +ACo-  

   80        8          4:+AD0AKgA9-  

   82        1          3: +ACo-  

   84        2          3: +ACo-  

   86        5          2: +ACoAPQ-  

   88        1          2: +ACo-                inset +AD0- represents 1 library sequences  

   90        0          1: +ACo-  

   92        1          1: +ACo-                :+ACo-  

   94        0          1: +ACo-                :+ACo-  

   96        0          1: +ACo-                :+ACo-  

   98        0          0:                    +ACo-  

  100        0          0:                    +ACo-  

  102        0          0:                    +ACo-  

  104        0          0:                    +ACo-  

  106        0          0:                    +ACo-  

  108        0          0:                    +ACo-  

  110        0          0:                    +ACo-  

  112        0          0:                    +ACo-
```

```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.27310.00363+ADs- mu+AD0- 6.0666
0.187
mean+AF8-var+AD0-43.804311.712, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193783
Kolmogorov-Smirnov statistic: 0.0534 (N+AD0-28) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)   59 21.8      3.1
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)   60 22.1      5.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)   55 20.7      6.7
gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.6
gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase a ( 339)
61 22.3      7.6
gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen allerge ( 339)
61 22.3      7.6
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)   56 21.0      7.7

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 59 Z-score: 93.5 bits: 21.8 E(): 3.1
Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (62-79:30-47)

```

```

          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKV
          :.  .:.  .:.  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAP
          10          20          30          40          50

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

```

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.6 bits: 22.1 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (26-57:133-160)

```

```

          10          20          30          40          50
AAD-12      VHLATLDDAGFAALHAAWLQHALLIFPGQHLSDNDQQITFAKRFGAIERIGGGDIV

```

```

                                : :: :...: . : :... :...
gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSRPPRRFQGQDQSQQQQDSHQK---VHRFDEGDLI
              110          120          130          140          150

```

```

              60          70          80
AAD-12 AISNVKADGTVRQHSPA EWDDMMKV
      :.

```

```

gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
              160          170          180          190          200          210

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 55 Z-score: 87.6 bits: 20.7 E(): 6.7
Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (62-79:30-47)

```

              40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV
                                :. :... :... :
gi+AHw-144 VKVTFKVEKGS DPKKLVL DIKYTRPGDTLAEVELRQHGSEWEPLTKKGNLWEVKSSKP
              10          20          30          40          50

```

```

gi+AHw-144 LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
              60          70          80          90

```

+AD4APg-gi+AHw-59895730+AHw-gb+AHw-AAX11262.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (1-33:238-270)

```

                                10          20          30
AAD-12                                VHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . : : : :... :... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
              210          220          230          240          250          260

```

```

              40          50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV
      :..
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFGGEYKNTGPGAAADKRVPTYTKQLTEADAKTFTSLEYI
              270          280          290          300          310          320

```

+AD4APg-gi+AHw-59895728+AHw-gb+AHw-AAX11261.1+AHw- pectin methylesterase
aller (339 aa)
initn: 61 init1: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
in 33 aa overlap (1-33:238-270)

```

                                10          20          30
AAD-12                                VHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . : : : :... :... .
gi+AHw-598 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEARVVFSYCN
              210          220          230          240          250          260

```

```

                40          50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV
      ...
gi+AHw-598 LSDAVKPEGWSDNNKPAAQKTIFFG EYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270          280          290          300          310          320

```

+AD4APg-gi+AHw-225810597+AHw-gb+AHw-ACO34813.1+AHw- Sal k 1 pollen
 allergen +AFs-S (339 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 86.6 bits: 22.3 E(): 7.6
 Smith-Waterman score: 61+ADs- 33.333+ACU- identity (57.576+ACU- similar)
 in 33 aa overlap (1-33:238-270)

```

                                10          20          30
AAD-12                                VHLATLDDAGFAALHAAWLQHALLIFPGQH
                                :: . .: : : :... : ...
gi+AHw-225 TELHVVPGDPMAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFEEAARVVFSSYCN
                210          220          230          240          250          260

```

```

                40          50          60          70          80
AAD-12 LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKV
      ...
gi+AHw-225 LSDAVKPEGWSDNNKPAAQKTIFFG EYKNTGPGAAADKRVPYTKQLTEADAKTFTSLEYI
                270          280          290          300          310          320

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 56 Z-score: 86.4 bits: 21.0 E(): 7.7
 Smith-Waterman score: 56+ADs- 26.866+ACU- identity (49.254+ACU- similar)
 in 67 aa overlap (17-78:33-99)

```

                                10          20          30          40
AAD-12                                VHLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                : .:: . : : : . :: : . :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                10          20          30          40          50          60

```

```

                50          60          70          80
AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKV
      . : .: .: .:: :. :. . .:
gi+AHw-273 KMLLKGVIGEEKVVELLRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
                70          80          90          100          110          120

```

```

gi+AHw-273 GATTLQHRRRR
                130

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 23 - 102 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0: +AD0-
      30      5      2: +ACoAPQ-
      32     20      8: +AD0APQAqAD0APQA9AD0-
      34     25     21: +AD0APQA9AD0APQA9ACoAPQA9-
      36     59     44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
      38     86
72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQ-
      40     107
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9-
      42     125
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
      44     169    136: +AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ-
      46     103
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      48     109
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      50      93
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
      52      89    106: +AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0- +ACo-
      54      77
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
- +ACo-
      56      61
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-

```

```

58      67
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
   60    63
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
   62    67
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
   64    27    32:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
   66    19    25:+AD0APQA9AD0APQA9AD0- +ACo-
   68    29    20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
   70    20    16:+AD0APQA9AD0APQAqAD0-
   72    16    12:+AD0APQA9ACoAPQA9-
   74     9    10:+AD0APQA9ACo-
   76     5     7:+AD0APQAq-
   78     4     6:+AD0AKg-
   80     7     4:+AD0AKgA9-
   82     1     3:+ACo-
   84     2     3:+ACo-
   86     1     2:+ACo-
   88     2     2:+ACo-          inset +AD0- represents 1 library sequences
   90     0     1:+ACo-
   92     1     1:+ACo-          :+ACo-
   94     0     1:+ACo-          :+ACo-
   96     0     1:+ACo-          :+ACo-
   98     0     0:              +ACo-
  100     0     0:              +ACo-
  102     0     0:              +ACo-
  104     0     0:              +ACo-
  106     0     0:              +ACo-
  108     0     0:              +ACo-
  110     0     0:              +ACo-
  112     0     0:              +ACo-
  114     0     0:              +ACo-
  116     0     0:              +ACo-
  118     0     0:              +ACo-
+AD4-120      0      0:              +ACo-
  331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.21120.00364+ADs- mu+AD0- 6.4473
0.188
mean+AF8-var+AD0-43.771711.792, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193855
Kolmogorov-Smirnov statistic: 0.0616 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)   59 21.8           3.2
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)   60 22.1           5.9
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)   57 21.2           6.5
```

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 55 20.7 6.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 59 Z-score: 93.4 bits: 21.8 E(): 3.2
Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (61-78:30-47)

```

                40          50          60          70          80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVI
                ..  ....  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAPK
                10          20          30          40          50

```

```

gi+AHw-126  LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60          70          80          90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.5 bits: 22.1 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (25-56:133-160)

```

                10          20          30          40          50
AAD-12          HLATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                :  ::  ....  .  :  ....  ....
gi+AHw-221  FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGGQDQSQQQQDSHQK----VHRFDEGDLI
                110          120          130          140          150

```

```

                60          70          80
AAD-12  AISNVKADGTVRQHSPAEDDDMMKVI
                :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                160          170          180          190          200          210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)
initn: 36 initl: 36 opt: 57 Z-score: 87.8 bits: 21.2 E(): 6.5
Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
in 70 aa overlap (16-80:33-102)

```

                10          20          30          40
AAD-12          HLATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                :  ::  ..  :  :  :  :  :  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQAATEKLKVG
                10          20          30          40          50          60

```

```

                50          60          70          80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPAEDDDMMKVI
                .  :  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-273  KMLLKGVIGEEKVVELRNMKEAGADIQELQKQVEKMLSEVTDEKQKEKVHEYGPACCKIF
                70          80          90          100          110          120

```


gi+AHw-273 GATTLQHRRRR
130

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 55 Z-score: 87.4 bits: 20.7 E(): 6.8
Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (61-78:30-47)

	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVI				
			
gi+AHw-144	VKVTFKVEKGS DPKKLVL DIKYTRPGDTLAEVELRQH GSEWEPLTKKGNLWEVKSSKP				
	10	20	30	40	50

gi+AHw-144	LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE				
	60	70	80	90	

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 24 - 103 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	1	0:+AD0-	
30	5	2:+ACoAPQ-	
32	20	8:+AD0APQAqAD0APQA9AD0-	
34	27	21:+AD0APQA9AD0-+AD0APQAqAD0APQ-	
36	62		

44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-

```

38      79
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
   40    110
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0-
   42    125
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
   44    170
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9A
D0-
   46    107
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9-          +ACo-
   48    101
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0-          +ACo-
   50     95
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ-          +ACo-
   52     94
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQ-          +ACo-
   54     71
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
   56     61
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-          +ACo-
   58     68
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
   60     59    50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   62     66
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
   64     29    32:+AD0APQA9AD0APQ-+AD0APQA9AD0APQAq-
   66     18    25:+AD0APQA9AD0APQA9-  +ACo-
   68     35    20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
   70     17    16:+AD0APQA9AD0APQAq-
   72     25    12:+AD0APQA9ACoAPQA9AD0APQA9-
   74      5    10:+AD0APQ- +ACo-
   76      4     7:+AD0APQAq-
   78      2     6:+AD0AKg-
   80      6     4:+AD0AKg-
   82      2     3:+ACo-
   84      1     3:+ACo-
   86      1     2:+ACo-
   88      2     2:+ACo-          inset +AD0- represents 1 library sequences
   90      0     1:+ACo-
   92      1     1:+ACo-          :+ACo-
   94      0     1:+ACo-          :+ACo-
   96      0     1:+ACo-          :+ACo-
   98      0     0:          +ACo-

```

```

100      0      0:      +ACo-
102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.29960.00371+ADs- mu+AD0- 6.0233
0.191
mean+AF8-var+AD0-44.174211.942, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.192970
Kolmogorov-Smirnov statistic: 0.0630 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)   59 21.8      3.2
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)   60 22.0      6.1
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)   57 21.2      6.6
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)   55 20.6      6.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 59 Z-score: 93.2 bits: 21.8 E(): 3.2
Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (60-77:30-47)

      30      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIV
      .. ..::: ..: :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAP
      10      20      30      40      50

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.2 bits: 22.0 E(): 6.1
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (24-55:133-160)

      10      20      30      40      50

```

```
AAD-12          LATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                  :  ::  :::::  .  :  ::::  ::::
gi+AHw-221 FGLIFPGCPSTYEPAQQGRRHQSRPFRFQGDQSQQQQDSHQK---VHRFDEGDLI
                  110      120      130      140      150
```

```

                  60      70      80
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIV
                  :.
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRFNLAGNHEQEFLRYQQQSRRR
                  160      170      180      190      200      210
```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)
initn: 36 initl: 36 opt: 57 Z-score: 87.6 bits: 21.2 E(): 6.6
Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
in 70 aa overlap (15-79:33-102)

```

                  10      20      30      40
AAD-12          LATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                  :  ::  .  :  :  :  :  :  :  :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                  10      20      30      40      50      60
```

```

                  50      60      70      80
AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKVIV
                  .  :  ::  .  ::  ::  ::  ::  ::  .  .  .  .
gi+AHw-273 KMLLKGVIGEEKVVELLRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
                  70      80      90      100      110      120
```

```
gi+AHw-273 GATTLQHRRRR
                  130
```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 55 Z-score: 87.3 bits: 20.6 E(): 6.9
Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (60-77:30-47)

```

                  30      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIV
                  :.  ::::  ::  .  :
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWELTKKGNLWEVKSSKP
                  10      20      30      40      50
```

```
gi+AHw-144 LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPPEE
                  60      70      80      90
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010

Total Scan time: 0.090 Total Display time: 0.000

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

54      76
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
-      +ACo-
56      60      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      79
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9-
60      59      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
62      68
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
64      28      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
66      18      25:+AD0APQA9AD0APQA9-      +ACo-
68      34      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      17      16:+AD0APQA9AD0APQA9-
72      24      12:+AD0APQA9ACoAPQA9AD0APQ-
74      5      10:+AD0APQ-      +ACo-
76      4      7:+AD0APQA9-
78      1      6:+AD0AKg-
80      7      4:+AD0AKgA9-
82      2      3:+ACo-
84      1      3:+ACo-
86      1      2:+ACo-
88      2      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      1      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120     0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.43470.00374+ADs- mu+AD0- 5.2968
0.193
mean+AF8-var+AD0-43.796911.810, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193799
Kolmogorov-Smirnov statistic: 0.0568 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 59 21.8 3.1

```

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.0 6
 gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 21.2 6.4
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-(96) 55 20.7 6.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 59 Z-score: 93.6 bits: 21.8 E(): 3.1
 Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
 in 18 aa overlap (59-76:30-47)

	30	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVG					
			 :
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAKP					
	10	20	30	40	50	

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.4 bits: 22.0 E(): 6
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (23-54:133-160)

	10	20	30	40	50
AAD-12	ATLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV				
			: ::	: ...
gi+AHw-221	FGLIFPGCPSTYEPAQQGRRHQSQRP RRFGQDQSQQQQDSHQK---VHRFDEGDLI				
	110	120	130	140	150
	60	70	80		
AAD-12	AISNVKADGTVRQHSPA EWDDMMKVIVG				
	..				
gi+AHw-221	AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR				
	160	170	180	190	200 210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 87.9 bits: 21.2 E(): 6.4
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (14-78:33-102)

	10	20	30	40
AAD-12	ATLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA			
		: ::	.. :	: : . :: : . :
gi+AHw-273	MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC			
	10	20	30	40 50 60
	50	60	70	80
AAD-12	IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKVIVG			

```

      . : .. .: .:: :. :. . . :...
gi+AHw-273 KMLLKGVIGEEKVVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
           70          80          90          100          110          120

```

```

gi+AHw-273 GATTLQHRRRR
           130

```

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
  initn: 55 initl: 55 opt: 55 Z-score: 87.6 bits: 20.7 E(): 6.6
Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (59-76:30-47)

```

```

      30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVG
              .. .:::. :.. . :
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKKGNLWEVKSSKP
           10          20          30          40          50

```

```

gi+AHw-144 LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
           60          70          80          90

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010
Total Scan time: 0.090 Total Display time: 0.000

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 26 - 105 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      5      2:+ACoAPQ-
      32     25      8:+AD0APQAqAD0APQA9AD0APQA9-
      34     25     21:+AD0APQA9AD0APQA9ACoAPQA9-

```



```

36      58      44: +AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
38      80
72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
40      97
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACo-
42      125
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
44      162
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA
9-
46      108
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
48      111
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
50      99
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9- +ACo-
52      86
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-
54      78      91: +AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
56      59      76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      73
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
60      63
50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      68
40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
64      29      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      18      25: +AD0APQA9AD0APQA9- +ACo-
68      33      20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
70      20      16: +AD0APQA9AD0APQAqAD0-
72      21      12: +AD0APQA9ACoAPQA9AD0-
74      6      10: +AD0APQ- +ACo-
76      4      7: +AD0APQAq-
78      1      6: +AD0AKg-
80      7      4: +AD0AKgA9-
82      2      3: +ACo-
84      1      3: +ACo-
86      0      2: +ACo-
88      3      2: +ACo- inset +AD0- represents 1 library sequences
90      0      1: +ACo-
92      1      1: +ACo- :+ACo-
94      0      1: +ACo- :+ACo-
96      0      1: +ACo- :+ACo-

```

```

 98      0      0:      +ACo-
100      0      0:      +ACo-
102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.46400.00375+ADs- mu+AD0- 5.0984
0.193
mean+AF8-var+AD0-43.770711.813, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193857
Kolmogorov-Smirnov statistic: 0.0487 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)   59 21.8           3
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)   60 22.0           5.9
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)   57 21.3           6.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)   55 20.7           6.5

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 59 Z-score: 93.7 bits: 21.8 E(): 3
Smith-Waterman score: 59+ADs- 44.444+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (58-75:30-47)

      30      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGN
      ..  .:..:  :..  : :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKKGNLWEVKSAP
      10      20      30      40      50

gi+AHw-126 LTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)
initn: 43 initl: 43 opt: 60 Z-score: 88.5 bits: 22.0 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (22-53:133-160)

```

```

              10      20      30      40      50
AAD-12      TLDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
              :  ::  :::::  .  :  ....  ::::
gi+AHw-221  FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI
              110      120      130      140      150
```

```

              60      70      80
AAD-12  AISNVKADGTVRQHSPA EWDDMMKVIVGN
              :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
              160      170      180      190      200      210
```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)
initn: 36 initl: 36 opt: 57 Z-score: 88.0 bits: 21.3 E(): 6.3
Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
in 70 aa overlap (13-77:33-102)

```

              10      20      30      40
AAD-12      TLDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
              :  ::  .  :  :  :  .  ::  :  .  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
              10      20      30      40      50      60
```

```

              50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKVIVGN
              .  :  ::  .  :::  ::  :.  .  .  :..
gi+AHw-273  KMLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
              70      80      90      100      110      120
```

```

gi+AHw-273  GATTLQHRRRR
              130
```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 55 Z-score: 87.7 bits: 20.7 E(): 6.5
Smith-Waterman score: 55+ADs- 38.889+ACU- identity (66.667+ACU- similar)
in 18 aa overlap (58-75:30-47)

```

              30      40      50      60      70      80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGN
              :.  ::::  ::.  .  :
gi+AHw-144  VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWELTKKGNLWEVKSSKP
              10      20      30      40      50
```

```

gi+AHw-144  LTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYTPEE
              60      70      80      90
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 27 - 106 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

56      59      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      72
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
60      63
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      70
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9-
64      29      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      21      25:+AD0APQA9AD0APQA9AD0- +ACo-
68      33      20:+AD0APQA9-+AD0APQA9ACoAPQA9AD0APQ-
70      19      16:+AD0APQA9AD0APQA9AD0-
72      21      12:+AD0APQA9ACoAPQA9AD0-
74      7       10:+AD0APQA9ACo-
76      4       7:+AD0APQA9-
78      2       6:+AD0AKg-
80      6       4:+AD0AKg-
82      2       3:+ACo-
84      1       3:+ACo-
86      0       2:+ACo-
88      3       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.53540.00374+ADs- mu+AD0- 4.7046
0.193
mean+AF8-var+AD0-43.527011.684, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.194399
Kolmogorov-Smirnov statistic: 0.0432 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 60 22.2 2.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 56 21.0 5.2

```

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 22.1 5.8
 gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 21.3 6.2

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 60 Z-score: 95.4 bits: 22.2 E(): 2.4
 Smith-Waterman score: 60+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (57-80:30-51)

	30	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNM					
			 : : : ...
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNLWEVKSA					
	10	20	30	40	50	

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 89.5 bits: 21.0 E(): 5.2
 Smith-Waterman score: 56+ADs- 37.500+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (57-80:30-51)

	30	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNM					
			 : ...
gi+AHw-144	VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNLWEVKSS					
	10	20	30	40	50	

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
 60 70 80 90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.6 bits: 22.1 E(): 5.8
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (21-52:133-160)

	10	20	30	40	50
AAD-12	LDDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV				
			: :: : : ...
gi+AHw-221	FGLIFPGCPSTYEPAQQGRRHQSRPFRFQGDQSQQQQDSHQK----VHRFDEGDLI				
	110	120	130	140	150

	60	70	80
AAD-12	AISNVKADGTVRQHSPA EWDDMMKVIVGNM		
	..		
gi+AHw-221	AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR		
	160	170	180 190 200 210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 88.2 bits: 21.3 E(): 6.2
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (12-76:33-102)

```

                                10      20      30      40
AAD-12      LDDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                : .:: .: : : : . :: : . :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
                10      20      30      40      50      60

                                50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPAEDDMMKVIVGNM
                . : .: .: .::: :. :. . . :. .
gi+AHw-273  KMLLKGVIGEEKVVELLRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
                70      80      90      100     110     120

gi+AHw-273  GATTLQHRRRR
                130

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:38 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 28 - 107 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	2	0:+AD0-	
30	9	2:+ACoAPQA9-	
32	19	8:+AD0APQAqAD0APQA9AD0-	
34	26	21:+AD0APQA9AD0APQA9ACoAPQA9-	

36 61
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
38 67 72:+AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
40 97
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
42 122
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
44 165
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
46 114
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +AD0APQA9AD0APQA9AD0APQA9- +ACo-
48 108
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
50 102
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
52 85
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
54 79
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ A9- +ACo-
56 58 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58 78
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ -
60 57 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62 71
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9-
64 29 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66 21 25:+AD0APQA9AD0APQA9AD0- +ACo-
68 33 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
70 19 16:+AD0APQA9AD0APQAqAD0-
72 21 12:+AD0APQA9ACoAPQA9AD0-
74 7 10:+AD0APQA9ACo-
76 4 7:+AD0APQAq-
78 2 6:+AD0AKg-
80 7 4:+AD0AKgA9-
82 1 3:+ACo-
84 1 3:+ACo-
86 0 2:+ACo-
88 3 2:+ACo- inset +AD0- represents 1 library sequences
90 0 1:+ACo-
92 0 1:+ACo- :+ACo-
94 1 1:+ACo- :+ACo-
96 0 1:+ACo- :+ACo-


```

 98      0      0:      +ACo-
100      0      0:      +ACo-
102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.52170.0037+ADs- mu+AD0- 4.7768
0.191
mean+AF8-var+AD0-43.563311.711, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.194318
Kolmogorov-Smirnov statistic: 0.0419 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  60 22.2      2.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  56 21.0      5.3
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.1      5.9
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)  57 21.3      6.2

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 60 Z-score: 95.4 bits: 22.2 E(): 2.4
Smith-Waterman score: 60+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (56-79:30-51)

      30      40      50      60      70      80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMA
      ..  .:..:  :..:  :  :  :..:
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNLWEVKSA
      10      20      30      40      50

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 56 Z-score: 89.4 bits: 21.0 E(): 5.3
Smith-Waterman score: 56+ADs- 37.500+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (56-79:30-51)

```

```

      30      40      50      60      70      80
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA
      ..  .:.  .:.  .:  .:
gi+AHw-144  VKVTFKVEKGS DPKKLVL DIKYTRPGDTLAEVELRQH GSEEW EPLTKK--GNLWEVKSS
      10      20      30      40      50

```

```

gi+AHw-144  KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGT TTYTPEE
      60      70      80      90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
Arachis (219 aa)

initn: 43 initl: 43 opt: 60 Z-score: 88.6 bits: 22.1 E(): 5.9
Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (20-51:133-160)

```

      10      20      30      40
AAD-12  DDAGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
      :  :  .:.  .:  .:  .:.  .:.
gi+AHw-221  FGLIFPGCPSTYEEPAQQGRRHQSQRP RRFQGDQSQQQQDSHQK----VHRFDEGDLI
      110      120      130      140      150

```

```

      50      60      70      80
AAD-12  AISNVKADGTVRQHSPA EWDDMMKVIVGNMA
      :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVA VSLTD TNNDNQLDQFP RRFNLAGNHEQEFLRYQQQSRRR
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)

initn: 36 initl: 36 opt: 57 Z-score: 88.1 bits: 21.3 E(): 6.2
Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
in 70 aa overlap (11-75:33-102)

```

      10      20      30
AAD-12  DDAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
      :  :.  .:  :  :  .:  :  .:
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLKVG C
      10      20      30      40      50      60

```

```

      40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMA
      .:  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-273  KMLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
      70      80      90      100      110      120

```

```

gi+AHw-273  GATT LQH HRRR
      130

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:38 2010 done: Fri Feb 5 12:55:39 2010

[illegible]

```

54      74
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      61      76:+AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
58      76
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
-
60      57      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      68
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
64      28      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      25      25:+AD0APQA9AD0APQA9AD0APQAq-
68      34      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      23      16:+AD0-+AD0APQA9AD0AKgA9AD0-
72      20      12:+AD0APQA9ACoAPQA9AD0-
74      5      10:+AD0APQ- +ACo-
76      4      7:+AD0APQAq-
78      1      6:+AD0AKg-
80      7      4:+AD0AKgA9-
82      1      3:+ACo-
84      1      3:+ACo-
86      0      2:+ACo-
88      2      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      1      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120     0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.45900.00374+ADs- mu+AD0- 5.1700
0.193
mean+AF8-var+AD0-44.058411.784, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.193223
Kolmogorov-Smirnov statistic: 0.0466 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 63 22.9 1.4

```

50 60 70 80
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
:
gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNDNQLDQFPRRFLAGNHEQEFLRYQQQSRRR
160 170 180 190 200 210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 87.8 bits: 21.2 E(): 6.5
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (10-74:33-102)

```

                                10      20      30
AAD-12      DAGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                : .:: . . : : : . :: : . :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLEKLVGC
              10      20      30      40      50      60

              40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAW
              . : .: .: .::: .: .: . . :.. .
gi+AHw-273  KMLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
              70      80      90      100     110     120

gi+AHw-273  GATTLQHRRRR
              130

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:39 2010 done: Fri Feb 5 12:55:39 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 30 - 109 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      2      0:+AD0-
      30      6      2:+ACoAPQ-
      32      21     8:+AD0APQAqAD0APQA9AD0-
      34      25    21:+AD0APQA9AD0APQA9ACoAPQA9-

```

```

36      61
44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
38      71
72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
40      98
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACo-
42      132
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
44      161
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA
9-
46      118
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
48      107
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
50      96
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ- +ACo-
52      99
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9- +ACo-
54      69
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
56      54      76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +AD0APQA9AD0APQA9-
+ACo-
58      71
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
60      53      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
62      69
40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
64      30      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      27      25: +AD0APQA9AD0APQA9AD0APQAq-
68      39      20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
70      19      16: +AD0APQA9AD0APQAqAD0-
72      14      12: +AD0APQA9ACoAPQ-
74      3      10: +AD0- +ACo-
76      3      7: +AD0- +ACo-
78      7      6: +AD0AKgA9-
80      8      4: +AD0AKgA9-
82      1      3: +ACo-
84      1      3: +ACo-
86      0      2: +ACo-
88      2      2: +ACo- inset +AD0- represents 1 library sequences
90      0      1: +ACo-
92      1      1: +ACo- :+ACo-
94      0      1: +ACo- :+ACo-
96      0      1: +ACo- :+ACo-
98      1      0: +AD0- +ACoAPO-

```

```

100      0      0:      +ACo-
102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.33500.00368+ADs- mu+AD0- 5.8232
0.190
mean+AF8-var+AD0-44.662411.986, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.191913
Kolmogorov-Smirnov statistic: 0.0480 (N+AD0-28) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.070
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  63 22.8      1.5
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  59 21.7      3.3
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 22.0      6.3
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)  57 21.2      6.8

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 63 Z-score: 99.0 bits: 22.8 E(): 1.5
Smith-Waterman score: 63+ADs- 42.308+ACU- identity (61.538+ACU- similar)
in 26 aa overlap (54-79:30-52)

```

```

          30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWH
          ..  ....  ...  :  :  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKS
          10          20          30          40          50

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

```

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 59 Z-score: 93.1 bits: 21.7 E(): 3.3
Smith-Waterman score: 59+ADs- 38.462+ACU- identity (61.538+ACU- similar)
in 26 aa overlap (54-79:30-52)

          30          40          50          60          70          80

```



```

AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWH
          ..  ....  ...  .  :  ...  :
gi+AHw-144  VKVTFKVEKGS DPKKLVL DIKYTRPGDTLAEVELRQHGSEEWEP LTKK--GNL-WEVKS
          10      20      30      40      50

```

```

gi+AHw-144  SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYTPEE
          60      70      80      90

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 88.0 bits: 22.0 E(): 6.3
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (18-49:133-160)

```

          10      20      30      40
AAD-12      AGFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
          :  ::  ....  .  :  ....  ....
gi+AHw-221  FGLIFPGCPSTYE E PAQQGRRHQSQRP RRFQGDQSQQQQDSHQK---VHRFDEGDLI
          110     120     130     140     150

```

```

          50      60      70      80
AAD-12  AISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWH
          ..
gi+AHw-221  AVPTGVAFWMYNDHDTDVVA VSLTDTNNNDNQLDQFP RRFNLAGNHEQEFLRYQQQSRRR
          160     170     180     190     200     210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
 Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 87.5 bits: 21.2 E(): 6.8
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (9-73:33-102)

```

          10      20      30
AAD-12      AGFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
          :  ::  ..  :  :  :  .  ::  :  .  :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
          10      20      30      40      50      60

```

```

          40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWH
          .  :  ..  .  :  :  :  :  .  .  :  :  .
gi+AHw-273  KMLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
          70      80      90      100     110     120

```

```

gi+AHw-273  GATTLQHRRRR
          130

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:40 2010 done: Fri Feb 5 12:55:40 2010

Total Scan time: 0.070 Total Display time: 0.010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

56      58      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      68
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      57      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      66
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
64      31      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      28      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      36      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      18      16:+AD0APQA9AD0APQAq-
72      15      12:+AD0APQA9ACoAPQ-
74      3      10:+AD0- +ACo-
76      3      7:+AD0- +ACo-
78      9      6:+AD0AKgA9-
80      6      4:+AD0AKg-
82      2      3:+ACo-
84      0      3:+ACo-
86      1      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120     0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.46220.00363+ADs- mu+AD0- 5.2174
0.187
mean+AF8-var+AD0-44.786411.931, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.191647
Kolmogorov-Smirnov statistic: 0.0425 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 63 22.8 1.5
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 59 21.7 3.3
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 21.9 6.4

```

gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 21.1 6.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 63 Z-score: 99.0 bits: 22.8 E(): 1.5
 Smith-Waterman score: 63+ADs- 42.308+ACU- identity (61.538+ACU- similar)
 in 26 aa overlap (53-78:30-52)

	30	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHA					
	: : : : :					
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKS					
	10	20	30	40	50	

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
 60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 59 Z-score: 93.1 bits: 21.7 E(): 3.3
 Smith-Waterman score: 59+ADs- 38.462+ACU- identity (61.538+ACU- similar)
 in 26 aa overlap (53-78:30-52)

	30	40	50	60	70	80
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHA					
	: : : : :					
gi+AHw-144	VKVTFKVEKGSDDPKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVKS					
	10	20	30	40	50	

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTITYTPEE
 60 70 80 90

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 87.9 bits: 21.9 E(): 6.4
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (17-48:133-160)

	10	20	30	40
AAD-12	GFAALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV			
	: : : : :			
gi+AHw-221	FGLIFPGCPSTYEPAQQGRRHQSRPFRFQGDQSQQQQDSHQK---VHRFDEGDLI			
	110	120	130	150

	50	60	70	80
AAD-12	AISNVKADGTVRQHSPAEDDMMKVIVGNMAWHA			
	: .			
gi+AHw-221	AVPTGVAFWMYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR			
	160	170	180	210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 87.4 bits: 21.1 E(): 6.8

Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
in 70 aa overlap (8-72:33-102)

```

                                10      20      30
AAD-12      GFAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                : .:: .: .: .: .: .:
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFDQLHGEEKQQATEKLVGC
              10      20      30      40      50      60

              40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHA
              .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-273  KMLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
              70      80      90      100     110     120

gi+AHw-273  GATTTLQHRRRR
              130

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:41 2010 done: Fri Feb 5 12:55:42 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 32 - 111 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      8      2:+ACoAPQA9-
      32     15      8:+AD0APQAqAD0APQ-
      34     29     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36     68
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
      38     63
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-

```

[illegible]

```

112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.54240.00366+ADs- mu+AD0- 4.9212
0.189
mean+AF8-var+AD0-48.425113.884, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.184306
Kolmogorov-Smirnov statistic: 0.0371 (N+AD0-27) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 63 22.5 2

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 59 21.4 4.1

gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (219) 60 21.6 7.9

gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (134) 57 20.9 8.3

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 63 Z-score: 97.0 bits: 22.5 E(): 2
Smith-Waterman score: 63+ADs- 42.308+ACU- identity (61.538+ACU- similar)
in 26 aa overlap (52-77:30-52)

```

                30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
                ..  ....  ...  :  :  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTKK--GNL-WEVK
                10          20          30          40          50

```

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 59 Z-score: 91.4 bits: 21.4 E(): 4.1
Smith-Waterman score: 59+ADs- 38.462+ACU- identity (61.538+ACU- similar)
in 26 aa overlap (52-77:30-52)

```

                30          40          50          60          70          80
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
                ..  ....  ...  .  :  ...  :
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKK--GNL-WEVK
                10          20          30          40          50

```

```

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE

```

```

      initn:  43 initl:  43 opt:   60 Z-score: 86.2  bits: 21.6 E():   7.9
Smith-Waterman score: 60+ADs-  34.375+ACU- identity (62.500+ACU- similar)
in 32 aa overlap (16-47:133-160)

```

50 60 70 80
 AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
 :.
 gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
 160 170 180 190 200 210

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)
initn: 36 initl: 36 opt: 57 Z-score: 85.8 bits: 20.9 E(): 8.3
Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
in 70 aa overlap (7-71:33-102)

AAD-12
 FAALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
 : .:: . : : : . :: : . :
 gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLKVGCG
 10 20 30 40 50 60

```

          40          50          60          70          80
AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHAD
          .  :   :.   .:   .::   :.   :.   .   .   :..   .
gi+AHw-273 KMLLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
          70          80          90          100          110          120

gi+AHw-273 GATTLLQHRRRR
          130

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:42 2010 done: Fri Feb 5 12:55:42 2010
Total Scan time: 0.090 Total Display time: 0.000

```

```
Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```



```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      7      2:+ACoAPQA9-
      32      16     8:+AD0APQAqAD0APQA9-
      34      27     21:+AD0APQA9AD0APQA9ACoAPQA9-
      36      67
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
      38      62
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      40      86     101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      42      132
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
      44      161
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA
9-
      46      137
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      48      96
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      50      119
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
      52      90
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9- +ACo-
      54      72
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      56      63
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      58      54     62:+AD0APQA9AD0APQ-+AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      60      69
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
      62      39     40:+AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0AKq-

```

```

64      30      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      38      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
68      30      20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
70      33      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      8       12:+AD0APQA9ACo-
74      7       10:+AD0APQ-+AD0AKg-
76     12       7:+AD0APQAqAD0-
78      2       6:+AD0AKg-
80      2       4:+AD0AKg-
82      1       3:+ACo-
84      4       3:+ACoAPQ-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.47430.00367+ADs- mu+AD0- 5.3943
0.189
mean+AF8-var+AD0-50.328914.482, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.180786
Kolmogorov-Smirnov statistic: 0.0357 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.3      1.1
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  63 22.2      2.3
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.7      8.5
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5

```

60 70 80
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADS
 .:. :. : : : .: :.
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

60 70 80
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADS
 . . . : : : . : :
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 initl: 43 opt: 60 Z-score: 85.4 bits: 21.5 E(): 8.8
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (15-46:133-160)

```

                                10      20      30      40
AAD-12      AALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                                : :: :...: . : :... :...
gi+AHw-221  FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGQDQSQQQQDSHQK----VHRFDEGDLI
              110      120      130      140      150

              50      60      70      80
AAD-12  AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
              :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
              160      170      180      190      200      210

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris lumb (134 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 84.9 bits: 20.7 E(): 9.3
 Smith-Waterman score: 57+ADs- 25.714+ACU- identity (50.000+ACU- similar)
 in 70 aa overlap (6-70:33-102)

```

                                10      20      30
AAD-12      AALHAAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
                                : .:: . . : : : . : : : . :
gi+AHw-273  MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLKVGC
              10      20      30      40      50      60

              40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
              . : :. . :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
gi+AHw-273  KMLLKGVIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
              70      80      90      100      110      120

gi+AHw-273  GATTLQHRRRR
              130

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:42 2010 done: Fri Feb 5 12:55:42 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 34 - 113 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

68      32      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
70      31      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      9       12:+AD0APQA9ACo-
74      7       10:+AD0APQA9ACo-
76     12       7:+AD0APQAqAD0-
78      2       6:+AD0AKg-
80      2       4:+AD0AKg-
82      1       3:+ACo-
84      4       3:+ACoAPQ-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.54220.00367+ADs- mu+AD0- 5.0367
0.190
mean+AF8-var+AD0-50.508214.517, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.180465
Kolmogorov-Smirnov statistic: 0.0385 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.3      1.1
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.8      1.6
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.7      8.5
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.7      8.5
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 21.5      8.9

```

60 70 80
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADST
 ::: :: : : : :: ::

gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 initl: 52 opt: 57 Z-score: 85.7 bits: 20.7 E(): 8.5
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (24-79:29-82)

10 20 30 40 50
AAD-12 ALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADST
... :: : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)

initn: 52 initl: 52 opt: 57 Z-score: 85.7 bits: 20.7 E(): 8.5
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (24-79:29-82)

10 20 30 40 50
AAD-12 ALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :.
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADST
... :: : : : : : :
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 initl: 52 opt: 57 Z-score: 85.7 bits: 20.7 E(): 8.5
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (24-79:29-82)

10 20 30 40 50
AAD-12 ALHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
10 20 30 40 50 60

60 70 80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADST
... :: : : : : : :

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank

[illegible]

```

60      61
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      28      40:+AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
64      26      32:+AD0APQA9AD0APQA9AD0APQA9-      +ACo-
66      44      25:+AD0-+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
68      23      20:+AD0APQA9AD0APQA9ACoAPQ-
70      33      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      9      12:+AD0APQA9ACo-
74      6      10:+AD0APQ-      +ACo-
76      11      7:+AD0APQAqAD0-
78      5      6:+AD0AKg-
80      3      4:+AD0AKg-
82      1      3:+ACo-
84      7      3:+ACoAPQA9-
86      2      2:+ACo-
88      0      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     1      0:+AD0-      +ACoAPQ-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120     0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.60300.00371+ADs- mu+AD0- 4.7526
0.191
mean+AF8-var+AD0-53.865115.304, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.174751
Kolmogorov-Smirnov statistic: 0.0323 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.0 1.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.5 1.9
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0 7.3
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8 8
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.8 8.7

```

AAD-12 LHAAWLQHALLIFPGQHLSDQQITFAKRFGAIERIGGGDIVAISNVKAD
 ::: ::: ::: ::: ::: :::

gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

60 70 80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTY
::: . . :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.2 bits: 21.8 E(): 8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (21-80:184-237)

10 20 30 40 50
AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
:::
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200

60 70 80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTY
::: . . :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.5 bits: 21.8 E(): 8.7
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (21-80:206-259)

10 20 30 40 50
AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
:::
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

60 70 80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTY
::: . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.9
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (23-78:29-82)

10 20 30 40 50
AAD-12 LHAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
.....

AAD-12 10 20 30 40 50
LHAAWLQHALLIFPGQHLSDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR

```

gi+AHw-400  MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
              10          20          30          40          50          60

              60          70          80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTY
        ...  ::  :  :  :  :  :  :
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDVVPEKYTIGATY
              70          80          90          100          110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:43 2010 done: Fri Feb 5 12:55:43 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 36 - 115 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      5      2:+ACoAPQ-
      32     12      8:+AD0APQAqAD0-
      34     24     21:+AD0APQA9AD0APQA9ACoAPQ-
      36     68
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
      38     61
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      40     92
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
      42    126
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
      44    162
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP

```


+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences

Kolmogorov-Smirnov statistic: 0.0303 (N+AD0-28) at 44

Scan time: 0.090

```
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
57 20.5      9.8
```

initn: 59 initl: 59 opt: 67 Z-score: 100.0 bits: 23.0 E(): 1.4
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (48-77:30-56)

80
AAD-12 TYM

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

```

initn: 55 init1: 55 opt: 65 Z-score: 97.3 bits: 22.5 E(): 1.9
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (48-78:30-57)

```

```

      20      30      40      50      60      70
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
      .. . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-144 VKVTFKVEKGS DPKKLVL DIKYTRPGDTLAEVELRQH GSEEW EPLTKK--GNL-WEVKS
      10      20      30      40      50

```

```

      80
AAD-12  TYM
      .
gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYTPEE
      60      70      80      90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 86.8 bits: 22.0 E(): 7.4
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (20-79:207-260)

```

      10      20      30      40
AAD-12  HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      .. . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230

```

```

      50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
      ::: . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.1 bits: 21.7 E(): 8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (20-79:184-237)

```

      10      20      30      40
AAD-12  HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      .. . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      160      170      180      190      200

```

```

      50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYM
      ::: . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
      210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.5 bits: 21.8 E(): 8.7
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (20-79:206-259)

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (22-77:29-82)

```

          10          20          30          40          50
AAD-12      HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              .....
gi+AHw-400  MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
          10          20          30          40          50          60

```

```

          60          70          80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYM
          ...  ::  :  :  :  :  :  :
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
          70          80          90          100          110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 initl: 52 opt: 57 Z-score: 84.5 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (22-77:29-82)

```

          10          20          30          40          50
AAD-12      HAAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              .....
gi+AHw-400  MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
          10          20          30          40          50          60

```

```

          60          70          80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYM
          ...  ::  :  :  :  :  :  :
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
          70          80          90          100          110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:43 2010 done: Fri Feb 5 12:55:43 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 37 - 116 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()

```

+ADw- 20      2      0: +AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      1      0: +AD0-
30      3      2: +ACo-
32      13     8: +AD0APQAqAD0APQ-
34      28     21: +AD0APQA9AD0APQA9ACoAPQA9AD0-
36      67
44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
38      64
72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
40      83
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0-      +ACo-
42      130
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
44      170
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA
9- +AD0APQA9-
46      132
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
48      104
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
50      121
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
52      91
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0-      +ACo-
54      75
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      63
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
58      61
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60      56      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      29      40: +AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
64      33      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      43      25: +AD0APQA9AD0APQA9AD0APQAqAD0APQ- +AD0APQA9AD0-
68      25      20: +AD0APQA9AD0APQA9ACoAPQA9-
70      32      16: +AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      12      12: +AD0APQA9ACo-
74      7       10: +AD0APQA9ACo-
76      8       7: +AD0APQAq-
78      2       6: +AD0AKg-
80      4       4: +AD0AKg-
82      1       3: +ACo-
84      7       3: +ACoAPQA9-

```

```

86      2      2:+ACo-
88      0      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.58210.00377+ADs- mu+AD0- 4.8582
0.194
mean+AF8-var+AD0-54.479415.446, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.173763
Kolmogorov-Smirnov statistic: 0.0357 (N+AD0-28) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 22.9      1.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.4      2
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0      7.5
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.7      8.2
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.7      8.9
gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-Ascaris (
134)  58 20.7      9.3

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 99.6 bits: 22.9 E(): 1.4
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (47-76:30-56)

```

```

      20      30      40      50      60      70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
      ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
      10      20      30      40      50

```

10
20
30
40

AAD-12
 AAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD

::
::
::
::
::
::
::
::

gi+AHw-458
 G
S
N
P
N
Y
L
A
L
L
V
K
F
V
A
G
D
G
D
V
V
A
V
D
I
K
E
K
G
K
D
K
W
I
A
L
K
E
S
W
G
A
I
W
R
I
D
T
P
E
V
L

K
G
P

160
170
180
190
200


```

      50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
      :::  . .      :  . . . . . :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
      210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.3 bits: 21.7 E(): 8.9
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (19-78:206-259)

```

      10      20      30      40
AAD-12  AAWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      . . . . . :  . . . . . :
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230

```

```

      50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
      :::  . .      :  . . . . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)
initn: 39 initl: 39 opt: 58 Z-score: 85.0 bits: 20.7 E(): 9.3
Smith-Waterman score: 58+ADs- 23.810+ACU- identity (47.619+ACU- similar)
in 84 aa overlap (2-80:33-116)

```

      10      20      30
AAD-12  AAWLQHALLIFPGQ-HLSNDQQITFAKRFGA
      :  . :  . :  :  . :  :  . :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLKVG
      10      20      30      40      50      60

```

```

      40      50      60      70      80
AAD-12  IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
      . :  . :  . :  . :  . :  . :
gi+AHw-273 KMLLKGVIGEEKVVELLRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
      70      80      90      100      110      120

```

```

gi+AHw-273 GATTLQHRRRR
      130

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:44 2010 done: Fri Feb 5 12:55:44 2010

Total Scan time: 0.080 Total Display time: 0.010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

56      61
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
58      66
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60      53      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
62      31      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
64      30      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
66      43      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
68      23      20:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
70      36      16:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
72      8      12:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
74      8      10:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
76      8      7:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
78      3      6:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
80      4      4:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
82      1      3:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
84      7      3:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
86      2      2:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
88      0      2:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
90      0      1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
92      0      1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
94      0      1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
96      1      1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
98      0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
100     1      0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
102     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
104     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
106     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
108     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
110     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
112     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
114     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
116     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
118     0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
+AD4-120      0      0:      +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.73250.0037+ADs- mu+AD0- 4.1430
0.191
mean+AF8-var+AD0-53.410415.308, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175494
Kolmogorov-Smirnov statistic: 0.0344 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.0 1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.5 1.9
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0 7.3

```

```
+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
  initn: 44 init1: 44 opt: 63 Z-score: 86.8 bits: 22.0 E(): 7.3
```

Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (18-77:207-260)

```

                        10      20      30      40
AAD-12                AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                        :. . . . . :. . . . . :.
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                        180      190      200      210      220      230

```

```

                        50      60      70      80
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                        ::: . . : . . . : . . . :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
                        240      250      260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 init1: 44 opt: 62 Z-score: 86.2 bits: 21.8 E(): 8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (18-77:184-237)

```

                        10      20      30      40
AAD-12                AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                        :. . . . . :. . . . . :.
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                        160      170      180      190      200

```

```

                        50      60      70      80
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                        ::: . . : . . . : . . . :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
                        210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 init1: 44 opt: 62 Z-score: 85.5 bits: 21.8 E(): 8.7
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (18-77:206-259)

```

                        10      20      30      40
AAD-12                AWLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                        :. . . . . :. . . . . :.
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                        180      190      200      210      220      230

```

```

                        50      60      70      80
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                        ::: . . : . . . : . . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
                        240      250      260

```

+AD4APg-gi+AHw-2735118+AHw-gb+AHw-AAB93839.1+AHw- ABA-1 allergen +AFs-
Ascaris lumb (134 aa)
initn: 39 init1: 39 opt: 58 Z-score: 85.3 bits: 20.7 E(): 9

Smith-Waterman score: 58+ADs- 23.810+ACU- identity (47.619+ACU- similar)
in 84 aa overlap (1-79:33-116)

```

                                10      20
AAD-12      AWLQHALLIFPGQ-HLSNDQQITFAKRFGA
              : .:. .: : : . :. : . :
gi+AHw-273 MEHYLKTYLSWLTEEQKEKLKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLVGC
              10      20      30      40      50      60

              30      40      50      60      70      80
AAD-12 IERIGG--GD--IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPV
              . : .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-273 KMLLKGVIGEEKVVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKIF
              70      80      90      100     110     120

gi+AHw-273 GATTLQHRRRR
              130

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.7
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (20-75:29-82)

```

                                10      20      30      40      50
AAD-12      AWLQHALLIFPGQHLSNDQQITFAKRFGA IERIGGGDIVAISNVKADGTVR
              .....: .: .: .: .: .: .: .:
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
              10      20      30      40      50      60

              60      70      80
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPV
              .:. :. : : : .: :.
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70      80      90      100     110

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.7
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (20-75:29-82)

```

                                10      20      30      40      50
AAD-12      AWLQHALLIFPGQHLSNDQQITFAKRFGA IERIGGGDIVAISNVKADGTVR
              .....: .: .: .: .: .: .: .:
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
              10      20      30      40      50      60

              60      70      80
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPV
              .:. :. : : : .: :.
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70      80      90      100     110

```

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]


```

72      11      12:+AD0APQA9ACo-
74      7       10:+AD0APQA9ACo-
76      6       7:+AD0APQAq-
78      4       6:+AD0AKg-
80      3       4:+AD0AKg-
82      3       3:+ACo-
84      6       3:+ACoAPQ-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.75990.00368+ADs- mu+AD0- 4.0059
0.189
mean+AF8-var+AD0-53.117415.091, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175977
Kolmogorov-Smirnov statistic: 0.0323 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.1      1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.6      1.8
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0      7.3
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8      7.9
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.8      8.6
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.5      9.6
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.5      9.6
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.5      9.6

```

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
57 20.5 9.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 100.3 bits: 23.1 E(): 1.3
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (45-74:30-56)

	20	30	40	50	60	70
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS					
:: : : : : : : : :					
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS					
	10	20	30	40	50	

80
AAD-12 TYMPVM

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 97.6 bits: 22.6 E(): 1.8
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (45-75:30-57)

	20	30	40	50	60	70
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS					
:: : : : : : : : :					
gi+AHw-144	VKVTFKVEKGSDDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS					
	10	20	30	40	50	

80
AAD-12 TYMPVM

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 86.9 bits: 22.0 E(): 7.3
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (17-76:207-260)

	10	20	30	40
AAD-12	WLQHALLIFPGQHLSDNDQQITFAKRFGAIERIGGGDIVAISNVKAD			
	.. : : : : : : : : : : : :			
gi+AHw-390	GSDNPYLLVVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP			
	180	190	200	210

	50	60	70	80
AAD-12	GTVRQHSPEWDDMMKVIVGNMAWHADSTYMPVM			
	: : : : : : : : : : : :			

gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.3 bits: 21.8 E(): 7.9
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (17-76:184-237)

AAD-12 10 20 30 40
WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
..::: :: ... :.
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200

AAD-12 50 60 70 80
GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
::: . . : .. . :.:.: :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.8 E(): 8.6
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (17-76:206-259)

AAD-12 10 20 30 40
WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
..::: :: ... :.
gi+AHw-158 KGNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

AAD-12 50 60 70 80
GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVM
::: . . : .. . :.:.: :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (19-74:29-82)

AAD-12 10 20 30 40 50
WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :.
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
10 20 30 40 50 60

AAD-12 60 70 80
QHSPAEWDDMMKVIVGNMAWHADSTYMPVM
... :: : : : .. ::

gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (19-74:29-82)

AAD-12 10 20 30 40 50
WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :. :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
10 20 30 40 50 60

AAD-12 60 70 80
QHSPAEWDDMMKVIVGNMAWHADSTYMPVM
... :: : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (19-74:29-82)

AAD-12 10 20 30 40 50
WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :. :. :.
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
10 20 30 40 50 60

AAD-12 60 70 80
QHSPAEWDDMMKVIVGNMAWHADSTYMPVM
... :: : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
70 80 90 100 110

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (19-74:29-82)

AAD-12 10 20 30 40 50
WLQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
..... :. :. :. :. :.
gi+AHw-400 MSMASSSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
10 20 30 40 50 60

AAD-12 60 70 80
QHSPAEWDDMMKVIVGNMAWHADSTYMPVM
... :: : : : : : :

```
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90             100             110
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:44 2010 done: Fri Feb 5 12:55:44 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 40 - 119 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      3      2:+ACo-
      32      7      8:+AD0APQAq-
      34      28     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      80
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9-
      38      68
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
      40      89
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9- +ACo-
      42      121
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
      44      158
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
      46      128
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
```

Kolmogorov-Smirnov statistic: 0.0330 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po

(97) 67 23.1 1.3

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-

(96) 65 22.5 1.8

gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI (263)

63 22.0 7.2

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)

62 21.8 7.9

gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262)

62 21.8 8.6

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P

(122) 57 20.5 9.6

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)

57 20.5 9.6

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)

57 20.5 9.6

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)

57 20.5 9.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:

Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 100.3 bits: 23.1 E(): 1.3

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)

in 30 aa overlap (44-73:30-56)

	20	30	40	50	60	70
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS					
			 : : ... :
gi+AHw-126	TKVDLTVEKGSDAKTLVLNLIKYPTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS					
	10	20	30	40	50	

80
AAD-12 TYMPVMA

gi+AHw-126	60	70	80	90
AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN				

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:

Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 97.6 bits: 22.5 E(): 1.8

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)

in 31 aa overlap (44-74:30-57)

	20	30	40	50	60	70
AAD-12	SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS					
			 : : ... :
gi+AHw-144	VKVTFKVEKGSDPKKLVLVDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKS					
	10	20	30	40	50	

80
AAD-12 TYMPVMA
gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPPEE
60 70 80 90
+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 87.0 bits: 22.0 E(): 7.2
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (16-75:207-260)

AAD-12 LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.3 bits: 21.8 E(): 7.9
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (16-75:184-237)

AAD-12 LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200

AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMA
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.8 E(): 8.6
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (16-75:206-259)

AAD-12 LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230


```

      50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
      :::  . .  : . . . . .
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (18-73:29-82)

```

      10      20      30      40
AAD-12  LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
      ..... . . . .
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
      10      20      30      40      50      60

```

```

      50      60      70      80
AAD-12  QHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
      .:. :: : : : .: ::
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
      70      80      90      100      110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (18-73:29-82)

```

      10      20      30      40
AAD-12  LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
      ..... . . . .
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
      10      20      30      40      50      60

```

```

      50      60      70      80
AAD-12  QHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
      .:. :: : : : .: ::
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
      70      80      90      100      110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (18-73:29-82)

```

      10      20      30      40
AAD-12  LQHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
      ..... . . . .
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
      10      20      30      40      50      60

```

initn: 52 initl: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.6
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (18-73;29-82)

50 60 70 80
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMA
 ... :: : : : .: ::
 gi+AHw-400 EHGSDEWVAMTKEGGG--VWTFDSEEP LQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-l2: 41 - 120 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	2	0:+AD0-	
30	2	2:+ACo-	

32 9 8:+AD0APQAq-
 34 36 21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
 36 73
 44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
 38 67
 72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
 40 92 101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 42 117
 123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 44 153
 136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
 46 128
 138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
 48 110
 132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
 50 120
 121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 52 92
 106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0- +ACo-
 54 86
 91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
 A9AD0APQ- +ACo-
 56 61
 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 58 74 62:+AD0APQA9AD0APQA9AD0-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
 60 44 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 62 38 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 64 34 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
 66 32 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
 68 25 20:+AD0APQA9AD0APQA9ACoAPQA9-
 70 30 16:+AD0APQA9AD0APQAqAD0APQA9AD0-
 72 11 12:+AD0APQA9ACo-
 74 7 10:+AD0APQA9ACo-
 76 4 7:+AD0APQAq-
 78 5 6:+AD0AKg-
 80 5 4:+AD0AKg-
 82 1 3:+ACo-
 84 7 3:+ACoAPQA9-
 86 2 2:+ACo-
 88 0 2:+ACo- inset +AD0- represents 1 library sequences
 90 0 1:+ACo-
 92 0 1:+ACo- :+ACo-
 94 0 1:+ACo- :+ACo-
 96 0 1:+ACo- :+ACo-
 98 1 0:+AD0- +ACoAPQ-
 100 1 0:+AD0- +ACoAPQ-

```

102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.78560.00371+ADs- mu+AD0- 3.9736
0.191
mean+AF8-var+AD0-52.183614.682, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.177545
Kolmogorov-Smirnov statistic: 0.0319 (N+AD0-28) at 36

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.1      1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.6      1.8
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.1      7.1
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8      7.7
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.8      8.4
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.5      9.4
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.5      9.4
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.5      9.4
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.5      9.4

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 100.6 bits: 23.1 E(): 1.3
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (43-72:30-56)

                20          30          40          50          60          70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
                10          20          30          40          50

```

AAD-12 TYMPVMAQ

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 97.9 bits: 22.6 E(): 1.8
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (43-73:30-57)

20 30 40 50 60 70
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
.. .:.. :. : :. :.
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEWEPLTKK--GNL-WEVKS
10 20 30 40 50

80
AAD-12 TYMPVMAQ

.
gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 87.1 bits: 22.1 E(): 7.1
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (15-74:207-260)

10 20 30 40
AAD-12 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.. :.. . :. :. :.
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

50 60 70 80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
::: . . : . . :.:.:.
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.4 bits: 21.8 E(): 7.7
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (15-74:184-237)

10 20 30 40
AAD-12 QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.. :.. . :. :. :.
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200
50 60 70 80

AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ

```

      ::: . . : . . . . . :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
      210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)

initn: 44 initl: 44 opt: 62 Z-score: 85.7 bits: 21.8 E(): 8.4
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (15-74:206-259)

```

                        10      20      30      40
AAD-12                QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                        :. . . . . :. . . . . :.
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230

```

```

      50      60      70      80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
      ::: . . : . . . . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)

initn: 52 initl: 52 opt: 57 Z-score: 84.9 bits: 20.5 E(): 9.4
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (17-72:29-82)

```

                        10      20      30      40
AAD-12                QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                        ..... :. :. . . . . :. :. :.
gi+AHw-117 MSMASSSSSSLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
      10      20      30      40      50      60

```

```

      50      60      70      80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQ
      :. :. :. :. :. :. :.
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
      70      80      90      100      110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)

initn: 52 initl: 52 opt: 57 Z-score: 84.9 bits: 20.5 E(): 9.4
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (17-72:29-82)

```

                        10      20      30      40
AAD-12                QHALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                        ..... :. :. . . . . :. :. :.
gi+AHw-400 MSMASSSSSSLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
      10      20      30      40      50      60

```

```

      50      60      70      80

```

```
Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

	opt	E()
+ADw-	20	2 0:+AD0-
22	0	0:
24	0	0:
26	0	0:
28	3	0:+AD0-
30	1	2:+ACo-
32	10	8:+AD0APQAqAD0-
34	38	21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
36	72	
44	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9- 38 65
72	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo- 40 95
101	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo- 42 112
123	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo- 44 155
136	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0- 46 120
138	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo- 48 113
132	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo- 50 121
121	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg- 52 97
106	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo- 54 82
91	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo- 56 61 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +AD0APQA9AD0APQA9- +ACo- 58 76
62	:	:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ -
60	49	50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62	35	40:+AD0APQA9AD0APQA9AD0APOA9AD0APQA9- +ACo-


```

64      38      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66      26      25: +AD0APQA9AD0APQA9AD0APQAq-
68      23      20: +AD0APQA9AD0APQA9ACoAPQ-
70      32      16: +AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      14      12: +AD0APQA9ACoAPQ-
74       5      10: +AD0APQ- +ACo-
76       5       7: +AD0APQAq-
78       5       6: +AD0AKg-
80       4       4: +AD0AKg-
82       1       3: +ACo-
84       6       3: +ACoAPQ-
86       3       2: +ACo-
88       0       2: +ACo-          inset +AD0- represents 1 library sequences
90       0       1: +ACo-
92       0       1: +ACo-          : +ACo-
94       0       1: +ACo-          : +ACo-
96       0       1: +ACo-          : +ACo-
98       1       0: +AD0-          +ACoAPQ-
100      1       0: +AD0-          +ACoAPQ-
102      0       0:              +ACo-
104      0       0:              +ACo-
106      0       0:              +ACo-
108      0       0:              +ACo-
110      0       0:              +ACo-
112      0       0:              +ACo-
114      0       0:              +ACo-
116      0       0:              +ACo-
118      0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.78320.00373+ADs- mu+AD0- 4.0331
0.193
mean+AF8-var+AD0-51.895314.562, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.178037
Kolmogorov-Smirnov statistic: 0.0333 (N+AD0-28) at 36

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.1      1.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.6      1.8
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.1      7.1
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8      7.7
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.8      8.4
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.6      9.3

```


[illegible]

gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
 10 20 30 40 50 60

50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ... :: : : : .: ::

gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.0 bits: 20.6 E(): 9.3
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (16-71:29-82)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :.
 gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
 10 20 30 40 50 60

50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ... :: : : : .: ::
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.0 bits: 20.6 E(): 9.3
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (16-71:29-82)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :.
 gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
 10 20 30 40 50 60

50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ... :: : : : .: ::
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.0 bits: 20.6 E(): 9.3
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (16-71:29-82)

10 20 30 40
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
 :. :. :.

gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
 10 20 30 40 50 60

 50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ... :: : : : : : : :

gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-
 Arachis (219 aa)

 initn: 43 initl: 43 opt: 60 Z-score: 84.4 bits: 21.3 E(): 10
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (6-37:133-160)

 10 20 30
 AAD-12 HALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
 : : : : : : : : : : : : : : :
 gi+AHw-221 FGLIFPGCPSTYEEPAQQGRRHQSQRRPFRFQGGDQSQQQQDSHQK----VHRFDEGDLI
 110 120 130 140 150

 40 50 60 70 80
 AAD-12 AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQG
 ..
 gi+AHw-221 AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
 160 170 180 190 200 210

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 43 - 122 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

 opt E()
 +ADw- 20 2 0:+AD0-
 22 0 0: one +AD0- represents 3 library sequences
 24 0 0:

inset +AD0- represents 1 library sequences

```

92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     1      0:+AD0-      +ACoAPQ-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.80130.00371+ADs- mu+AD0- 3.7601
0.192
mean+AF8-var+AD0-51.499514.551, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.178720
Kolmogorov-Smirnov statistic: 0.0305 (N+AD0-29) at 36

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.2      1.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.7      1.7
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.1      6.7
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.9      7.3
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.9      8
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.6      8.9
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.6      8.9
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.6      8.9
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.6      8.9
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219)  60 21.4      9.5

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 101.1 bits: 23.2 E(): 1.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (41-70:30-56)

```

```

                20          30          40          50          60          70
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126  TKVDLTVEKGS DAKTLVLN IKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKS
                10          20          30          40          50

```

```

                80
AAD-12  TYMPVMAQGA

gi+AHw-126  AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 init1: 55 opt: 65 Z-score: 98.4 bits: 22.7 E(): 1.7
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (41-71:30-57)

```

                20          30          40          50          60          70
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                ..  ....  ...  :  :  ...  ...  :
gi+AHw-144  VKVTFKVEKGS DPKKLVL DIKYTRPGDTLAEVELRQH GSEEWEP LTKK--GNL-WEVKS
                10          20          30          40          50

```

```

                80
AAD-12  TYMPVMAQGA

gi+AHw-144  SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTP EE
                60          70          80          90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 init1: 44 opt: 63 Z-score: 87.5 bits: 22.1 E(): 6.7
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (13-72:207-260)

```

                10          20          30          40
AAD-12  ALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                ..  ...  .  ....  ::  ...  :..
gi+AHw-390  GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                180          190          200          210          220          230

```

```

                50          60          70          80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
                :::  .  .  :  .  .  .  ....  :
gi+AHw-390  FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
                240          250          260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 init1: 44 opt: 62 Z-score: 86.9 bits: 21.9 E(): 7.3
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (13-72:184-237)


```

                                10      20      30      40
AAD-12      ALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . : : : : :
gi+AHw-458  GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                                160      170      180      190      200
```

```

                                50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
                                : : : : :
gi+AHw-458  FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
                                210      220      230      240
```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 init1: 44 opt: 62 Z-score: 86.1 bits: 21.9 E(): 8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (13-72:206-259)

```

                                10      20      30      40
AAD-12      ALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . : : : : :
gi+AHw-158  KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                                180      190      200      210      220      230
```

```

                                50      60      70      80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
                                : : : : :
gi+AHw-158  FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
                                240      250      260
```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.9
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (15-70:29-82)

```

                                10      20      30      40
AAD-12      ALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... : : : : :
gi+AHw-117  MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
                                10      20      30      40      50      60
```

```

                                50      60      70      80
AAD-12  QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA
                                : : : : :
gi+AHw-117  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100      110
```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.9
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (15-70:29-82)

```

                10         20         30         40
AAD-12          ALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... : : : : : : : : : : : :
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                ... : : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKY
                70         80         90         100        110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.9
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (15-70:29-82)

```

                10         20         30         40
AAD-12          ALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... : : : : : : : : : : : :
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                ... : : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKY
                70         80         90         100        110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.9
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (15-70:29-82)

```

                10         20         30         40
AAD-12          ALLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                ..... : : : : : : : : : : : :
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE
                10         20         30         40         50         60

```

```

                50         60         70         80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                ... : : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKY
                70         80         90         100        110

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs- Arachis (219 aa)

initn: 43 init1: 43 opt: 60 Z-score: 84.8 bits: 21.4 E(): 9.5
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (5-36:133-160)

```

                                10      20      30
AAD-12      ALLIFPGQHLSDQITFAKRFGAIERIGGGDIV
                                : :: :...: . : :... :...
gi+AHw-221  FGLIFPGCPSTYEPAQQGRRHQSRPFRFQGQDQSQQQQDSHQK----VHRFDEGDLI
                                110      120      130      140      150

                                40      50      60      70      80
AAD-12  AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                                :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQQSRRR
                                160      170      180      190      200      210

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 44 - 123 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      2      0:+AD0-
      30      1      2:+ACo-
      32      8      8:+AD0APQAq-
      34      30     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      82
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-
      38      70
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
      40      87
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-

```

```

42      107
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
    44     149
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
    46     138
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
    48     101
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
    50     135
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AKgA9AD0APQA9-
    52     93
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
    54     72
91 :+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
   56     67
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
   58     67
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
   60     58       50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   62     28       40:+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
   64     38       32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
   66     31       25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
   68     26       20:+AD0APQA9AD0APQA9ACoAPQA9-
   70     35       16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
   72     14       12:+AD0APQA9ACoAPQ-
   74      5       10:+AD0APQ- +ACo-
   76      5        7:+AD0APQAq-
   78      5        6:+AD0AKg-
   80      4        4:+AD0AKg-
   82      1        3:+ACo-
   84      4        3:+ACoAPQ-
   86      3        2:+ACo-
   88      1        2:+ACo-          inset +AD0- represents 1 library sequences
   90      0        1:+ACo-
   92      0        1:+ACo-          :+ACo-
   94      0        1:+ACo-          :+ACo-
   96      0        1:+ACo-          :+ACo-
   98      1        0:+AD0-         +ACoAPQ-
100     1        0:+AD0-         +ACoAPQ-
102      0        0:              +ACo-
104      0        0:              +ACo-
106      0        0:              +ACo-
108      0        0:              +ACo-
110      0        0:              +ACo-
112      0        0:              +ACo-
114      0        0:              +ACo-
116      0        0:              +ACo-
```

```

118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.88930.00367+ADs- mu+AD0- 3.3122
0.189
mean+AF8-var+AD0-51.554114.639, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.178625
Kolmogorov-Smirnov statistic: 0.0326 (N+AD0-29) at 36

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.2 1.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.7 1.6
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.1 6.8
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.9 7.4
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.9 8.1
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 57 20.6 8.8
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.6 8.8
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.6 8.8
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.6 8.8
gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arac (
219) 60 21.4 9.6

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 101.2 bits: 23.2 E(): 1.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (40-69:30-56)

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
      .. ..::: ..::: ..::: ..:::
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
      10      20      30      40      50

      70      80
AAD-12 TYMPVMAQGAV

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 98.5 bits: 22.7 E(): 1.6
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (40-70:30-57)

```
      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADS
      .. .::: .:: . : .:: .:: :
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEWEPLTKK--GNL-WEVKS
      10      20      30      40      50
```

```
      70      80
AAD-12 TYMPVMAQGAV
      .
gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYTPPE
      60      70      80      90
```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 87.4 bits: 22.1 E(): 6.8
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (12-71:207-260)

```
      10      20      30      40
AAD-12 LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      .. ... .::: :: ... :
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230
```

```
      50      60      70      80
AAD-12 GTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
      ::: . . : .. .::: .::
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
      240      250      260
```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.8 bits: 21.9 E(): 7.4
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (12-71:184-237)

```
      10      20      30      40
AAD-12 LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      .. ... .::: :: ... :
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      160      170      180      190      200
```

```
      50      60      70      80
AAD-12 GTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
      ::: . . : .. .::: .::
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
      210      220      230      240
```

50 60 70 80
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAV
 :: :: :: :: :: ::
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (14-69:29-82)

```

                                10      20      30      40
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... : : : : : : : : : :
gi+AHw-400  MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                                10      20      30      40      50      60

```

```

                                50      60      70      80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
                                ... : : : : : : : :
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100     110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.4 bits: 20.6 E(): 8.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (14-69:29-82)

```

                                10      20      30      40
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... : : : : : : : : : :
gi+AHw-400  MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                                10      20      30      40      50      60

```

```

                                50      60      70      80
AAD-12  QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
                                ... : : : : : : : :
gi+AHw-400  EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100     110

```

+AD4APg-gi+AHw-22135348+AHw-gb+AHw-AAM93157.1+AHw- trypsin inhibitor +AFs-Arachis (219 aa)
 initn: 43 init1: 43 opt: 60 Z-score: 84.7 bits: 21.4 E(): 9.6
 Smith-Waterman score: 60+ADs- 34.375+ACU- identity (62.500+ACU- similar)
 in 32 aa overlap (4-35:133-160)

```

                                10      20      30
AAD-12      LLIFPGQHLSNDQQITFAKRFGAIERIGGGDIV
                                : : : : : : : : : :
gi+AHw-221  FGLIFPGCPSTYEPAQQGRRHQSQRPFRFQGDQSQQQQDSHQK---VHRFDEGDLI
                                110     120     130     140     150

```

```

                                40      50      60      70      80
AAD-12  AISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAV
                                :.
gi+AHw-221  AVPTGVAFWMYNDHDTDVVAVSLTDTNNNDNQLDQFPRFRNLAGNHEQEFLRYQQQSRRR
                                160     170     180     190     200     210

```


	opt	E ()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	2	0:+AD0-	
30	1	2:+ACo-	
32	9	8:+AD0APQAq-	
34	34	21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-	
36	76		
44	:	+	AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
-			
38	70		
72	:	+	AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
40	94		
101	:	+	AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ-			+ACo-
42	97		
123	:	+	AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ-			+AD0APQA9AD0- +ACo-
44	146		
136	:	+	AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-			
46	141		
138	:	+	AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-			
48	113		
132	:	+	AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-			+ACo-

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-  
ktup: 1
```

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po

(97) 67 23.2 1.2

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-

(96) 65 22.7 1.7

gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI (263)

63 22.0 7.2

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)

62 21.8 7.8

gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262)

62 21.8 8.5

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P

(122) 57 20.6 9.1

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)

57 20.6 9.1

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)

57 20.6 9.1

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)

57 20.6 9.1

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:

Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 101.0 bits: 23.2 E(): 1.2

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)

in 30 aa overlap (39-68:30-56)

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
      ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
      10      20      30      40      50

      70      80
AAD-12 TYMPVMAQGAVF

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:

Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 98.3 bits: 22.7 E(): 1.7

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)

in 31 aa overlap (39-69:30-57)

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
      ..  ....  ...  .  :  ...  ...  :
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK
      10      20      30      40      50

      70      80
AAD-12 TYMPVMAQGAVF

```

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)

initn: 44 initl: 44 opt: 63 Z-score: 87.0 bits: 22.0 E(): 7.2
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (11-70:207-260)

AAD-12 10 20 30 40
LIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.. : : : :
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

AAD-12 50 60 70 80
GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
: : : : : : : : : : : : : :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.4 bits: 21.8 E(): 7.8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (11-70:184-237)

AAD-12 10 20 30 40
LIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.. : : : :
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200

AAD-12 50 60 70 80
GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
: : : : : : : : : : : : : :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.7 bits: 21.8 E(): 8.5
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (11-70:206-259)

AAD-12 10 20 30 40
LIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.. : : : :
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

AAD-12 50 60 70 80
GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF

```
      ::: . . : . . . : . . . :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
              240              250              260
```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (13-68:29-82)

```

              10              20              30              40
AAD-12          LIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              . . . . . : . : . . . : . : . : . :
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
              10              20              30              40              50              60
```

```

              50              60              70              80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
              . . : : : : : : : :
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110
```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (13-68:29-82)

```

              10              20              30              40
AAD-12          LIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              . . . . . : . : . . . : . : . : . :
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
              10              20              30              40              50              60
```

```

              50              60              70              80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
              . . : : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70              80              90              100              110
```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (13-68:29-82)

```

              10              20              30              40
AAD-12          LIFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
              . . . . . : . : . . . : . : . : . :
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
              10              20              30              40              50              60
```

```

              50              60              70              80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVF
```

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	2	0:+AD0-	
30	2	2:+ACo-	
32	9	8:+AD0APQAq-	
34	27	21:+AD0APOA9AD0APOA9ACoAPOA9-	

36 82
 44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
 A9AD0-
 38 79
 72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
 +AD0APQA9-
 40 79
 101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9- +ACo-
 42 113
 123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
 44 138
 136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
 46 142
 138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
 48 116
 132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 50 113
 121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
 52 99
 106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9- +ACo-
 54 67
 91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
 +ACo-
 56 56 76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-+AD0APQ-
 +ACo-
 58 83
 62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
 A9AD0-
 60 52 50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
 62 37 40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
 64 37 32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
 66 33 25: +AD0APQA9AD0APQA9AD0APQAqAD0APQ-
 68 32 20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
 70 32 16: +AD0APQA9AD0APQAqAD0APQA9AD0APQ-
 72 10 12: +AD0APQA9ACo-
 74 5 10: +AD0APQ- +ACo-
 76 4 7: +AD0APQAq-
 78 5 6: +AD0AKg-
 80 4 4: +AD0AKg-
 82 1 3: +ACo-
 84 6 3: +ACoAPQ-
 86 2 2: +ACo-
 88 0 2: +ACo- inset +AD0- represents 1 library sequences
 90 0 1: +ACo-
 92 0 1: +ACo- :+ACo-
 94 0 1: +ACo- :+ACo-
 96 0 1: +ACo- :+ACo-

```

  98      1      0:+AD0-      +ACoAPQ-
 100      1      0:+AD0-      +ACoAPQ-
 102      0      0:          +ACo-
 104      0      0:          +ACo-
 106      0      0:          +ACo-
 108      0      0:          +ACo-
 110      0      0:          +ACo-
 112      0      0:          +ACo-
 114      0      0:          +ACo-
 116      0      0:          +ACo-
 118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.05830.00364+ADs- mu+AD0- 2.4473
0.188
mean+AF8-var+AD0-52.644514.782, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.176766
Kolmogorov-Smirnov statistic: 0.0366 (N+AD0-28) at 38

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.1      1.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.6      1.7
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0      7.2
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.8      7.8
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.8      8.6
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.6      9.2
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.6      9.2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.6      9.2
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.6      9.2

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 100.8 bits: 23.1 E(): 1.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (38-67:30-56)

```

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
      ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIK YTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVK S
      10      20      30      40      50

```


70 80
AAD-12 TYMPVMAQGAVFS

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 98.1 bits: 22.6 E(): 1.7
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (38-68:30-57)

10 20 30 40 50 60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADS
:: :. :. :. :. :. :. :. :. :. :.
gi+AHw-144 VKVTFKVEKGSDDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWELTKK--GNL-WEVKS
10 20 30 40 50

70 80
AAD-12 TYMPVMAQGAVFS

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTITYTPEE
60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 86.9 bits: 22.0 E(): 7.2
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (10-69:207-260)

10 20 30
AAD-12 IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
:: :. :. :. :. :. :. :. :. :. :.
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

40 50 60 70 80
AAD-12 GTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
::: . . : . . . :. :. :.
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.3 bits: 21.8 E(): 7.8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (10-69:184-237)

10 20 30
AAD-12 IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
:: :. :. :. :. :. :. :. :. :. :.
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200

AAD-12
IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTEKGSNEKHLAVLVKYEGDTMAEVELR

50 60 70 80
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
 ... :: : : : .: ::
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 85.1 bits: 20.6 E(): 9.2
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (12-67:29-82)

10
20
30
40

AAD-12
 IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR

.
.
.
.

gi+AHw-400
 MSMASSSSSGLLAMAVLAALFAGAWCVPKVFTFVEKGSNEKHLAVLVKYE
GDTMAEVELR

10
20
30
40
50
60

50 60 70 80
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
 .. :: : : : .: ::
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

```
+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group
II)      (122 aa)
  initn:  52 init1:  52 opt:   57 Z-score: 85.1  bits: 20.6 E():  9.2
Smith-Waterman score: 57+ADs-  26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (12-67:29-82)
```

10
20
30
40

AAD-12
 IFPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR

.
.
.
.

gi+AHw-400
 MSMASSSSSLLAMAVLAALFAGAWCVPKVFTFVEKGSNEKHLAVLVKYE
GDTMAEVELR

10
20
30
40
50
60

50 60 70 80
 AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFS
 ... :: : : : .: ::
 gi+AHw-400 EHGSEDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010
Total Scan time: 0.090 Total Display time: 0.000

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

```
+ADw-      opt          E()
   20       2           0:+AD0-
    22     0         0:              one +AD0- represents 3 library sequences
    24     0         0:
    26     0         0:
    28     1        0:+AD0-
    30     3        2:+ACo-
    32     7        8:+AD0APQAq-
    34    20       21:+AD0APQA9AD0APQA9ACo-
    36    72
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
   38    92
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQA9AD0-
   40    83
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0-      +ACo-
   42    118
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
   44    142    136:+AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
   46    135
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
   48    104
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
   50    120
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
   52    102    106:+AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
   54     62
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
   56     63
76:+AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0APOA9-      +ACo-
```

```

58      83
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9AD0-
   60    52    50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
   62    45    40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
   64    37    32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
   66    25    25:+AD0APQA9AD0APQA9AD0APQAq-
   68    27    20:+AD0APQA9AD0APQA9ACoAPQA9-
   70    30    16:+AD0APQA9AD0APQAqAD0APQA9AD0-
   72    13    12:+AD0APQA9ACoAPQ-
   74     8    10:+AD0APQA9ACo-
   76     5     7:+AD0APQAq-
   78     6     6:+AD0AKg-
   80     3     4:+AD0AKg-
   82     1     3:+ACo-
   84     6     3:+ACoAPQ-
   86     2     2:+ACo-
   88     0     2:+ACo-          inset +AD0- represents 1 library sequences
   90     0     1:+ACo-
   92     0     1:+ACo-          :+ACo-
   94     0     1:+ACo-          :+ACo-
   96     0     1:+ACo-          :+ACo-
   98     1     0:+AD0-          +ACoAPQ-
  100     1     0:+AD0-          +ACoAPQ-
  102     0     0:              +ACo-
  104     0     0:              +ACo-
  106     0     0:              +ACo-
  108     0     0:              +ACo-
  110     0     0:              +ACo-
  112     0     0:              +ACo-
  114     0     0:              +ACo-
  116     0     0:              +ACo-
  118     0     0:              +ACo-
+AD4-120    0    0:              +ACo-
  331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.13570.00374+ADs- mu+AD0- 1.9525
0.193
mean+AF8-var+AD0-52.834814.750, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.176447
Kolmogorov-Smirnov statistic: 0.0325 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.2 1.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.7 1.7
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw-pollen allergen Phl pI ( 263)
63 22.0 7.2
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw-unnamed protein produc ( 240)
62 21.8 7.8

```

10 20 30

AAD-12 FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 :. :. :.
 gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

40 50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
 :. :. :.
 gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
 product +AFs-P (240 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 86.3 bits: 21.8 E(): 7.8
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (9-68:184-237)

10 20 30
 AAD-12 FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 :. :. :.
 gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 160 170 180 190 200

40 50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
 :. :. :.
 gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
 210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
 (262 aa)
 initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.8 E(): 8.6
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (9-68:206-259)

10 20 30
 AAD-12 FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
 :. :. :.
 gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

40 50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
 :. :. :.
 gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (11-66:29-82)

10 20 30 40

```

AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                               ..... : : : . . . . : :
gi+AHw-117 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
              10          20          30          40          50          60

```

```

              50          60          70          80
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
       ... : : : : : : : :
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (11-66:29-82)

```

              10          20          30          40
AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                               ..... : : : . . . . : :
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
              10          20          30          40          50          60

```

```

              50          60          70          80
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
       ... : : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (11-66:29-82)

```

              10          20          30          40
AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                               ..... : : : . . . . : :
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELR
              10          20          30          40          50          60

```

```

              50          60          70          80
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
       ... : : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (11-66:29-82)

10 20 30 40


```

AAD-12                      FPGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                               ..... :. :. . . . :. :.
gi+AHw-400 MSMASSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
                               10      20      30      40      50      60

                               50      60      70      80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSA
                               ...  ::  :  :  :  :  :  :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                               70      80      90      100     110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:45 2010

Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 48 - 127 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      2      0:+AD0-
      30      4      2:+ACoAPQ-
      32      5      8:+AD0APQAq-
      34      22     21:+AD0APQA9AD0APQA9ACoAPQ-
      36      91
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9AD0-
      38      74
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
      40      86
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ-      +ACo-
      42      113
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-

```

inset +AD0- represents 1 library sequences

Kolmogorov-Smirnov statistic: 0.0345 (N+AD0-28) at 38

```
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.6      9.1
```

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (36-65:30-56)

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (36-66:30-57)

```

      10      20      30      40      50      60
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADS
      ..  ....  ...  .  :  ...  ...  :
gi+AHw-144  VKVTFKVEKGSDPKKLVLVDIKYTRPGDTLAEVELRQHGSEEWELTKK--GNL-WEVKS
      10      20      30      40      50

```

```

      70      80
AAD-12  TYMPVMAQGAVFSAE
      .
gi+AHw-144  SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYTPPEE
      60      70      80      90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 87.2 bits: 22.1 E(): 7
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (8-67:207-260)

```

      10      20      30
AAD-12  PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      ..  ...  .  ....  ::  ...  :
gi+AHw-390  GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230

```

```

      40      50      60      70      80
AAD-12  GTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
      :::  .  .  :  .  .  .  ....  :
gi+AHw-390  FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.5 bits: 21.8 E(): 7.6
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (8-67:184-237)

```

      10      20      30
AAD-12  PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      ..  ...  .  ....  ::  ...  :
gi+AHw-458  GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      160      170      180      190      200

```

```

      40      50      60      70      80
AAD-12  GTVRQHSAPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
      :::  .  .  :  .  .  .  ....  :
gi+AHw-458  FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
      210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.8 bits: 21.8 E(): 8.3
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (8-67:206-259)

```

                                10      20      30
AAD-12      PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . : : : : ..
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                                180      190      200      210      220      230

```

```

                                40      50      60      70      80
AAD-12      GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                                ::: . . : .. . : : : : :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
                                240      250      260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (10-65:29-82)

```

                                10      20      30      40
AAD-12      PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... . : : . . . . : :
gi+AHw-117 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                                10      20      30      40      50      60

```

```

                                50      60      70      80
AAD-12      QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                                ... : : : : : : :
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100      110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (10-65:29-82)

```

                                10      20      30      40
AAD-12      PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... . : : . . . . : :
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                                10      20      30      40      50      60

```

```

                                50      60      70      80
AAD-12      QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                                ... : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100      110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 52 init1: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (10-65:29-82)

```

                        10      20      30      40
AAD-12                PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                        ..... : : : : : : : : : : : :
gi+AHw-400 MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
                        10      20      30      40      50      60

```

```

                        50      60      70      80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                        ... : : : : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                        70      80      90      100     110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 85.2 bits: 20.6 E(): 9.1
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (10-65:29-82)

```

                        10      20      30      40
AAD-12                PGQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                        ..... : : : : : : : : : : : :
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
                        10      20      30      40      50      60

```

```

                        50      60      70      80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE
                        ... : : : : : : : : : :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                        70      80      90      100     110

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:45 2010 done: Fri Feb 5 12:55:46 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 49 - 128 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

[illegible]

```

80      2      4:+AD0AKg-
82      1      3:+ACo-
84      5      3:+ACoAPQ-
86      2      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.12710.00376+ADs- mu+AD0- 2.0908
0.194
mean+AF8-var+AD0-53.630514.904, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175133
Kolmogorov-Smirnov statistic: 0.0516 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.1      1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.6      1.8
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0      7.6
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.7      8.2
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.7      9
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.5      9.5
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
57 20.5      9.5
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
57 20.5      9.5
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.5      9.5

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

```


initn: 59 initl: 59 opt: 67 Z-score: 100.4 bits: 23.1 E(): 1.3
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (35-64:30-56)

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
      .. .. : : : : :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIK YTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
      10      20      30      40      50

```

```

      70      80
AAD-12 TYMPVMAQGAVFSAEV

```

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 97.7 bits: 22.6 E(): 1.8
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (35-65:30-57)

```

      10      20      30      40      50      60
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
      .. .. : : : : :
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
      10      20      30      40      50

```

```

      70      80
AAD-12 TYMPVMAQGAVFSAEV

```

```

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
      60      70      80      90

```

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
 +AFs-Phl (263 aa)

initn: 44 initl: 44 opt: 63 Z-score: 86.6 bits: 22.0 E(): 7.6
 Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (7-66:207-260)

```

      10      20      30
AAD-12 GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
      .. : : : : :
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
      180      190      200      210      220      230

```

```

      40      50      60      70      80
AAD-12 GTVRQHSPEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
      : : : : :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
      240      250      260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
 product +AFs-P (240 aa)

initn: 44 initl: 44 opt: 62 Z-score: 86.0 bits: 21.7 E(): 8.2
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
 in 60 aa overlap (7-66:184-237)

```

                                10      20      30
AAD-12                      GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . : : : : ..
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                                160      170      180      190      200

```

```

                                40      50      60      70      80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
                                ::: . . : .. . : : : : :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
                                210      220      230      240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
 (262 aa)

initn: 44 initl: 44 opt: 62 Z-score: 85.2 bits: 21.7 E(): 9
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (7-66:206-259)

```

                                10      20      30
AAD-12                      GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . : : : : ..
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                                180      190      200      210      220      230

```

```

                                40      50      60      70      80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
                                ::: . . : .. . : : : : :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
                                240      250      260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)

initn: 52 initl: 52 opt: 57 Z-score: 84.8 bits: 20.5 E(): 9.5
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (9-64:29-82)

```

                                10      20      30      40
AAD-12                      GQHLSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... : : . . . . : :
gi+AHw-117 MSMASSSSSSLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEEDTMAEVELR
                                10      20      30      40      50      60

```

```

                                50      60      70      80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
                                ... : : : : : : :
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
                                70      80      90      100      110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
 II) (122 aa)

50 60 70 80
 AAD-12 QHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEV
 ... :: : : : .: ::
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEP LQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 50 - 129 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	2	0:+AD0-	
30	4	2:+ACoAPQ-	
32	8	8:+AD0APQAq-	
34	30	21:+AD0APQA9AD0APQA9ACoAPQA9AD0-	
36	72		
44:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
38	108		
72:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQA9AD0APQA9AD0APQA9-			
40	88		
101:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9-			+ACo-
42	104		
123:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ-			+ACo-
44	133		
136:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-			
46	126		
138:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-			+ACo-
48	120		
132:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-			+ACo-
50	114		
121:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-			+ACo-

```

52      82
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
QA9AD0-      +ACo-
54      86
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQ- +ACo-
56      51      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      80
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9-
60      60      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
62      38      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      46      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66      24      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
68      21      20:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
70      29      16:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
72      11      12:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
74      9       10:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
76      6       7:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
78      5       6:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
80      2       4:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
82      1       3:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
84      6       3:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
86      1       2:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
88      0       2:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
90      0       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
92      0       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
94      0       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
96      1       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
98      0       0:      +ACo-
100     1       0:+AD0-      +ACoAPQ-
102     0       0:      +ACo-
104     0       0:      +ACo-
106     0       0:      +ACo-
108     0       0:      +ACo-
110     0       0:      +ACo-
112     0       0:      +ACo-
114     0       0:      +ACo-
116     0       0:      +ACo-
118     0       0:      +ACo-
+AD4-120     0       0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.07850.00366+ADs- mu+AD0- 2.4584
0.189
mean+AF8-var+AD0-54.320615.236, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.174017
Kolmogorov-Smirnov statistic: 0.0522 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)

```

10 20 30

```
AAD-12                      QHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . : : : : : : : : : : : :
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           180           190           200           210           220           230
```

```
           40           50           60           70           80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV
           : : : . . : . . . : : : : : : :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
           240           250           260
```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.6 E(): 8.6
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (6-65:184-237)

```
                               10           20           30
AAD-12                      QHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . : : : : : : : : : : : :
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           160           170           180           190           200
```

```
           40           50           60           70           80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV
           : : : . . : . . . : : : : : : :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
           210           220           230           240
```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 84.9 bits: 21.6 E(): 9.4
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (6-65:206-259)

```
                               10           20           30
AAD-12                      QHLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                               .. ... . : : : : : : : : : : : :
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           180           190           200           210           220           230
```

```
           40           50           60           70           80
AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVV
           : : : . . : . . . : : : : : : :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
           240           250           260
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010

Total Scan time: 0.090 Total Display time: 0.000

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
```

```
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
```

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

```
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

1+AD4APqA+-AAD-12: 51 - 130 80 aa - 80 aa

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	1	0:+AD0-	
26	0	0:	
28	1	0:+AD0-	
30	6	2:+ACoAPQ-	
32	5	8:+AD0APQAq-	
34	33	21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-	
36	69		
44	:	:	:
38	113	72	:
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0-			
40	82		
101	:	:	:
42	108		
123	:	:	:
44	139		
136	:	:	:
46	124		
138	:	:	:
48	109		
132	:	:	:
50	124		
121	:	:	:
52	81		
106	:	:	:
54	90		
91	:	:	:


```

56      43      76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
58      79
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9-
60      55      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      42      40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      50      32: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
66      24      25: +AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
68      19      20: +AD0APQA9AD0APQA9AD0APQA9ACo-
70      30      16: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
72      10      12: +AD0APQA9ACo-
74      9       10: +AD0APQA9ACo-
76      7       7: +AD0APQAq-
78      4       6: +AD0AKg-
80      2       4: +AD0AKg-
82      1       3: +ACo-
84      6       3: +ACoAPQ-
86      1       2: +ACo-
88      0       2: +ACo-      inset +AD0- represents 1 library sequences
90      0       1: +ACo-
92      0       1: +ACo-      : +ACo-
94      0       1: +ACo-      : +ACo-
96      1       1: +ACo-      : +ACo-
98      1       0: +AD0-      +ACoAPQ-
100     0       0:      +ACo-
102     0       0:      +ACo-
104     0       0:      +ACo-
106     0       0:      +ACo-
108     0       0:      +ACo-
110     0       0:      +ACo-
112     0       0:      +ACo-
114     0       0:      +ACo-
116     0       0:      +ACo-
118     0       0:      +ACo-
+AD4-120     0       0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.92320.00367+ADs- mu+AD0- 3.2489
0.190
mean+AF8-var+AD0-55.187515.506, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172645
Kolmogorov-Smirnov statistic: 0.0550 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.9 1.5
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.4 2.1
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 21.9 8.2

```

gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc (240)

62 21.6 8.8

gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I (262)

62 21.6 9.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:

Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 99.3 bits: 22.9 E(): 1.5

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)

in 30 aa overlap (33-62:30-56)

```

                10         20         30         40         50         60
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10         20         30         40         50

```

```

                70         80
AAD-12  TYMPVMAQGAVFSAEVVP

```

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN

60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:

Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 96.7 bits: 22.4 E(): 2.1

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)

in 31 aa overlap (33-63:30-57)

```

                10         20         30         40         50         60
AAD-12  SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADS
                ..  ....  ...  .  :  ...  ...  :
gi+AHw-144  VKVTFKVEKGSDDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
                10         20         30         40         50

```

```

                70         80
AAD-12  TYMPVMAQGAVFSAEVVP

```

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE

60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)

initn: 44 initl: 44 opt: 63 Z-score: 86.0 bits: 21.9 E(): 8.2

Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)

in 60 aa overlap (5-64:207-260)

```

                10         20         30
AAD-12  HLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                ..  ...  .  ....  ::  ...  :
gi+AHw-390  GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                180         190         200         210         220         230

```

40 50 60 70 80

AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP

```

      ::: . . : . . . . .
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
           240       250       260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)

initn: 44 initl: 44 opt: 62 Z-score: 85.4 bits: 21.6 E(): 8.8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (5-64:184-237)

```

                                10      20      30
AAD-12                        HLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . . . . .
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           160       170       180       190       200

```

```

      40      50      60      70      80
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP
      ::: . . : . . . . .
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
           210       220       230       240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)

initn: 44 initl: 44 opt: 62 Z-score: 84.7 bits: 21.6 E(): 9.7
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (5-64:206-259)

```

                                10      20      30
AAD-12                        HLSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. ... . . . . .
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
           180       190       200       210       220       230

```

```

      40      50      60      70      80
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVP
      ::: . . : . . . . .
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
           240       250       260

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 52 - 131 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	2	0:+AD0-	
30	5	2:+ACoAPQ-	
32	6	8:+AD0APQAq-	
34	30	21:+AD0APQA9AD0APQA9ACoAPQA9AD0-	
36	79		
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ			
A9-			
38	86		
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ			
A9AD0APQ-			
40	78		
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
Q- +ACo-			
42	121		
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-			
44	142		
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-			
46	139	138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-	
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A			
D0APQAqAD0-			
48	107		
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-			
50	129		
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-			
52	82		
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0- +ACo-			
54	80		
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ			
-+AD0- +ACo-			
56	51	76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-	
+ACo-			
58	71		
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-			
60	52	50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-	

```

62      43      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      42      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      29      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      21      20:+AD0APQA9AD0APQA9ACo-
70      30      16:+AD0APQA9AD0APQAqAD0APQA9AD0-
72      11      12:+AD0APQA9ACo-
74      9       10:+AD0APQA9ACo-
76      8       7:+AD0APQAq-
78      3       6:+AD0AKg-
80      3       4:+AD0AKg-
82      1       3:+ACo-
84      5       3:+ACoAPQ-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.81550.00372+ADs- mu+AD0- 3.7393
0.192
mean+AF8-var+AD0-53.665915.199, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175075
Kolmogorov-Smirnov statistic: 0.0414 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 23.0      1.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.5      1.9
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 22.0      7.5
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.7      8.1
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.7      8.9
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  57 20.5      9.8

```

```

                                10      20      30
AAD-12                        LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                :: :.. . .::: ::  ...      ::
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
                   180      190      200      210      220      230

```

```

          40          50          60          70          80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSAE VVPA
          :::  . .      : . . . . : : : : :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
          240          250          260

```

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.0 bits: 21.7 E(): 8.1
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (4-63:184-237)

```

                                10          20          30
AAD-12                                LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. :.. . : : : : : : : : :
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
          160          170          180          190          200

```

```

          40          50          60          70          80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSAE VVPA
          :::  . .      : . . . . : : : : :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
          210          220          230          240

```

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.3 bits: 21.7 E(): 8.9
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (4-63:206-259)

```

                                10          20          30
AAD-12                                LSNDQQITFAKRFGAIERIGGGDIVAISNVKAD
                                .. :.. . : : : : : : : : :
gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
          180          190          200          210          220          230

```

```

          40          50          60          70          80
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGA VFSAE VVPA
          :::  . .      : . . . . : : : : :
gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
          240          250          260

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 52 initl: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.8
Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
in 56 aa overlap (6-61:29-82)

```

                                10          20          30
AAD-12                                LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                ..... : : : : : : : : : :
gi+AHw-117 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELR
          10          20          30          40          50          60

```

```

      40          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVPA
      ...  ::  :  :  :  :  :  :
gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (6-61:29-82)

```

                                10          20          30
AAD-12                          LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                .....  .  .  .  .  .  .  .  .  .  .  .  .
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
              10          20          30          40          50          60

```

```

      40          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVPA
      ...  ::  :  :  :  :  :  :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (6-61:29-82)

```

                                10          20          30
AAD-12                          LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                .....  .  .  .  .  .  .  .  .  .  .  .  .
gi+AHw-400 MSMASSSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
              10          20          30          40          50          60

```

```

      40          50          60          70          80
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVPA
      ...  ::  :  :  :  :  :  :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 52 init1: 52 opt: 57 Z-score: 84.6 bits: 20.5 E(): 9.8
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (6-61:29-82)

```

                                10          20          30
AAD-12                          LSNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR
                                .....  .  .  .  .  .  .  .  .  .  .  .  .
gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
              10          20          30          40          50          60

```



```

      40          50          60          70          80
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPA
      ...  ::  :  :  :  :  :  :
gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
              70          80          90          100          110
  
```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 53 - 132 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      5      2:+ACoAPQ-
      32      7      8:+AD0APQAq-
      34      28     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      83
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-
      38      72
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
      40      87     101:+AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      42      120
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
      44      136
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
  
```

```
mean+AF8-var+AD0-53.664315.282, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
```

Kolmogorov-Smirnov statistic: 0.0333 (N+AD0-28) at 36

Scan time: 0.090

```
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
57 20.5      9.7
```

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (31-60:30-56)

AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW HADS
 10 20 30 40 50 60
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKS
 10 20 30 40 50

gi+AHw-126 AKPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (31-61:30-57)

AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
 : . .::: .::: . : : :::

gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEWELTKK--GNL-WEVKS
10 20 30 40 50

70 80
AAD-12 TYMPVMAQGAVFSAEVVPAV

gi+AHw-144 SKPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYPPEE
60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)

initn: 44 initl: 44 opt: 63 Z-score: 86.8 bits: 22.0 E(): 7.4
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (3-62:207-260)

10 20 30
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.. : : : :
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230

40 50 60 70 80
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV
: : : : : : : : : : : : : :
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 86.2 bits: 21.8 E(): 8
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (3-62:184-237)

10 20 30
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.. : : : :
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200

40 50 60 70 80
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV
: : : : : : : : : : : : : :
gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
(262 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.5 bits: 21.8 E(): 8.7
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (3-62:206-259)

10 20 30
AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKAD
.. : : : :
.. : : : :

gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

40 50 60 70 80
 AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV
 ::: . . :

gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
 240 250 260

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.7
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (5-60:29-82)

10 20 30
 AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR

 gi+AHw-117 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV
 ... :: : : : .: ::
 gi+AHw-117 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
 II) (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.7
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (5-60:29-82)

10 20 30
 AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR

 gi+AHw-400 MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELR
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAV
 ... :: : : : .: ::
 gi+AHw-400 EHGSDEWVAMTKGEGG--VWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATY
 70 80 90 100 110

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
 II) (122 aa)
 initn: 52 initl: 52 opt: 57 Z-score: 84.7 bits: 20.5 E(): 9.7
 Smith-Waterman score: 57+ADs- 26.786+ACU- identity (55.357+ACU- similar)
 in 56 aa overlap (5-60:29-82)

10 20 30
 AAD-12 SNDQQITFAKRFGAIERIGGGDIVAISNVKADGTVR

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	

```

26      0      0:
28      2      0:+AD0-
30      5      2:+ACoAPQ-
32     12      8:+AD0APQAqAD0-
34     29     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
36     85
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQ-
38     75
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
40     81
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9-      +ACo-
42     130
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
44     135
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
46     133
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
48     117
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
50     111
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
52     73
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
54     95
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQ-
56     58     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58     80
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9-
60     43     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62     32     40:+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
64     56     32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
66     22     25:+AD0APQA9AD0APQA9AD0APQAq-
68     20     20:+AD0APQA9AD0APQA9ACo-
70     34     16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
72     7      12:+AD0APQA9ACo-
74     9      10:+AD0APQA9ACo-
76     9      7:+AD0APQAq-
78     3      6:+AD0AKg-
80     3      4:+AD0AKg-
82     1      3:+ACo-
84     6      3:+ACoAPQ-
86     1      2:+ACo-
88     0      2:+ACo-      inset +AD0- represents 1 library sequence

```

```

90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.86120.00374+ADs- mu+AD0- 3.6807
0.194
mean+AF8-var+AD0-54.053015.372, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.174447
Kolmogorov-Smirnov statistic: 0.0414 (N+AD0-28) at 38

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.9 1.4
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.4 2
gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI ( 263)
63 21.9 7.9
gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein produc ( 240)
62 21.7 8.6
gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I ( 262)
62 21.7 9.4

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 99.7 bits: 22.9 E(): 1.4
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (30-59:30-56)

10 20 30 40 50 60
AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
.. .. : : : : :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
10 20 30 40 50

70 80
AAD-12 YMPVMAQGAVFSAEVVPAVG

```


gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 97.0 bits: 22.4 E(): 2
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (30-60:30-57)

10 20 30 40 50 60
AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADST
:: :: . : :: ... ::
gi+AHw-144 VKVTFKVEKGSDDPKKLVLVDIKYTRPGDTLAEVELRQHGSEWEPLTKK--GNL-WEVKSS
10 20 30 40 50
70 80
AAD-12 YMPVMAQGAVFSAEVVPAVG

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-3901094+AHw-emb+AHw-CAA81613.1+AHw- pollen allergen Phl pI
+AFs-Phl (263 aa)
initn: 44 initl: 44 opt: 63 Z-score: 86.3 bits: 21.9 E(): 7.9
Smith-Waterman score: 63+ADs- 26.667+ACU- identity (56.667+ACU- similar)
in 60 aa overlap (2-61:207-260)

10 20 30
AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKAD
:: :: ... ::
gi+AHw-390 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
180 190 200 210 220 230
40 50 60 70 80
AAD-12 GTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
::: . . : . . . :::::
gi+AHw-390 FTVRYTTEGGTKGEAKDVIPE-GWKADTAYESK
240 250 260

+AD4APg-gi+AHw-45823012+AHw-emb+AHw-CAG24374.1+AHw- unnamed protein
product +AFs-P (240 aa)
initn: 44 initl: 44 opt: 62 Z-score: 85.6 bits: 21.7 E(): 8.6
Smith-Waterman score: 62+ADs- 26.667+ACU- identity (55.000+ACU- similar)
in 60 aa overlap (2-61:184-237)

10 20 30
AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKAD
:: :: ... ::
gi+AHw-458 GSNPNYLALLVKFVAGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
160 170 180 190 200
40 50 60 70 80
AAD-12 GTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
::: . . : . . . :::::

gi+AHw-458 FTVRYTTEGGTKGEAKDVIPE-GWKADTCYESK
 210 220 230 240

+AD4APg-gi+AHw-1582250+AHw-prf+AHwAfA-2118271A allergen PhI p I
 (262 aa)

initn: 44 init1: 44 opt: 62 Z-score: 84.9 bits: 21.7 E(): 9.4
 Smith-Waterman score: 62+ADs- 26.667+ACU- identity (56.667+ACU- similar)
 in 60 aa overlap (2-61:206-259)

AAD-12 NDQQITFAKRFGAIERIGGGDIVAISNVKAD
 :.::: :: . . . :.
 gi+AHw-158 KGSNPNYLALLVKFSGDGDVVAVDIKEKGKDKWIALKESWGAIWRIDTPEVL-----KGP
 180 190 200 210 220 230

AAD-12 GTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVG
 ::: . . : . . .::: . . .
 gi+AHw-158 FTVRYTTEGGTKARAKDVIPE-GWKADTAYESK
 240 250 260

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 55 - 134 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	2	0:+AD0-	
30	7	2:+ACoAPQA9-	
32	11	8:+AD0APQAqAD0-	
34	37	21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-	

36 85
44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQ-
38 81
72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
40 97
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACo-
42 130
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
44 148
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
46 104
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
48 123 132: +AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
50 86
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-
52 74
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
54 71
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
56 75
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58 72
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
60 64
50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
62 58 40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64 35 32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
66 29 25: +AD0APQA9AD0APQA9AD0APQAqAD0-
68 25 20: +AD0APQA9AD0APQA9ACoAPQA9-
70 8 16: +AD0APQA9- +ACo-
72 18 12: +AD0APQA9ACoAPQ- +AD0-
74 10 10: +AD0APQA9ACo-
76 5 7: +AD0APQAq-
78 3 6: +AD0AKg-
80 4 4: +AD0AKg-
82 4 3: +ACoAPQ-
84 1 3: +ACo-
86 0 2: +ACo-
88 0 2: +ACo- inset +AD0- represents 1 library sequences
90 0 1: +ACo-
92 0 1: +ACo- :+ACo-
94 1 1: +ACo- :+ACo-

```

96      1      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.09890.00385+ADs- mu+AD0- 3.1493
0.199
mean+AF8-var+AD0-60.104217.939, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.165433
Kolmogorov-Smirnov statistic: 0.0623 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)   67 22.3      2.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)   65 21.9      3

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 96.4 bits: 22.3 E(): 2.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (29-58:30-56)

          10          20          30          40          50
AAD-12  DQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
          ..  .....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
          10          20          30          40          50

          60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGG

          60          70          80          90
gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 93.9 bits: 21.9 E(): 3
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (29-59:30-57)

```

```

      10      20      30      40      50
AAD-12  DQQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPEWDDMMKVIVGNMAWHADST
      . . . . .
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEWEPLTKK--GNL-WEVKSS
      10      20      30      40      50

      60      70      80
AAD-12  YMPVMAQGAVFSAEVPVAVGG

      60      70      80      90
gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYPPEE

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:46 2010 done: Fri Feb 5 12:55:46 2010
Total Scan time: 0.090 Total Display time: 0.000

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 56 - 135 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

inset +AD0- represents 1 library sequences

```

116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.72280.00378+ADs- mu+AD0- 4.9785
0.196
mean+AF8-var+AD0-57.859817.442, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.168611
Kolmogorov-Smirnov statistic: 0.0729 (N+AD0-26) at 42

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.5 2

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.0 2.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 97.1 bits: 22.5 E(): 2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (28-57:30-56)

```

          10          20          30          40          50
AAD-12  QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
          ..  .....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
          10          20          30          40          50

```

```

          60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGGR

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 94.6 bits: 22.0 E(): 2.7
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (28-58:30-57)

```

          10          20          30          40          50
AAD-12  QQITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
          ..  .....  ...  .  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
          10          20          30          40          50

```

```

          60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGGR

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE

```

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

  1+AD4APgA+-AAD-12: 57  - 136 80 aa - 80 aa
vs  /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

opt      E()
+ADw- 20      2      0:+AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      1      0:+AD0-
26      1      0:+AD0-
28      2      0:+AD0-
30      7      2:+ACoAPQA9-
32      15     8:+AD0APQAqAD0APQ-
34      27     21:+AD0APQA9AD0APQA9ACoAPQA9-
36      90
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ
A9AD0APQA9-
38      89
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQA9-
40      89
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9- +ACo-
42      147
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
44      124
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
46      148      138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqA
D0APQA9AD0-

```


inset +AD0- represents 1 library sequences

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po

(97) 67 22.4 2

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-

(96) 65 21.9 2.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:

Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 96.8 bits: 22.4 E(): 2

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)

in 30 aa overlap (27-56:30-56)

```

                10      20      30      40      50
AAD-12  QITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10      20      30      40      50
```

```

                60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRT
```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60      70      80      90
```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 94.3 bits: 21.9 E(): 2.8

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)

in 31 aa overlap (27-57:30-57)

```

                10      20      30      40      50
AAD-12  QITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                10      20      30      40      50
```

```

                60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRT
```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60      70      80      90
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:47 2010

Total Scan time: 0.090 Total Display time: 0.000

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

opt      E()
+ADw- 20      2      0:+AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      1      0:+AD0-
26      1      0:+AD0-
28      4      0:+AD0APQ-
30      6      2:+ACoAPQ-
32      21     8:+AD0APQAqAD0APQA9AD0-
34      27     21:+AD0APQA9AD0APQA9ACoAPQA9-
36      71     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
+AD0APQA9AD0APQA9AD0APQA9-
38      82
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0-
40      94
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ- +ACo-
42      180
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA
9AD0APQA9AD0APQA9-
44      127
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
46      136
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
48      98
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9- +ACo-
50      80
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9- +ACo-
52      65
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
54      76
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
- +ACo-

```

```

56      51      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      90
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9AD0APQA9-
60      44      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62      58      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      54      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
66      30      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      19      20:+AD0APQA9AD0APQA9ACo-
70      16      16:+AD0APQA9AD0APQAq-
72      5       12:+AD0APQ- +ACo-
74      15      10:+AD0APQA9ACoAPQ-
76      4       7:+AD0APQAq-
78      5       6:+AD0AKg-
80      7       4:+AD0AKgA9-
82      0       3:+ACo-
84      0       3:+ACo-
86      0       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.25130.00364+ADs- mu+AD0- 7.6333
0.189
mean+AF8-var+AD0-55.200316.529, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172625
Kolmogorov-Smirnov statistic: 0.0791 (N+AD0-25) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.6 1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.1 2.6

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 97.6 bits: 22.6 E(): 1.9
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (26-55:30-56)

```

      10      20      30      40      50
AAD-12  ITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
              .. .:..: .:..: .:..: .:..: .:..:
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
              10      20      30      40      50

```

```

      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTC

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 95.0 bits: 22.1 E(): 2.6
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (26-56:30-57)

```

      10      20      30      40      50
AAD-12  ITFAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
              .. .:..: .:..: .:..: .:..: .:..:
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSS
              10      20      30      40      50

```

```

      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTC

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
      60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:47 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 59 - 138 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      4      0:+AD0APQ-
      30      6      2:+ACoAPQ-
      32      21     8:+AD0APQAqAD0APQA9AD0-
      34      32     21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      36      73
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
      38      79
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
      40      102
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACo-
      42      180
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA
9AD0APQA9AD0APQA9-
      44      133     136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
Co-
      46      125
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      48      93
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
      50      81
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9- +ACo-
      52      68
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-+AD0APQ-
+ACo-
      54      70
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      56      65
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      58      79
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9-
      60      45     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      62      56     40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
      64      47     32:+AD0APQA9AD0APQA9AD0-+AD0APQA9ACoAPQA9AD0APQA9-
      66      31     25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
      68      22     20:+AD0APQA9AD0APQA9ACoAPQ-

```

```

70      16      16:+AD0APQA9AD0APQAq-
72      9      12:+AD0APQA9ACo-
74      17      10:+AD0APQA9ACoAPQA9-
76      3      7:+AD0- +ACo-
78      5      6:+AD0AKg-
80      3      4:+AD0AKg-
82      0      3:+ACo-
84      0      3:+ACo-
86      0      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.27160.00364+ADs- mu+AD0- 7.6296
0.189
mean+AF8-var+AD0-55.037316.386, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172880
Kolmogorov-Smirnov statistic: 0.0872 (N+AD0-25) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 22.5      1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.0      2.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 97.5 bits: 22.5 E(): 1.9
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (25-54:30-56)

          10          20          30          40          50
AAD-12      TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
          ..  ....  ...  :  :  ...  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
          10          20          30          40          50

```

60 70 80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCF

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 94.9 bits: 22.0 E(): 2.6
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (25-55:30-57)

10 20 30 40 50
AAD-12 TFAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
:: :
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGSEEW EPLTKK--GNL-WEVKSS
10 20 30 40 50

60 70 80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCF

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:47 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 60 - 139 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	1	0:+AD0-	
26	0	0:	
28	2	0:+AD0-	

inset +AD0- represents 1 library sequences

```

92      0      1:+ACo-      :+ACo-
94      1      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.39000.00367+ADs- mu+AD0- 7.0780
0.190
mean+AF8-var+AD0-55.449216.399, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.172237
Kolmogorov-Smirnov statistic: 0.0906 (N+AD0-25) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 22.5      1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.0      2.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 97.4 bits: 22.5 E(): 1.9
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (24-53:30-56)

          10          20          30          40          50
AAD-12      FAKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
          ..  ....  ...  :  :  ...  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
          10          20          30          40          50

          60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFA

gi+AHw-126  KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
          60          70          80          90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 94.7 bits: 22.0 E(): 2.7

```

Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (24-54:30-57)

```

                10      20      30      40      50
AAD-12      FAKRFGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEWEPLTKK--GNL-WEVKSS
                10      20      30      40      50

                60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFA

gi+AHw-144  KPLTGPFNFRFMSKGGMRNVFDEVIPATFKIGTTTYPTEE
                60      70      80      90

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:47 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 61 - 140 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      1      0:+AD0-
      26      0      0:
      28      4      0:+AD0APQ-
      30      7      2:+ACoAPQA9-
      32      25     8:+AD0APQAqAD0APQA9AD0APQA9-
      34      29    21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      75
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
      38      77
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
-

```

inset +AD0- represents 1 library sequences

```

110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.39400.00368+ADs- mu+AD0- 7.1676
0.190
mean+AF8-var+AD0-56.738116.423, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.170270
Kolmogorov-Smirnov statistic: 0.0866 (N+AD0-26) at 42

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.4 2.1

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 21.9 2.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 96.7 bits: 22.4 E(): 2.1
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (23-52:30-56)

```

              10      20      30      40      50
AAD-12      AKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
              ..  ....  ...  :  :  ...  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
              10      20      30      40      50

              60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFAD

gi+AHw-126  KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
              60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 94.1 bits: 21.9 E(): 2.9
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (23-53:30-57)

```

              10      20      30      40      50
AAD-12      AKRFGAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
              ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
              10      20      30      40      50

              60      70      80

```

```

opt      E ()
+ADw- 20      2      0:+AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      1      0:+AD0-
26      0      0:
28      4      0:+AD0APQ-
30      7      2:+ACoAPQA9-
32      24      8:+AD0APQAqAD0APQA9AD0APQ-
34      25      21:+AD0APQA9AD0APQA9ACoAPQA9-
36      82
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-
38      80
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
40      110
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0-
42      169      123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9A
D0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
44      127
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-

```

inset +AD0- represents 1 library sequences

Kolmogorov-Smirnov statistic: 0.0893 (N+AD0-26) at 42

(96) 65 21.8 3

in 30 aa overlap (22-51:30-56)

in 31 aa overlap (22-52:30-57)

```
80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
```


[illegible]

```

54      57      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      88
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0APQA9-
58      59
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60      45      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62      50      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64      38      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66      29      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      25      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      10      16:+AD0APQA9AD0- +ACo-
72      19      12:+AD0APQA9ACoAPQA9AD0-
74      5       10:+AD0APQ- +ACo-
76      3       7:+AD0- +ACo-
78      5       6:+AD0AKg-
80      3       4:+AD0AKg-
82      6       3:+ACoAPQ-
84      0       3:+ACo-
86      0       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.01420.0036+ADs- mu+AD0- 9.0770
0.186
mean+AF8-var+AD0-56.567716.446, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.170526
Kolmogorov-Smirnov statistic: 0.0893 (N+AD0-26) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.100
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.4 2.1
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 21.9 3

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 96.5 bits: 22.4 E(): 2.1
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (21-50:30-56)

```

                10      20      30      40      50
AAD-12          RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                10      20      30      40      50

```

```

                60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMR

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 93.9 bits: 21.9 E(): 3
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (21-51:30-57)

```

                10      20      30      40      50
AAD-12          RFGAIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                ..  ....  ...  :  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                10      20      30      40      50

```

```

                60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMR

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:47 2010 done: Fri Feb 5 12:55:48 2010
 Total Scan time: 0.100 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 64 - 143 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	1	0:+AD0-	
26	1	0:+AD0-	
28	2	0:+AD0-	
30	4	2:+ACoAPQ-	
32	27	8:+AD0APQAqAD0APQA9AD0APQA9-	
34	28	21:+AD0APQA9AD0APQA9ACoAPQA9AD0-	
36	69		
44:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
38	88		
72:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQA9-			
40	114		
101:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q-			+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
42	167		
123:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA			
9AD0APQ-			
44	133		
136:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-			
46	130		
138:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-			
48	106	132:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-			+ACo-
50	75		
121:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-			
52	77		
106:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q-			+ACo-
54	57	91:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-			
56	90		
76:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0APQA9-			
58	59		
62:			+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60	41	50:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
62	51	40:	+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64	39	32:	+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66	33	25:	+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68	25	20:	+AD0APQA9AD0APQA9ACoAPQA9-


```

        60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
        60          70          80          90

```

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
  initn: 55 initl: 55 opt: 65 Z-score: 93.8 bits: 21.9 E(): 3
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (20-50:30-57)

```

```

        10          20          30          40          50
AAD-12      FGAIERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
              .. .:.:. .:. . : .:. .:. .:
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWELTKK--GNL-WEVKSS
        10          20          30          40          50

```

```

        60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
        60          70          80          90

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
Total Scan time: 0.090 Total Display time: 0.010

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 65 - 144 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      3      0:+AD0-

```

one +AD0- represents 4 library sequences

```

30      4      2: +ACo-
32     25     8: +AD0AKgA9AD0APQA9AD0-
34     26    21: +AD0APQA9AD0APQAqAD0-
36     66    44: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
38     87
72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
40    108
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQAqAD0-
42    185
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
44    129
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACo-
46    132
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9- +ACo-
48    110
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0- +ACo-
50     70    121: +AD0APQA9AD0APQA9AD0APQ- +AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
52     76    106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
54     54     91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
56     86
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
58     64    62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60     41    50: +AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
62     51    40: +AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
64     42    32: +AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66     30    25: +AD0APQA9AD0APQA9ACoAPQ-
68     23    20: +AD0APQA9AD0AKgA9-
70     12    16: +AD0APQA9ACo-
72     19    12: +AD0APQAqAD0APQ-
74      4    10: +AD0- +ACo-
76      4      7: +AD0AKg-
78      5      6: +AD0AKg-
80      3      4: +ACo-
82      6      3: +ACoAPQ-
84      0      3: +ACo-
86      0      2: +ACo-
88      0      2: +ACo-
90      0      1: +ACo-
92      0      1: +ACo-
94      1      1: +ACo-
96      1      1: +ACo-
98      0      0:
100     0      0:
102     0      0:
104     0      0:
106     0      0:
108     0      0:

```

inset +AD0- represents 1 library sequences

```

110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.06520.00358+ADs- mu+AD0- 8.7658
0.185
mean+AF8-var+AD0-56.579316.473, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.170508
Kolmogorov-Smirnov statistic: 0.0920 (N+AD0-26) at 42

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.4 2.1

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 21.9 2.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

initn: 59 initl: 59 opt: 67 Z-score: 96.6 bits: 22.4 E(): 2.1
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (19-48:30-56)

```

                        10      20      30      40
AAD-12      GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                        ..  ....  ...  :  :  ...  ...  :
gi+AHw-126  TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                        10      20      30      40      50

                        50      60      70      80
AAD-12  YMPVMAQQGAVFSAEVVPAVGGRTCFADMRAA

gi+AHw-126  KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                        60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 94.0 bits: 21.9 E(): 2.9
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (19-49:30-57)

```

                        10      20      30      40
AAD-12      GAIERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
                        ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144  VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                        10      20      30      40      50

                        50      60      70      80

```



```

48      107
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9-      +ACo-
   50     65    121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
   52     73    106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
   54     56    91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
   56     80    76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
   58     64    62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
   60     41    50:+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
   62     49    40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
   64     43    32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   66     35    25:+AD0APQA9AD0APQA9ACoAPQA9-
   68     23    20:+AD0APQA9AD0AKgA9-
   70     12    16:+AD0APQA9ACo-
   72     19    12:+AD0APQAqAD0APQ-
   74       4    10:+AD0- +ACo-
   76       4     7:+AD0AKg-
   78       5     6:+AD0AKg-
   80       3     4:+ACo-
   82       6     3:+ACoAPQ-
   84       0     3:+ACo-
   86       0     2:+ACo-
   88       0     2:+ACo-          inset +AD0- represents 1 library sequences
   90       0     1:+ACo-
   92       0     1:+ACo-           :+ACo-
   94       1     1:+ACo-           :+ACo-
   96       1     1:+ACo-           :+ACo-
   98       0     0:               +ACo-
  100       0     0:               +ACo-
  102       0     0:               +ACo-
  104       0     0:               +ACo-
  106       0     0:               +ACo-
  108       0     0:               +ACo-
  110       0     0:               +ACo-
  112       0     0:               +ACo-
  114       0     0:               +ACo-
  116       0     0:               +ACo-
  118       0     0:               +ACo-
+AD4-120    0     0:             +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.03900.00354+ADs- mu+AD0- 8.8605
0.184
mean+AF8-var+AD0-56.813616.737, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.170156
Kolmogorov-Smirnov statistic: 0.0927 (N+AD0-26) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                               opt bits E(1471)
```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
 (97) 67 22.4 2.1
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 65 21.9 2.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 96.6 bits: 22.4 E(): 2.1
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (18-47:30-56)

	10	20	30	40
AAD-12	AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST			
		 : : .. . : .
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQH
	10	20	30	40
				50

	50	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY			

gi+AHw-126	KPLTGPMNFR	FLSKGGMKN	VFDEVIPTA	FTVGKTYT
	60	70	80	90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 94.0 bits: 21.9 E(): 2.9
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (18-48:30-57)

	10	20	30	40
AAD-12	AIERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST			
		 : : .. . : .
gi+AHw-144	VKVTFKVEKGS	DPKKLVLD	IKYTRPGD	TLAEVELRQH
	10	20	30	40
				50

	50	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY			

gi+AHw-144	KPLTGPFNFR	FMSKGGMRN	VFDEVIPTA	FKIGTTYT
	60	70	80	90

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

	opt	E ()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	0	0:	
26	1	0:+AD0-	
28	3	0:+AD0-	
30	3	2:+ACo-	
32	20	8:+AD0AKgA9AD0APQ-	
34	30	21:+AD0APQA9AD0APQAqAD0APQ-	
36	69	44:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-	
38	80	72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-	
40	120		
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-			
42	187		
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-			
44	134		
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-			
46	132		
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-			
48	110		
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-			
50	72	121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-	
+ACo-			
52	64	106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-	
+ACo-			
54	61	91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-	
56	79	76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-	
58	66	62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-	
60	36	50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-	
62	47	40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-	
64	43	32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-	
66	34	25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-	
68	21	20:+AD0APQA9AD0AKgA9-	
70	13	16:+AD0APQA9ACo-	
72	18	12:+AD0APQAqAD0APQ-	
74	6	10:+AD0APQAq-	
76	4	7:+AD0AKg-	
78	5	6:+AD0AKg-	
80	3	4:+ACo-	

```

82      6      3:+ACoAPQ-
84      0      3:+ACo-
86      0      2:+ACo-
88      0      2:+ACo-      inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      1      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.11830.00359+ADs- mu+AD0- 8.5000
0.186
mean+AF8-var+AD0-55.900016.510, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.171541
Kolmogorov-Smirnov statistic: 0.0968 (N+AD0-26) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.4 2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 21.9 2.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 96.9 bits: 22.4 E(): 2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (17-46:30-56)

      10      20      30      40
AAD-12      IERIGGGDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST
      .. ..:.. :. : : :. :. :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
      10      20      30      40      50

      50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
      60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 94.3 bits: 21.9 E(): 2.8
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (17-47:30-57)

```

                                10      20      30      40
AAD-12      IERIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                :.  .:..:  :.  . :  :.  :.  :.
gi+AHw-144  VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEW EPLTKK--GNL-WEVKSS
                                10      20      30      40      50

                                50      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGR TCFADMRAAYD

gi+AHw-144  KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGT TTYTPEE
                                60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 68 - 147 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	4	0:+AD0APQ-	
30	3	2:+ACo-	
32	18	8:+AD0APQAqAD0APQA9-	
34	35	21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-	
36	59	44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-	

```

38      87
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQ-
   40    127
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
   42    175
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
   44    145
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
   46    127
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
   48    104
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
   50     70    121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
   52     75
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
   54     53     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
   56     81
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9-
   58     67
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
   60     43     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
   62     43     40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
   64     38     32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
   66     37     25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
   68     21     20:+AD0APQA9AD0APQA9ACo-
   70     13     16:+AD0APQA9AD0APQAq-
   72     13     12:+AD0APQA9ACoAPQ-
   74     10     10:+AD0APQA9ACo-
   76       5       7:+AD0APQAq-
   78       2       6:+AD0AKg-
   80       4       4:+AD0AKg-
   82       4       3:+ACoAPQ-
   84       4       3:+ACoAPQ-
   86       0       2:+ACo-
   88       0       2:+ACo- inset +AD0- represents 1 library sequences
   90       0       1:+ACo-
   92       0       1:+ACo- :+ACo-
   94       1       1:+ACo- :+ACo-
   96       1       1:+ACo- :+ACo-
   98       0       0: +ACo-
  100       0       0: +ACo-
  102       0       0: +ACo-
  104       0       0: +ACo-

```

10
20
30
40

AAD-12
 ERIGGGDIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST

:
:::
:::
:
:
:::
:::
:::

gi+AHw-144
 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEWEPLTKK--GNL-WEVKSS

10
20
30
40
50


```

opt      E ()
+ADw- 20      2      0: +AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      3      0: +AD0-
30      4      2: +ACoAPQ-
32      19     8: +AD0APQAqAD0APQA9AD0-
34      32     21: +AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
36      66
44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0-
38      81
72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
40      126
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
42      174     123: +AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
44      139
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-

```

```
mean+AF8-var+AD0-54.217916.231, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
```

Lambda+AD0- 0.174182

Kolmogorov-Smirnov statistic: 0.0969 (N+AD0-27) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 22.5 1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 22.0 2.6

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 97.5 bits: 22.5 E(): 1.9
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (15-44:30-56)

	10	20	30	40
AAD-12	RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST			
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
	10	20	30	40

	50	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL			

gi+AHw-126	KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
	60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 94.9 bits: 22.0 E(): 2.6
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (15-45:30-57)

	10	20	30	40
AAD-12	RIGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST			
gi+AHw-144	VKVTFKVEKGS	DPKKLVLD	IKYTRPGD	TAEVELRQHGSEEWEPMTK--KGNL-WEVKSS
	10	20	30	40

	50	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL			

gi+AHw-144	KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
	60 70 80 90

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-

```

opt      E()
+ADw-   20       2       0:+AD0-
    22        0       0:               one +AD0- represents 3 library sequences
    24         0       0:
    26         0       0:
    28         3       0:+AD0-
    30         4       2:+ACoAPQ-
    32        19       8:+AD0APQAqAD0APQA9AD0-
    34        35      21:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
    36        67
44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
    38         81
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9-
    40        129
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
    42        180
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA
9AD0APQA9AD0APQA9-
    44        140
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
    46        133
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
    48         98
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ-+AD0-             +ACo-
    50         71
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+Aco-
    52         74
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+Aco-
```

```

54      55      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58      57      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-+AD0APQA9AD0APQA9-
+ACo-
60      47      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62      42      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      40      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      33      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
68      23      20:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
70      12      16:+AD0APQA9AD0- +ACo-
72      14      12:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
74      10      10:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
76      6       7:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
78      2       6:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
80      2       4:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
82      5       3:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
84      3       3:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
86      0       2:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
88      0       2:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
90      0       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
92      0       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
94      1       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
96      1       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
98      0       0:      +ACo-
100     0       0:      +ACo-
102     0       0:      +ACo-
104     0       0:      +ACo-
106     0       0:      +ACo-
108     0       0:      +ACo-
110     0       0:      +ACo-
112     0       0:      +ACo-
114     0       0:      +ACo-
116     0       0:      +ACo-
118     0       0:      +ACo-
+AD4-120    0       0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.85670.0036+ADs- mu+AD0- 9.9306
0.186
mean+AF8-var+AD0-54.351216.130, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.173968
Kolmogorov-Smirnov statistic: 0.1031 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 22.5 1.9
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 22.0 2.7

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 97.3 bits: 22.5 E(): 1.9
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (14-43:30-56)

```

                                10      20      30      40
AAD-12                      IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                :.  .:.:.  :.  .  :  :.  :.  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIK YTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

                                50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 94.6 bits: 22.0 E(): 2.7
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (14-44:30-57)

```

                                10      20      30      40
AAD-12                      IGGGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                :.  .:.:.  :.  .  :  :.  :.  :
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSS
                                10      20      30      40      50

                                50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGT TYTPEE
                                60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:48 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 71 - 150 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

opt      E()
+ADw- 20    2      0:+AD0-
   22     0       0:          one +AD0- represents 3 library sequences
   24     0       0:
   26     0       0:
   28     4       0:+AD0APQ-
   30     3       2:+ACo-
   32    20       8:+AD0APQAqAD0APQA9AD0-
   34    29      21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
   36    58     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
   38    87
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ
A9AD0APQ-
   40    101
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9-+AD0APQA9ACo-
   42    173
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA
9AD0APQA9AD0-
   44    147
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
   46    118
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-        +ACo-
   48    121
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-   +ACo-
   50     86
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ-            +ACo-
   52     75
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
   54     61
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
   56     59      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
   58     85      62:+AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
   60     41      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
   62     33      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
   64     53      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
   66     21      25:+AD0APQA9AD0APQA9AD0-   +ACo-
   68     32      20:+AD0APQA9AD0APQA9ACoAPOA9AD0APO-

```

```

70      15      16:+AD0APQA9AD0APQAq-
72      6      12:+AD0APQ- +ACo-
74      21      10:+AD0APQ-+AD0AKgA9AD0APQ-
76      4      7:+AD0APQAq-
78      3      6:+AD0AKg-
80      3      4:+AD0AKg-
82      2      3:+ACo-
84      6      3:+ACoAPQ-
86      0      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120 0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.52430.00364+ADs- mu+AD0- 6.0564
0.187
mean+AF8-var+AD0-53.128716.237, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.175958
Kolmogorov-Smirnov statistic: 0.0786 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 22.8      1.6
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 22.3      2.2
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)  57 20.3      9
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 20.5      9.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  58 20.5      9.5
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 20.5      9.5
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 20.5      9.5

```



```

          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
          :.  .:  :.  .  :  :  :.  :  :.  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFVKVGTTRYKPE
          60          70          80          90

```

```

          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDE
          ..  ::  :.  .  .  :  .  .  :.
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDVVPEKYTIGATYAPEE
          90          100          110          120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 84.9 bits: 20.5 E(): 9.5
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (13-71:55-107)

```

                                10      20      30      40
AAD-12      GGGDIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400  WCVPKVTFTEVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
                                ..  ::  ..  .  :  ..  :  :
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:48 2010 done: Fri Feb 5 12:55:49 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 72 - 151 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      3      0:+AD0-
      30      2      2:+ACo-
      32      18     8:+AD0AKgA9AD0APQ-
      34      25    21:+AD0APQA9AD0APQAqAD0-
      36      63    44:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
      38      77    72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
      40      94   101:+AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-

```

inset +AD0- represents 1 library sequences

Kolmogorov-Smirnov statistic: 0.0689 (N+AD0-28) at 42

Scan time: 0.090

```

The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)      67 23.1      1.2
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-P
( 96)      65 22.6      1.8
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)      57 20.5      7.6
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 20.8      7.9
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)     58 20.8      7.9
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 20.8      7.9
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 20.8      7.9
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419)      64 22.5      8.3

```

```
+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
  initn: 59 initl: 59 opt: 67 Z-score: 100.7 bits: 23.1 E(): 1.2
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (12-41:30-56)
```

```

                                10      20      30      40
AAD-12      GGDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126  TKVDLTVEKGS DAKTLVLN I KYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50
                                50      60      70      80
AAD-12      YMPVMAQGAVFSAE VVPAVGGRTCFADMR AAYDALDEA
                                50      60      70      80
gi+AHw-126  KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                60      70      80      90

```

```
+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
  initn: 55 initl: 55 opt: 65 Z-score: 98.0 bits: 22.6 E(): 1.8
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (12-42:30-57)
```

10 20 30 40
AAD-12 GGDIVAI SNVKADGTVROHSPA EWDDMMKVIVGNMAWHADST

```

                                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGS DPKKLVL D I KYTRPGDTLAEVELRQH GSEEW EPLTKK--GNL-WEVKSS
                                10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTTYTP EE
                    60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 86.5 bits: 20.5 E(): 7.6
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (12-73:31-86)

```

                                10      20      30      40
AAD-12  GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-126 AAPVEFTVEKGSDEKNLALS I KYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA
                    ..  .:  ..  .  :  :  :  :  :  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGT TYKPE
                    60      70      80      90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 86.3 bits: 20.8 E(): 7.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (12-70:55-107)

```

                                10      20      30      40
AAD-12  GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-400 WCVPKVTF TVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                    50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA
                    ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVP EKYTIGATYAPEE
                    90      100      110      120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 86.3 bits: 20.8 E(): 7.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (12-70:55-107)

```

                                10      20      30      40
AAD-12  GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS

```

```

                                ..  ....  ::  :  :  :  :  :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                    50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA

```

```

                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 86.3 bits: 20.8 E(): 7.9
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (12-70:55-107)

```

                                10      20      30      40
AAD-12  GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                    50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA

```

```

                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 86.3 bits: 20.8 E(): 7.9
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (12-70:55-107)

```

                                10      20      30      40
AAD-12  GGDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                    50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA

```

```

                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)

initn: 39 init1: 39 opt: 64 Z-score: 85.8 bits: 22.5 E(): 8.3
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (11-69:89-149)

```

                                10      20      30
AAD-12  GGDIVAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA

```

```

gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPAWKNK--KIWL-QFAQLT
          60          70          80          90          100          110
          40          50          60          70          80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA
          : . : . . : . : . : : :
gi+AHw-114 DFNLMGTGVIDGQGQGWAGQCKVVGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
          120          130          140          150          160          170
gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
          180          190          200          210          220          230

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:49 2010 done: Fri Feb 5 12:55:49 2010
Total Scan time: 0.090 Total Display time: 0.010

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-l2: 73 - 152 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are: opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 67 25.4 0.25
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 65 24.8 0.38
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
(97) 57 22.4 2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
58 22.6 2.2
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 58 22.6 2.2
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
58 22.6 2.2
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
58 22.6 2.2
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
64 24.1 2.7
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
59 22.8 3.1
gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
(514) 64 24.1 3.5
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.3 3.7
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
(379) 61 23.2 4.5
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
56 22.0 4.6
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
(158) 55 21.7 5.6
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.4 7
gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor (279)
57 22.1 7.2
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
53 21.1 7.6
gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
(379) 58 22.3 8.4
gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
58 22.3 8.4
gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (386)
58 22.3 8.6
+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 59 init1: 59 opt: 67 Z-score: 113.1 bits: 25.4 E(): 0.25
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (11-40:30-56)

	10	20	30	40
AAD-12	GDIVAISNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADST			

```

                                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNLIK YTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
           60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 109.9 bits: 24.8 E(): 0.38
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (11-41:30-57)

```

                                10      20      30      40
AAD-12  GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  ....  ...  :  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
           60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 96.8 bits: 22.4 E(): 2
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (11-72:31-86)

```

                                10      20      30      40
AAD-12  GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-126 AAPVEFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT

```

```

                                ..  ..  ..  .  :  :  ..  :  ..  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGT TYKPE
           60      70      80      90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (11-69:55-107)

```

                                10      20      30      40
AAD-12  GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS

```

```

                                ..  ....  ::  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                                ..  ::  ..  .  .  :  ..  :  :

```

```

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (11-69:55-107)

```

                                10      20      30      40
AAD-12                                GDIVAIISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (11-69:55-107)

```

                                10      20      30      40
AAD-12                                GDIVAIISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (11-69:55-107)

```

                                10      20      30      40
AAD-12                                GDIVAIISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS

```

```
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYEgDTMAEVELREHGSDewVAMTKGEGG--VWTFDS
              30          40          50          60          70          80
```

```
50          60          70          80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
      ..  ::  ..  .  .  :  ..  :  ..
```

```
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90          100          110          120
```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-
Chamaecy (419 aa)

initn: 39 initl: 39 opt: 64 Z-score: 94.6 bits: 24.1 E(): 2.7
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (10-68:89-149)

```
10          20          30
AAD-12          GDIVAIISNVKADGT-VRQHSPAewDDMMKVIVGNMAWHA
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
              60          70          80          90          100          110
```

```
40          50          60          70          80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-114 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
              120          130          140          150          160          170
```

```
gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
              180          190          200          210          220          230
```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)

initn: 36 initl: 36 opt: 59 Z-score: 93.5 bits: 22.8 E(): 3.1
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (11-72:31-86)

```
10          20          30          40
AAD-12          GDIVAIISNVKADGTVRQHSPAewDDMMKVIVGNMAWHAADS
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-109 EAPVTFTVEKGSDEKNLALSIIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
              10          20          30          40          50
```

```
50          60          70          80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMKNVFDDVVVPADFKVGTTYKPEEAAAASASRRRSSEVFQF
              60          70          80          90          100          110
```

```
gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLD RFFFDGLEIIYKIFKMMFQ
              120          130          140          150          160          170
```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
Full+AD0-Poly (514 aa)

initn: 39 initl: 39 opt: 64 Z-score: 92.7 bits: 24.1 E(): 3.5
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (10-68:119-179)

```

                                10      20      30
AAD-12      GDIVAI SNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : :
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
          90      100      110      120      130      140

          40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
          : . : . : : : : : : : : :
gi+AHw-476 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
          150      160      170      180      190      200

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
          210      220      230      240      250      260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 92.1 bits: 22.3 E(): 3.7
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (34-62:23-50)

```

          10      20      30      40      50      60
AAD-12 VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA DSTYMPVMAQGAVFSAEVVPAVGGR
                                .. : : : : : : : : : :
gi+AHw-444      MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGV
              10      20      30      40      50

          70      80
AAD-12 TCFADMRAAYDALDEAT

gi+AHw-444 GTIKKISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADG
          60      70      80      90      100      110

```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
 max+AF0- (379 aa)

initn: 49 initl: 49 opt: 61 Z-score: 90.6 bits: 23.2 E(): 4.5
 Smith-Waterman score: 61+ADs- 20.779+ACU- identity (61.039+ACU- similar)
 in 77 aa overlap (4-79:120-194)

```

                                10      20      30
AAD-12      GDIVAI SNVKADGTVRQHSPA EWDDMMKVIVGN
                                : : : : : : : : : :
gi+AHw-309 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKMKMKKEQYSCDHPPASWDWRKKGVITQ
          90      100      110      120      130      140

          40      50      60      70      80
AAD-12 MAWHAD-STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
          . . . . : : : : : : : : : :
gi+AHw-309 VKYQGGCGSGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFE
          150      160      170      180      190      200

```

gi+AHw-309 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
210 220 230 240 250 260

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 90.5 bits: 22.0 E(): 4.6
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (38-62:27-50)

10 20 30 40 50 60
AAD-12 NVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCF
::: .: .: .: : : : :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIK
10 20 30 40 50
70 80
AAD-12 DMRAAYDALDEAT

gi+AHw-165 KITFGEQSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSIL
60 70 80 90 100 110

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 initl: 39 opt: 55 Z-score: 89.0 bits: 21.7 E(): 5.6
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (19-46:114-147)

10 20 30 40
AAD-12 GDIVAI SNVKADGTVRQHSPAEDDDMMKVIV----GNMAWHA--DSTY
:::: .: .: .: : : : :
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
90 100 110 120 130 140
50 60 70 80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
:::
gi+AHw-250 APVLDFVFSTLKNEL
150

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 initl: 52 opt: 54 Z-score: 87.2 bits: 21.4 E(): 7
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (34-62:23-50)

10 20 30 40 50 60
AAD-12 VAISNVKADGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGR
.. :: : : : : : : : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDGGV
10 20 30 40 50
70 80
AAD-12 TCFADMRAAYDALDEAT

gi+AHw-444 GTIKKISFGEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVSADG
60 70 80 90 100 110

+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor
+AFs-Tr (279 aa)

initn: 57 initl: 57 opt: 57 Z-score: 87.0 bits: 22.1 E(): 7.2
Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
in 55 aa overlap (9-63:225-279)

AAD-12 10 20 30
GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
: : :
gi+AHw-106 IMQQEQQEQRQGVQILVPLSQQQVQGGLVQGGQIIQPQQPAQLE VIRSSVLQTLATMC
200 210 220 230 240 250

AAD-12 40 50 60 70 80
DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
. : . . : . : . : . : . :
gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
260 270

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)

initn: 53 initl: 53 opt: 53 Z-score: 86.6 bits: 21.1 E(): 7.6
Smith-Waterman score: 53+ADs- 26.667+ACU- identity (66.667+ACU- similar)
in 30 aa overlap (40-69:5-34)

AAD-12 10 20 30 40 50 60
KADGTVRQHSPA EWDDMMKVIVGNMAWHA DSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
: . : . . : . : . : . : . : . : . :
gi+AHw-189 MASKSSITPLLLAAVLASVF AAAAATGQYCYAGM
10 20 30

AAD-12 70 80
RAAYDALDEAT

gi+AHw-189 GLPSNPLEGCREYVAQQTCGV TIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFIG
40 50 60 70 80 90

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)

initn: 49 initl: 49 opt: 58 Z-score: 85.7 bits: 22.3 E(): 8.4
Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
in 77 aa overlap (4-79:120-194)

AAD-12 10 20 30
GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGN
: . : . . : . : . : . : . : . : . :
gi+AHw-129 LGLNKFADITPQEF SKKY LQAPKDVSQQIKMANKMKMKKEQYSCDHPPASWDWRKKGVITQ
90 100 110 120 130 140

AAD-12 40 50 60 70 80
MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT


```

      . . . . .      : : : . . . . . : : . . . . . : : : :
gi+AHw-129 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
      150      160      170      180      190      200

```

```

gi+AHw-129 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
      210      220      230      240      250      260

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vacuola (379 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 85.7 bits: 22.3 E(): 8.4
 Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
 in 77 aa overlap (4-79:120-194)

```

                                10      20      30
AAD-12                        GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGN
                                . : . . . : . . : : : : : . . .
gi+AHw-119 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQ
      90      100      110      120      130      140

```

```

      40      50      60      70      80
AAD-12 MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
      . . . . .      : : : . . . . . : : . . . . . : : : :
gi+AHw-119 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
      150      160      170      180      190      200

```

```

gi+AHw-119 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
      210      220      230      240      250      260

```

+AD4APg-gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosum+AF0- (386 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 85.6 bits: 22.3 E(): 8.6
 Smith-Waterman score: 58+ADs- 25.000+ACU- identity (58.333+ACU- similar)
 in 48 aa overlap (7-54:262-309)

```

                                10      20      30
AAD-12                        GDIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
                                . : . : : . : : . . . . .
gi+AHw-169 ATRLAQEDPAFSSIKSLDYKQMLLSLGTGTNSEFDKTYTAQEAAKWGPLRWMLAIQQMT
      240      250      260      270      280      290

```

```

      40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
      . : : : : . . : : :
gi+AHw-169 NAASSYMTDYYISTVFAQRHSSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
      300      310      320      330      340      350

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:49 2010 done: Fri Feb 5 12:55:49 2010

Total Scan time: 0.090 Total Display time: 0.010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

60      45      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62      43      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      70
32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
66      31      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68      30      20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
70      38      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0-
72      21      12:+AD0APQA9ACoAPQA9AD0-
74      17      10:+AD0APQA9ACoAPQA9-
76      19      7:+AD0APQAqAD0APQA9AD0-
78      11      6:+AD0AKgA9AD0-
80      6       4:+AD0AKg-
82      5       3:+ACoAPQ-
84      14      3:+ACoAPQA9AD0APQ-
86      5       2:+ACoAPQ-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      3       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      2       1:+ACo-          :+ACoAPQ-
96      5       1:+ACoAPQ-      :+ACoAPQA9AD0APQ-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     1       0:+AD0-          +ACoAPQ-
112     1       0:+AD0-          +ACoAPQ-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.55780.00328+ADs- mu+AD0- 2.9452
0.169
mean+AF8-var+AD0-37.2076 9.431, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.210261
Kolmogorov-Smirnov statistic: 0.0944 (N+AD0-29) at 60

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.5 0.25
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.9 0.37
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.4 2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.7 2.1
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.7 2.1

```

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 58 22.7 2.1
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 58 22.7 2.1
 gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
 64 24.2 2.5
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 59 22.9 3
 gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0- (514)
 64 24.2 3.2
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.3 3.6
 gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0- (379)
 61 23.3 4.3
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 56 22.0 4.4
 gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-G1 (158)
 55 21.7 5.4
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.4 6.8
 gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor (279)
 57 22.2 6.9
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
 53 21.1 7.4
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34 (379)
 58 22.4 8
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 58 22.4 8
 gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (386)
 58 22.4 8.2

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 113.3 bits: 25.5 E(): 0.25
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (10-39:30-56)

	10	20	30	40
AAD-12	DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST			
	:. .:.. :. : : :. :. :			
gi+AHw-126	TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA			
	10	20	30	40
	50	60	70	80
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR			
gi+AHw-126	KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN			
	60	70	80	90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 110.1 bits: 24.9 E(): 0.37
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (10-40:30-57)

```

                        10      20      30      40
AAD-12                DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADST
                        ..  ....  ::  .  :  ::  ...  :.
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEWELTKK--GNL-WEVKSS
                        10      20      30      40      50

```

```

                        50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                        60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 96.9 bits: 22.4 E(): 2
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (10-71:31-86)

```

                        10      20      30
AAD-12                DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                        ..  ....  ::  .  :  ::  ...  :
gi+AHw-126 AAPVEFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                        10      20      30      40      50

```

```

                        40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                        ..  .:  ..  .  :  :  ::  :  ::  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
                        60      70      80      90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (10-68:55-107)

```

                        10      20      30
AAD-12                DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                        ..  ....  ::  :  :  :  :  :  ::
gi+AHw-400 WCVPKVTFTEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                        30      40      50      60      70      80

```

```

                        40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                        ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPKYTIGATYAPEE
                        90      100      110      120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (10-68:55-107)

```

                                10      20      30
AAD-12      DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-117  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

      40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      ..  ::  ..  .  .  :  ..  :  :
gi+AHw-117  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
      90      100      110      120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (10-68:55-107)

```

                                10      20      30
AAD-12      DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

      40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
      90      100      110      120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (10-68:55-107)

```

                                10      20      30
AAD-12      DIVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :
gi+AHw-400  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

      40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
      90      100      110      120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)
 initn: 39 initl: 39 opt: 64 Z-score: 95.1 bits: 24.2 E(): 2.5
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (9-67:89-149)

```

                                10      20      30
AAD-12      DIVAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : :
gi+AHw-114  ASAVLVVPANKKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                60      70      80      90      100     110

```

```

                                40      50      60      70      80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                                : . : . : : : : : : :
gi+AHw-114  DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                120     130     140     150     160     170

```

```

gi+AHw-114  FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                180     190     200     210     220     230

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)
initn: 36 initl: 36 opt: 59 Z-score: 93.8 bits: 22.9 E(): 3
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (10-71:31-86)

```

                                10      20      30
AAD-12      DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                : . : : : : : : : : :
gi+AHw-109  EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                                : . : : : : : : : : :
gi+AHw-109  DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAAASASRRRSSEVFQF
                                60      70      80      90      100     110

```

```

gi+AHw-109  LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTDRFFFDGLEIIYKIFKMMFQ
                                120     130     140     150     160     170

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
Full+AD0-Poly (514 aa)
initn: 39 initl: 39 opt: 64 Z-score: 93.2 bits: 24.2 E(): 3.2
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (9-67:119-179)

```

                                10      20      30
AAD-12      DIVAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : :
gi+AHw-476  ASAVLLVPANKKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                90      100     110     120     130     140

```

```

                                40      50      60      70      80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                                : . : . : : : : : : :
gi+AHw-476  DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                150     160     170     180     190     200

```

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
 210 220 230 240 250 260

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 92.4 bits: 22.3 E(): 3.6
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (33-61:23-50)

10 20 30 40 50 60
 AAD-12 VAISNVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGR
 .. .:: : .: .: .: .::: . :
 gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIPQSVKSAEIVEGDGGV
 10 20 30 40 50

70 80
 AAD-12 TCFADMRAAYDALDEATR

gi+AHw-444 GTIKKISFGEESHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADG
 60 70 80 90 100 110

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
 max+AF0- (379 aa)

initn: 49 initl: 49 opt: 61 Z-score: 91.1 bits: 23.3 E(): 4.3
 Smith-Waterman score: 61+ADs- 20.779+ACU- identity (61.039+ACU- similar)
 in 77 aa overlap (3-78:120-194)

10 20 30
 AAD-12 DIVAISNVKADGTVRQHSPAEDDMMKVIVGN
 .: .::: . : : : : : : :
 gi+AHw-309 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKMKKEQYSCDHPPASWDWRKKGVITQ
 90 100 110 120 130 140

40 50 60 70 80
 AAD-12 MAWHAD-STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
 : : : : : : : : : : : :
 gi+AHw-309 VKYQGGCGSGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFE
 150 160 170 180 190 200

gi+AHw-309 WVLEHGGIATDDDPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
 210 220 230 240 250 260

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)

initn: 55 initl: 55 opt: 56 Z-score: 90.7 bits: 22.0 E(): 4.4
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (37-61:27-50)

10 20 30 40 50 60
 AAD-12 NVKADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFA
 .: .: .: .: .: .: .: .:
 gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIK
 10 20 30 40 50

70 80
AAD-12 DMRAAYDALDEATR

gi+AHw-165 KITFGEQSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSIL
60 70 80 90 100 110

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 initl: 39 opt: 55 Z-score: 89.2 bits: 21.7 E(): 5.4
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (18-45:114-147)

10 20 30 40
AAD-12 DIVAISNVKADGTVRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
::: : : : : : : : : :
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
90 100 110 120 130 140

50 60 70 80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
:::
gi+AHw-250 APVLDFVFSTLKNEL
150

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 initl: 52 opt: 54 Z-score: 87.5 bits: 21.4 E(): 6.8
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (33-61:23-50)

10 20 30 40 50 60
AAD-12 VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHDSTYMPVMAQGAVFSAEVVPAVGGGR
.. : : : : : : : : : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDGGV
10 20 30 40 50

70 80
AAD-12 TCFADMRAAYDALDEATR

gi+AHw-444 GTIKISFGEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVSADG
60 70 80 90 100 110

+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor
+AFs-Tr (279 aa)
initn: 57 initl: 57 opt: 57 Z-score: 87.3 bits: 22.2 E(): 6.9
Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
in 55 aa overlap (8-62:225-279)

10 20 30
AAD-12 DIVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
: : : : : : : : : :
gi+AHw-106 IMQQEQEQRQGVQILVPLSQQQQVGQGLTVQGQGIQPPQPAQLE VIRSSSVLQTLATMC
200 210 220 230 240 250

```

      40      50      60      70      80
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      .   :   .   .   :   .:   .:   .:
gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
      260      270

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 53 initl: 53 opt: 53 Z-score: 86.8 bits: 21.1 E(): 7.4
Smith-Waterman score: 53+ADs- 26.667+ACU- identity (66.667+ACU- similar)
in 30 aa overlap (39-68:5-34)

```

      10      20      30      40      50      60
AAD-12 KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
      .:   .:   .:   .:   .:   .:   .:   .:
gi+AHw-189 MASKSSITPLLLAAVLASVF AAAAATGQYCYAGM
      10      20      30

```

```

      70      80
AAD-12 RAA YDALDEATR

gi+AHw-189 GLPSNPLEGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIG
      40      50      60      70      80      90

```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)
initn: 49 initl: 49 opt: 58 Z-score: 86.2 bits: 22.4 E(): 8
Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
in 77 aa overlap (3-78:120-194)

```

      10      20      30
AAD-12 DIVAISNVKADGTVRQHSPA EWDDMMKVIVGN
      .:   .:   .:   .:   .:   .:   .:   .:
gi+AHw-129 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKMKMKKEQYSCDHPPASWDWRKKGVITQ
      90      100      110      120      130      140

```

```

      40      50      60      70      80
AAD-12 MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      .   .   .   .   .   .   .   .   .   .   .   .
gi+AHw-129 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
      150      160      170      180      190      200

gi+AHw-129 WVLEHGGIATDDDYPIRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
      210      220      230      240      250      260

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
initn: 49 initl: 49 opt: 58 Z-score: 86.2 bits: 22.4 E(): 8
Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
in 77 aa overlap (3-78:120-194)

```

      10      20      30
AAD-12 DIVAISNVKADGTVRQHSPA EWDDMMKVIVGN

```

```

      .: .:.: . .: :: :
gi+AHw-119 LGLNKFADITPQEFSSKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQ
      90      100      110      120      130      140

```

```

      40      50      60      70      80
AAD-12 MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      . . . . . : :. . . . . :. . . . . : :. . . . .
gi+AHw-119 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
      150      160      170      180      190      200

```

```

gi+AHw-119 WVLEHGGIATDDDDYPYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAIL
      210      220      230      240      250      260

```

+AD4APg-gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum
tuberosum+AF0- (386 aa)
initn: 58 initl: 58 opt: 58 Z-score: 86.0 bits: 22.4 E(): 8.2
Smith-Waterman score: 58+ADs- 25.000+ACU- identity (58.333+ACU- similar)
in 48 aa overlap (6-53:262-309)

```

      10      20      30
AAD-12 DIVAISNVKADGTVRQHSPAEWDDMMKVIVGNMAW
      .: .: : . :. . . . .
gi+AHw-169 ATRLAQEDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAQEAAKWGPLRWMLAIQQMT
      240      250      260      270      280      290

```

```

      40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
      .: :.:.: . .:.:.:
gi+AHw-169 NAASSYMTDYYISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
      300      310      320      330      340      350

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:49 2010 done: Fri Feb 5 12:55:49 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 75 - 154 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

[illegible]

```

102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      1      0:+AD0-      +ACoAPQ-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.61550.00328+ADs- mu+AD0- 2.7599
0.170
mean+AF8-var+AD0-38.0417 9.711, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.207943
Kolmogorov-Smirnov statistic: 0.0991 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.3 0.27
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.7 0.41
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.3 2.2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.6 2.3
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419) 64 24.1 2.8
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
59 22.7 3.3
gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
( 514) 64 24.0 3.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.2 3.9
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 61 23.2 4.7
gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (
386) 61 23.2 4.8
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 21.9 4.8
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
( 158) 55 21.6 5.8
gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product +AFs- (
386) 60 22.9 5.9

```

gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum tuberosu (386) 60 22.9 5.9
gi+AHw-158517845+AHw-sp+AHw-P15476.2+AHw-PATB1+AF8-SOLTU RecName: Full (386) 59 22.6 7.2
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.3 7.3
gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor (279) 57 22.1 7.5
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 53 21.0 7.9
gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379) 58 22.3 8.7
gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34 (379) 58 22.3 8.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
initn: 59 initl: 59 opt: 67 Z-score: 112.5 bits: 25.3 E(): 0.27
Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
in 30 aa overlap (9-38:30-56)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  .:.:.  .:.  . :  .:.  .:.  :
gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                60      70      80      90
```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 109.4 bits: 24.7 E(): 0.41
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (9-39:30-57)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  .:.:.  .:.  . :  .:.  .:.  ..
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEPMTK--GNL-WEVKSS
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                                60      70      80      90
```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 96.3 bits: 22.3 E(): 2.2

Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (9-70:31-86)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-126 AAPVEFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50
```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                ..  ::  ..  .  :  :  :  :  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTITYKPE
                                60      70      80      90
```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 95.8 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (9-67:55-107)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80
```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                ..  ::  ..  .  :  :  :  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVP EKYTIGATYAPEE
                                90      100      110      120
```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-Polle (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 95.8 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (9-67:55-107)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80
```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                ..  ::  ..  .  :  :  :  :  :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVP EKYTIGATYAPEE
                                90      100      110      120
```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 95.8 bits: 22.6 E(): 2.3

Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (9-67:55-107)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 95.8 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (9-67:55-107)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs- Chamaecy (419 aa)

initn: 39 initl: 39 opt: 64 Z-score: 94.3 bits: 24.1 E(): 2.8
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (8-66:89-149)

```

                                10      20      30
AAD-12                        IVAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                :  :  :  :  :  :  :  :  :  :
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                60      70      80      90      100     110

```

```

                                40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                :  .  :  .  :  :  :  :  :
gi+AHw-114 DFNLMGTGVIDGQGQWQWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                120     130     140     150     160     170

```

```

                                180     190     200     210     220     230
gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN

```



```

initn: 36 initl: 36 opt: 59 Z-score: 93.1 bits: 22.7 E(): 3.3
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (9-70:31-86)

```

```

      40          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
      . . . . . : . . . . . : . . . . . :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMARNVFVDVVPADFKVGTTYKPEEAAASASRRRSSEVFQF
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
Full+AD0-Poly (514 aa)
initn: 39 initl: 39 opt: 64 Z-score: 92.5 bits: 24.0 E(): 3.6
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (8-66:119-179)

40 50 60 70 80
 AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
 : . : . . : . : . : : :
 gi+AHw-476 DFNLMTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
 150 160 170 180 190 200

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 initl: 55 opt: 57 Z-score: 91.7 bits: 22.2 E(): 3.9
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (32-60:23-50)

AAD-12 VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVP AVGG R
gi+AHw-444 MGVFTYADESTS VIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGV

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (36-60;27-50)

```

      10      20      30      40      50      60
AAD-12 NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFA
      ... .. : : : : : :
gi+AHw-165 MGVFTHENEITS AIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIK
      10      20      30      40      50
```

```

      70      80
AAD-12 DMRAAYDALDEATRA

gi+AHw-165 KITFGEQSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSIL
      60      70      80      90      100      110
```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 initl: 39 opt: 55 Z-score: 88.6 bits: 21.6 E(): 5.8
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (17-44:114-147)

```

      10      20      30      40
AAD-12 IVAISNVKADGTVRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
      .... : : : : : :
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
      90      100      110      120      130      140
```

```

      50      60      70      80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFA DMRAAYDALDEATRA
      ...
gi+AHw-250 APVLDFVFSTLKNEL
      150
```

+AD4APg-gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product
+AFs-Sola (386 aa)
initn: 60 initl: 60 opt: 60 Z-score: 88.6 bits: 22.9 E(): 5.9
Smith-Waterman score: 60+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (5-80:262-337)

```

      10      20      30
AAD-12 IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
      . : . : : . : : . . . .
gi+AHw-215 ATRLAQEDPAFSSIKSLDYQM LLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQMT
      240      250      260      270      280      290
```

```

      40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFA DMRAAYDALDEATRA
      . : : : . . : : . : : :
gi+AHw-215 NAASSYMTDYYISTVFQARHSQNNYLRVQENALNGTTTEMDDASEANMELLVQVGETLLK
      300      310      320      330      340      350
```

```

gi+AHw-215 KPVS KDSPET YEEALKRFAKLLSDRKKLRANKASH
      360      370      380
```

+AD4APg-gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum
tuberosum+AF0- (386 aa)
initn: 60 initl: 60 opt: 60 Z-score: 88.6 bits: 22.9 E(): 5.9

Smith-Waterman score: 60+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (5-80:262-337)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
                                .: . : : . :. . . . .
gi+AHw-215 ATRLAQDDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAK WGPLRWMLAIQQMT
                                240      250      260      270      280      290

                                40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                .: .: . . . . . .: . . . :. :. :.
gi+AHw-215 NAASSYMTDYYISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
                                300      310      320      330      340      350

gi+AHw-215 KPVS KDSPET YEEALKRFAKLLSDRKKLRANKASH
                                360      370      380

```

+AD4APg-gi+AHw-158517845+AHw-sp+AHw-P15476.2+AHw-PATB1+AF8-SOLTU RecName:
Full+AD0-Pat (386 aa)
initn: 59 initl: 59 opt: 59 Z-score: 87.0 bits: 22.6 E(): 7.2
Smith-Waterman score: 59+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (5-80:262-337)

```

                                10      20      30
AAD-12                        IVAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
                                .: . : : . :. . . . .
gi+AHw-158 ATRLAQEDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAK WGPLRWMLAIQQLT
                                240      250      260      270      280      290

                                40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
                                .: .: . . . . . .: . . . :. :. :.
gi+AHw-158 NAASSYMTDYYISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
                                300      310      320      330      340      350

gi+AHw-158 KPVS KDSPET YEEALKRFAKLLSNRKKLRANKASY
                                360      370      380

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 initl: 52 opt: 54 Z-score: 86.9 bits: 21.3 E(): 7.3
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (32-60:23-50)

```

                                10      20      30      40      50      60
AAD-12 VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGR
                                .. :. : :. :. :. :. :. :.
gi+AHw-444      MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDGGV
                                10      20      30      40      50

                                70      80
AAD-12 TCFADMRAAYDALDEATRA

```

40
50
60
70
80
 AAD-12 MAWHADSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
 :..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	1	0:+AD0-	

[illegible]

```

108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      1      0:+AD0-      +ACoAPQ-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.71290.00328+ADs- mu+AD0- 2.2319
0.169
mean+AF8-var+AD0-37.9027 9.671, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.208324
Kolmogorov-Smirnov statistic: 0.0997 (N+AD0-29) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.4 0.26
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.8 0.4
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.4 2.1
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.6 2.3
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419) 64 24.1 2.8
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
59 22.8 3.2
gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
( 514) 64 24.0 3.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.2 3.8
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 61 23.2 4.7
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 21.9 4.7
gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (
386) 61 23.2 4.8
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
( 158) 55 21.6 5.7
gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product +AFs- (
386) 60 22.9 5.9
gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum tuberosu (
386) 60 22.9 5.9

```


gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.3 7.2
 gi+AHw-158517845+AHw-sp+AHw-P15476.2+AHw-PATB1+AF8-SOLTU RecName: Full (386)
 59 22.6 7.2
 gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor (279)
 57 22.1 7.5
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
 53 21.0 7.8
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 58 22.3 8.7
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34 (379)
 58 22.3 8.7

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 init1: 59 opt: 67 Z-score: 112.8 bits: 25.4 E(): 0.26
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (8-37:30-56)

	10	20	30	
AAD-12	VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST			
	:	:	:	:
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
	10	20	30	40 50

	40	50	60	70	80
AAD-12	YMPVMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRAL				

gi+AHw-126	KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
	60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 init1: 55 opt: 65 Z-score: 109.6 bits: 24.8 E(): 0.4
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (8-38:30-57)

	10	20	30	
AAD-12	VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST			
	:	:	:	:
gi+AHw-144	VKVTFKVEKGS	DPKKLVLDIKYTRPGD	TLAEVELRQHGSEEWEPMTK--GNL-WEVKSS	
	10	20	30	40 50

	40	50	60	70	80
AAD-12	YMPVMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRAL				

gi+AHw-144	KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
	60 70 80 90

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 36 init1: 36 opt: 57 Z-score: 96.5 bits: 22.4 E(): 2.1
 Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
 in 62 aa overlap (8-69:31-86)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-126  AAPVEFTVEKGSDEKNLALS I KYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                ..  ..  ..  .  :  :  ::  :  ..  :
gi+AHw-126  DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
                                60      70      80      90

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (8-66:55-107)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  ::
gi+AHw-400  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                ..  ::  ..  .  :  ..  :  ..
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100      110      120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (8-66:55-107)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  ::
gi+AHw-117  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                ..  ::  ..  .  :  ..  :  ..
gi+AHw-117  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100      110      120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (8-66:55-107)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400  WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (8-66:55-107)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400  WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs- Chamaecy (419 aa)
 initn: 39 initl: 39 opt: 64 Z-score: 94.3 bits: 24.1 E(): 2.8
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (7-65:89-149)

```

                                10      20      30
AAD-12      VAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                :  ::  :  :  :  :  :  :  :
gi+AHw-114  ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                60      70      80      90      100     110

```

```

                                40      50      60      70      80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                :  :  .  :  :  :  :  :  :
gi+AHw-114  DFNLMGTGVIDGQGQWQWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                120     130     140     150     160     170

```

```

                                180     190     200     210     220     230
gi+AHw-114  FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
 (196 aa)

initn: 36 initl: 36 opt: 59 Z-score: 93.2 bits: 22.8 E(): 3.2
 Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
 in 62 aa overlap (8-69:31-86)

```

                                10      20      30
AAD-12      VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-109  EAPVTFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                ..  .:  .:  .  :  :  ::  ....  :
gi+AHw-109  DK-PL--KGP-FNFRFVSEKGM RNVFVDVVPADFKVGT TYKPEEAAAASASRRRSSEVFQF
                                60      70      80      90      100     110

gi+AHw-109  LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTDRFFFDGLEIIYKIFKMMFQ
                                120     130     140     150     160     170

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
 Full+AD0-Poly (514 aa)
 initn: 39 initl: 39 opt: 64 Z-score: 92.4 bits: 24.0 E(): 3.6
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (7-65:119-179)

```

                                10      20      30
AAD-12      VAISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                .....  :  .....  .  ..  ....  .
gi+AHw-476  ASAVLLVPANKKFFVN NLFVRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                90      100     110     120     130     140

                                40      50      60      70      80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                                :  .  :  .  ::  .  :  .....  :
gi+AHw-476  DFNLMGTGVIDGQQQW WAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                150     160     170     180     190     200

gi+AHw-476  FHLVFGECEGVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                210     220     230     240     250     260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 91.9 bits: 22.2 E(): 3.8
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (31-59:23-50)

```

                                10      20      30      40      50      60
AAD-12  VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGR
                                ..  ...  :  .:  .:  .:  .....  .  ::
gi+AHw-444      MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGV
                                10      20      30      40      50

                                70      80
AAD-12  TCFADMRAAYDALDEATRAL

```

10
20
30

AAD-12
 VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW

.
.
.

gi+AHw-169
 ATRLAQEDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAQEAAKWGPLRWMLAIQQMT

240
250
260
270
280
290

```

      40      50      60      70      80
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
      .: :.: . .: .: .:
gi+AHw-169 NAASSYMTDYYISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
      300      310      320      330      340      350

```

```

gi+AHw-169 KPVS KDSPET YEEALKRFAKLLSDRKKLRANKASY
      360      370      380

```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 initl: 39 opt: 55 Z-score: 88.7 bits: 21.6 E(): 5.7
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (16-43:114-147)

```

      10      20      30
AAD-12  VAISNVKADGTVRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
      .: .: .: .: .: .:
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
      90      100      110      120      130      140

```

```

      40      50      60      70      80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
      .: .:
gi+AHw-250 APVLDFVFSTLKNEL
      150

```

+AD4APg-gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product
+AFs-Sola (386 aa)
initn: 60 initl: 60 opt: 60 Z-score: 88.6 bits: 22.9 E(): 5.9
Smith-Waterman score: 60+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (4-79:262-337)

```

      10      20      30
AAD-12  VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
      .: .: .: .: .: .:
gi+AHw-215 ATRLAQEDPAFSSIKSLDYQMLLLSLGTGTNSEFDKTYAEEAAKWGPLRWMLAIQQMT
      240      250      260      270      280      290

```

```

      40      50      60      70      80
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
      .: :.: . .: .: .:
gi+AHw-215 NAASSYMTDYYISTVFQARHSQNNYLRVQENALNGTTTEMDDASEANMELLVQVGETLLK
      300      310      320      330      340      350

```

```

gi+AHw-215 KPVS KDSPET YEEALKRFAKLLSDRKKLRANKASH
      360      370      380

```

+AD4APg-gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum
tuberosum+AF0- (386 aa)
initn: 60 initl: 60 opt: 60 Z-score: 88.6 bits: 22.9 E(): 5.9
Smith-Waterman score: 60+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (4-79:262-337)

gi+AHw-158 KPVSKDSPETEEEEALKRFAKLLSNRKKLRANKASY
360 370 380

+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor
 +AFs-Tr (279 aa)
 initn: 57 initl: 57 opt: 57 Z-score: 86.7 bits: 22.1 E(): 7.5
 Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
 in 55 aa overlap (6-60:225-279)

```

                                10      20      30
AAD-12                        VAISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
                                :. . . . .
gi+AHw-106 IMQQEQQEQRQGVQILVPLSQQQVQGQTLVQGGQGI IQPQQPAQLE VIRSSVLQTLATMC
                200      210      220      230      240      250

```

```

                40      50      60      70      80
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                . : . . : . : . : .
gi+AHw-106 NVYVPPYCSTIRAPPFASIVAGIGGQ
                260      270

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 53 initl: 53 opt: 53 Z-score: 86.3 bits: 21.0 E(): 7.8
 Smith-Waterman score: 53+ADs- 26.667+ACU- identity (66.667+ACU- similar)
 in 30 aa overlap (37-66:5-34)

```

                10      20      30      40      50      60
AAD-12 KADGTVRQHSPA EWDDMMKVIVGNMAWHA DSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
                                :. :. . . :. . :. :. :. :
gi+AHw-189                        MASKSSITPLLLAAVLASVF AAAAATGQYCYAGM
                                10      20      30

```

```

                70      80
AAD-12 RAA YDALDEATRAL

gi+AHw-189 GLPSNPLEGCREYVAQQTCGV TIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFIG
                40      50      60      70      80      90

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
 vacuola (379 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 85.5 bits: 22.3 E(): 8.7
 Smith-Waterman score: 58+ADs- 20.779+ACU- identity (58.442+ACU- similar)
 in 77 aa overlap (1-76:120-194)

```

                                10      20      30
AAD-12                        VAISNVKADGTVRQHSPA EWDDMMKVIVGN
                                :. :. . . :. :. :. :. :
gi+AHw-119 LGLNKFADITPQEFSKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQ
                90      100      110      120      130      140

                40      50      60      70      80
AAD-12 MAWHA DSTY-MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
                . . . : :. :. :. :. :. :. :. :
gi+AHw-119 VKYQGGCGRGWAFSATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFE
                150      160      170      180      190      200

```


	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	1	0:+AD0-	
26	0	0:	
28	1	0:+AD0-	

```

30      5      2:+ACoAPQ-
32      3      8:+AD0AKg-
34      8      21:+AD0APQ-   +ACo-
36     31     44:+AD0APQ-+AD0APQA9AD0APQA9-   +ACo-
38     39     72:+AD0APQA9AD0APQA9AD0APQA9AD0-   +ACo-
40     77    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
42     74    123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
44     117
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9-   +ACo-
46     154
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
48     188
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
50     113
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-
52     100
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
54     63     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-   +ACo-
56     72     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
58     54     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60     48     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62     41     40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
64     68     32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
66     47     25:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
68     17     20:+AD0APQA9AD0AKg-
70     40     16:+AD0APQA9ACoAPQA9AD0APQA9AD0-
72     18     12:+AD0APQAqAD0APQ-
74     20     10:+AD0APQAqAD0APQ-
76     17     7:+AD0AKgA9AD0APQ-
78     7      6:+AD0AKg-
80     5      4:+ACoAPQ-
82     10     3:+ACoAPQA9-
84     9      3:+ACoAPQA9-
86     4      2:+ACo-
88     5      2:+ACoAPQ-           inset +AD0- represents 1 library
sequences
90     2      1:+ACo-
92     3      1:+ACo-           :+ACoAPQA9-
94     1      1:+ACo-           :+ACo-
96     5      1:+ACoAPQ-       :+ACoAPQA9AD0APQ-
98     0      0:               +ACo-
100    0      0:               +ACo-
102    0      0:               +ACo-
104    0      0:               +ACo-
106    0      0:               +ACo-
108    1      0:+AD0-         +ACoAPQ-
110    0      0:               +ACo-

```

```

112      1      0:+AD0-      +ACoAPQ-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.79730.0033+ADs- mu+AD0- 1.8060
0.170
mean+AF8-var+AD0-37.9943 9.688, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.208073
Kolmogorov-Smirnov statistic: 0.1025 (N+AD0-29) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 25.4 0.26
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 24.8 0.4
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.4 2.1
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 22.6 2.3
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
58 22.6 2.3
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419) 64 24.0 2.9
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
59 22.8 3.3
gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
( 514) 64 24.0 3.7
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.2 3.9
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 21.9 4.8
gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosu (
386) 61 23.2 4.9
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
( 158) 55 21.6 5.8
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 60 22.9 5.9
gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product +AFs- (
386) 60 22.9 6
gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum tuberosu (
386) 60 22.9 6
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 54 21.3 6.4

```

AAD-12 10 20 30
AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS

⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮
⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮

AAD-12

 10 20 30
AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
 :: :: :: :: :: :: :: : :: ::

```

      initn: 36 initl: 36 opt: 59 Z-score: 93.1 bits: 22.8 E(): 3.3
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (7-68:31-86)

```

```

                                10      20      30
AAD-12      AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                :.  ....  ::  .  :  :.  ...  :
gi+AHw-109  EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50
```

```

                                40      50      60      70      80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
                                :.  .:  :.  .  :  :.  :.  :.  :
gi+AHw-109  DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGT TYKPEEAAAASASRRRSSEVFQF
                                60      70      80      90      100     110
```

```

gi+AHw-109  LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
                                120     130     140     150     160     170
```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
Full+AD0-Poly (514 aa)
initn: 39 init1: 39 opt: 64 Z-score: 92.2 bits: 24.0 E(): 3.7
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (6-64:119-179)

```

                                10      20      30
AAD-12      AISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-476  ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                90      100     110     120     130     140
```

```

                                40      50      60      70      80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
                                :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-476  DFNLMGTGVIDGQGQWQWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                150     160     170     180     190     200
```

```

gi+AHw-476  FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                210     220     230     240     250     260
```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 init1: 55 opt: 57 Z-score: 91.8 bits: 22.2 E(): 3.9
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (30-58:23-50)

```

                                10      20      30      40      50      60
AAD-12  AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRT
                                ..  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-444      MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVG
                                10      20      30      40      50
```

```

                                70      80
AAD-12  CFADMRAAYDALDEATRALV

gi+AHw-444  TIKKISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGG
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (34-58:27-50)

```

      10      20      30      40      50      60
AAD-12 NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFA
      ... .. : : : : : :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIK
      10      20      30      40      50

      70      80
AAD-12 DMRAAYDALDEATRALV

```

```

gi+AHw-165 KITFGEQSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosum+AF0- (386 aa)
 initn: 61 initl: 61 opt: 61 Z-score: 90.0 bits: 23.2 E(): 4.9
 Smith-Waterman score: 61+ADs- 21.053+ACU- identity (53.947+ACU- similar)
 in 76 aa overlap (3-78:262-337)

```

      10      20      30
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
      . : . : . : . : . : . : . : . :
gi+AHw-169 ATRLAQEDPAFSSIKSLDYKQMLLSLGTGTNSEFDKTYTAQEAAKWGPLRWMLAIQQMT
      240      250      260      270      280      290

      40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
      . : . : . : . : . : . : . : . :
gi+AHw-169 NAASSYMTDYYISTVFQARHSQNNYLVRVQENALTGTTTEMDDASEANMELLVQVGETLLK
      300      310      320      330      340      350

gi+AHw-169 KPVSKDSPETYYEALKRFAKLLSDRKKLRANKASY
      360      370      380

```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
 Full+AD0-Globin (158 aa)
 initn: 39 initl: 39 opt: 55 Z-score: 88.7 bits: 21.6 E(): 5.8
 Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
 in 34 aa overlap (15-42:114-147)

```

      10      20      30
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
      . : . : . : . : . : . : . : . :
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
      90      100      110      120      130      140

      40      50      60      70      80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
      . : .

```


AAD-12

10 20 30

AISNVKADGTVRQHSPA EWDDMMKVIVGNMAW

⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮ ⋮

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 initl: 52 opt: 54 Z-score: 86.9 bits: 21.3 E(): 7.2
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (30-58;23-50)

```

      10      20      30      40      50      60
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAW HADSTYMPVMAQGAVFSAEVVPAVGGRT
      .. : : : : : : : : : : : :
gi+AHw-444      MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVG
      10      20      30      40      50
```

```

      70      80
AAD-12 CFADMRAAYDALDEATRALV

gi+AHw-444 TIKKISFGEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGG
      60      70      80      90      100      110
```

+AD4APg-gi+AHw-158517845+AHw-sp+AHw-P15476.2+AHw-PATB1+AF8-SOLTU RecName:
Full+AD0-Pat (386 aa)
initn: 59 initl: 59 opt: 59 Z-score: 86.8 bits: 22.6 E(): 7.4
Smith-Waterman score: 59+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (3-78:262-337)

```

      10      20      30
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
      . : . : . : . : . : . : . :
gi+AHw-158 ATRLAQEDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQLT
      240      250      260      270      280      290
```

```

      40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
      . : : : . : : : . : : : . : : :
gi+AHw-158 NAASSYMTDYIISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
      300      310      320      330      340      350
```

```

gi+AHw-158 KPVS KDSPET YEEALKRFAKLLSNRKKLRANKASY
      360      370      380
```

+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor
+AFs-Tr (279 aa)
initn: 57 initl: 57 opt: 57 Z-score: 86.6 bits: 22.0 E(): 7.6
Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
in 55 aa overlap (5-59:225-279)

```

      10      20      30
AAD-12 AISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
      . : : : . : : : . : : : . : : :
gi+AHw-106 IMQQEQQEQRQGVQILVPLSQQQQVGQGT LVQGGI IQPQQPAQLE VIRSSVLQTLATMC
      200      210      220      230      240      250
```

```

      40      50      60      70      80
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
      . : . : . : . : . : . :
gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
      260      270
```

80 residues in 1 query sequences

[illegible]

```

60      50      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      44      40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
64      67      32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
66      45      25:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
68      20      20:+AD0APQA9AD0AKg-
70      41      16:+AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
72      17      12:+AD0APQAqAD0APQ-
74      20      10:+AD0APQAqAD0APQ-
76      17      7:+AD0AKgA9AD0APQ-
78      7       6:+AD0AKg-
80      4       4:+ACo-
82     13      3:+ACoAPQA9AD0-
84      7       3:+ACoAPQ-
86      4       2:+ACo-
88      5       2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      2       1:+ACo-
92      3       1:+ACo-          :+ACoAPQA9-
94      1       1:+ACo-          :+ACo-
96      5       1:+ACoAPQ-        :+ACoAPQA9AD0APQ-
98      0       0:                +ACo-
100     0       0:                +ACo-
102     0       0:                +ACo-
104     0       0:                +ACo-
106     0       0:                +ACo-
108     1       0:+AD0-          +ACoAPQ-
110     0       0:                +ACo-
112     1       0:+AD0-          +ACoAPQ-
114     0       0:                +ACo-
116     0       0:                +ACo-
118     0       0:                +ACo-
+AD4-120    0       0:                +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.86300.00331+ADs- mu+AD0- 1.4079
0.171
mean+AF8-var+AD0-38.2664 9.716, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.207332
Kolmogorov-Smirnov statistic: 0.1018 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 25.4      0.27
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 24.8      0.4
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)  57 22.4      2.1
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 22.6      2.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  58 22.6      2.3

```



```

          40          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVH
          ..  ::  :.  .  .  :  .  .  :.
gi+AHw-400  EE-PL--QGP-FNFRFLTEKGMKNVFDVVPEKYTIGATYAPEE
          90          100          110          120

```

40 50 60 70 80
 AAD-12 TYPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVH
 :. :: :. . . : . : :.
 gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVPEKYTIGATYAPEE
 90 100 110 120

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-
Chamaecy (419 aa)
initn: 39 initl: 39 opt: 64 Z-score: 94.0 bits: 24.0 E(): 2.9
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (5-63:89-149)

```

                                10      20      30
AAD-12                        ISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                :.:.:.: . :.:.:.:
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
           60      70      80      90     100     110
```

```

                   40      50      60      70      80
AAD-12 DSTYMP--VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
           :.:.: . :.:.: . :.:.:.: :
gi+AHw-114 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
           120     130     140     150     160     170
```

```

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
           180     190     200     210     220     230
```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)
initn: 36 initl: 36 opt: 59 Z-score: 93.1 bits: 22.7 E(): 3.3
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (6-67:31-86)

```

                                10      20      30
AAD-12                        ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                :. :.:.:.: :. :. :. :. :. :. :
gi+AHw-109 EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
           10      20      30      40      50
```

```

                   40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
           :. :. :. :. :. :. :. :. :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGT TYKPEEAAASASRRRSSEVFQF
           60      70      80      90     100     110
```

```

gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
           120     130     140     150     160     170
```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
Full+AD0-Poly (514 aa)
initn: 39 initl: 39 opt: 64 Z-score: 92.0 bits: 23.9 E(): 3.8
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (5-63:119-179)

```

                                10      20      30
AAD-12                        ISNVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                :.:.:.: . :.:.:.: . :.:.:.:
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
           90      100     110     120     130     140
```

```

          40          50          60          70          80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
      : . : . . : . : . : : : : :
gi+AHw-476 DFNLMGTGVIDGQGQWWAGQCKVVGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
      150          160          170          180          190          200

```

```

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
      210          220          230          240          250          260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 91.8 bits: 22.2 E(): 3.9
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (29-57:23-50)

```

          10          20          30          40          50          60
AAD-12 ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTC
      .. . : : . : . : . : : : :
gi+AHw-444      MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGT
      10          20          30          40          50

```

```

          70          80
AAD-12 FADMRAAYDALDEATRALVH

```

```

gi+AHw-444 IKKISFGE GSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGS
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)

initn: 55 initl: 55 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (33-57:27-50)

```

          10          20          30          40          50          60
AAD-12 NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCF
      : : . : . : . : : : :
gi+AHw-165      MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIK
      10          20          30          40          50

```

```

          70          80
AAD-12 DMRAAYDALDEATRALVH

```

```

gi+AHw-165 KITFGE GSKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSIL
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-169500+AHw-gb+AHw-AAA33819.1+AHw- patatin +AFs-Solanum tuberosum+AF0- (386 aa)

initn: 61 initl: 61 opt: 61 Z-score: 89.9 bits: 23.1 E(): 5
 Smith-Waterman score: 61+ADs- 21.053+ACU- identity (53.947+ACU- similar)
 in 76 aa overlap (2-77:262-337)

```

          10          20          30
AAD-12      ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
      . : . : : . : : . . . . .

```

```
+AD4APg-gi+AHw-21510+AHw-emb+AHw-CAA31575.1+AHw- unnamed protein product
+AFs-Sola (386 aa)
  initn: 60 init1: 60 opt: 60 Z-score: 88.3 bits: 22.8 E(): 6.1
```

Smith-Waterman score: 60+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (2-77:262-337)

```

                                10      20      30
AAD-12                        ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
                                .: . : : . :. . . . .
gi+AHw-215 ATRLAQEDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQMT
                                240      250      260      270      280      290

                                40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
                                .: .: . . . . . .: . . . :. :. :
gi+AHw-215 NAASSYMTDYYISTVFQARHSQNNYLRVQENALNGTTTEMDDASEANMELLVQVGETLLK
                                300      310      320      330      340      350

gi+AHw-215 KPVS KDSPET YEEALKRFAKLLSDRKKLRANKASH
                                360      370      380
```

+AD4APg-gi+AHw-21514+AHw-emb+AHw-CAA27588.1+AHw- patatin +AFs-Solanum
tuberosum+AF0- (386 aa)
initn: 60 initl: 60 opt: 60 Z-score: 88.3 bits: 22.8 E(): 6.1
Smith-Waterman score: 60+ADs- 21.053+ACU- identity (53.947+ACU- similar)
in 76 aa overlap (2-77:262-337)

```

                                10      20      30
AAD-12                        ISNVKADGTVRQHSPA EWDDMMKVIVGNMAW
                                .: . : : . :. . . . .
gi+AHw-215 ATRLAQDDPAFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQMT
                                240      250      260      270      280      290

                                40      50      60      70      80
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
                                .: .: . . . . . .: . . . :. :. :
gi+AHw-215 NAASSYMTDYYISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
                                300      310      320      330      340      350

gi+AHw-215 KPVS KDSPET YEEALKRFAKLLSDRKKLRANKASH
                                360      370      380
```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 53 initl: 53 opt: 54 Z-score: 87.9 bits: 21.3 E(): 6.4
Smith-Waterman score: 54+ADs- 26.667+ACU- identity (57.778+ACU- similar)
in 45 aa overlap (35-79:5-48)

```

                                10      20      30      40      50      60
AAD-12 KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
                                .: . . . . . :. . . :. :. :. :
gi+AHw-189 MASKSSITPLLLAAVLASVF AAAAAATGQYCYAGM
                                10      20      30

                                70      80
AAD-12 RAA YDALDEATRALVH
                                . : . . : :
```

AAD-12 HADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVH

 40 50 60 70 80

 ::: ::: ::: ::: :::

gi+AHw-158 NAASSYMTDYYISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLK
 300 310 320 330 340 350

gi+AHw-158 KPVS KDSPET YEEALKRFAKLLSNRKKLRANKASY
 360 370 380

+AD4APg-gi+AHw-1063270+AHw-dbj+AHw-BAA11251.1+AHw- gamma-gliadin precursor
 +AFs-Tr (279 aa)
 initn: 57 initl: 57 opt: 57 Z-score: 86.5 bits: 22.0 E(): 7.7
 Smith-Waterman score: 57+ADs- 18.182+ACU- identity (58.182+ACU- similar)
 in 55 aa overlap (4-58:225-279)

AAD-12 ISNVKADGTVRQHSPA EWDDMMKVIVGNMAWHA
 :...: .. :...: :
 gi+AHw-106 IMQQEQQEQRQGVQILVPLSQQQVQGQTLVQGGQGI IQPQQPAQLE VIRSSVLQTLATMC
 200 210 220 230 240 250

AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
 . : . . : . : . : . :
 gi+AHw-106 NVYVPPYCSTIRAPFASIVAGIGGQ
 260 270

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:50 2010 done: Fri Feb 5 12:55:50 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 79 - 158 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	1	0:+AD0-	
26	0	0:	
28	1	0:+AD0-	
30	6	2:+ACoAPQ-	

```

32      6      8:+AD0AKg-
34     12     21:+AD0APQA9-  +ACo-
36     43     44:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
38     74     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
40     69    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42     129    123:+AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqA
D0APQ-
44     170
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
46     202
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
48     124
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0- +ACo-
50     98
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0-      +ACo-
52     81
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
54     60     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
56     57     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
58     54     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60     71     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
62     50     40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
64     19     32:+AD0APQA9AD0APQ- +ACo-
66     37     25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68     26     20:+AD0APQA9AD0AKgA9AD0-
70     22     16:+AD0APQA9ACoAPQA9-
72      9     12:+AD0APQAq-
74      4     10:+AD0- +ACo-
76     14      7:+AD0AKgA9AD0-
78      7      6:+AD0AKg-
80      7      4:+ACoAPQ-
82      3      3:+ACo-
84      3      3:+ACo-
86      2      2:+ACo-
88      6      2:+ACoAPQ-      inset +AD0- represents 1 library
sequences
90      0      1:+ACo-
92      0      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     1      0:+AD0-      +ACoAPQ-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-

```

AAD-12 SNVKADGTVRQHS¹⁰PAEWDDMMKVIVGNMAWHADST³⁰
 :. :. :. :. :. :. :. :. :.
 gi+AHw-126 TKVDLTVEKGS¹⁰DAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA⁵⁰
 40 50 60 70 80

AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 100.7 bits: 23.1 E(): 1.2
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (5-35:30-57)

AAD-12 SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
10 20 30
:. .:. .:. .: .:. .:.
gi+AHw-144 VKVTFKVEKGS DPKKLVL DIKYTRPGDTLAEVELRQH GSEWEPLTKK--GNL-WEVKSS
10 20 30 40 50

AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
40 50 60 70 80

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 89.1 bits: 21.0 E(): 5.5
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (5-66:31-86)

AAD-12 SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
10 20 30
:. .:. .:. .: .:. .:
gi+AHw-126 AAPVEFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
10 20 30 40 50

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
40 50 60 70 80
:. .: .: .: .: .: .: .:
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGT TYKPE
60 70 80 90

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 59 Z-score: 88.6 bits: 21.5 E(): 5.8
Smith-Waterman score: 59+ADs- 27.660+ACU- identity (57.447+ACU- similar)
in 47 aa overlap (34-80:5-50)

AAD-12 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
10 20 30 40 50 60
:. .:. .:. .: .: .: .: .:
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGM
10 20 30

70 80

AAD-12 RAAYDALDEATRALVHQ

```
      . : . : . :  
gi+AHw-189 GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFI  
          40          50          60          70          80          90
```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:

Full+AD0-Polle (122 aa)

```
  initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8  
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)  
in 59 aa overlap (5-63:55-107)
```

```
          10          20          30  
AAD-12      SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS  
          ..  ....  ::  :  :  :  :  :  
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS  
          30          40          50          60          70          80
```

```
          40          50          60          70          80  
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ  
          ..  ::  :.  .  .  :  .  :  :.  
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE  
          90          100          110          120
```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

```
  initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8  
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)  
in 59 aa overlap (5-63:55-107)
```

```
          10          20          30  
AAD-12      SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS  
          ..  ....  ::  :  :  :  :  :  
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS  
          30          40          50          60          70          80  
  
          40          50          60          70          80  
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ  
          ..  ::  :.  .  .  :  .  :  :.  
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE  
          90          100          110          120
```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

```
  initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8  
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)  
in 59 aa overlap (5-63:55-107)
```

```
          10          20          30  
AAD-12      SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHADS  
          ..  ....  ::  :  :  :  :  :  
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS  
          30          40          50          60          70          80  
  
          40          50          60          70          80
```

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ

.. :: : .. : ..

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (5-63:55-107)

AAD-12 SNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADS
.. :: : : : : : :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
30 40 50 60 70 80

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
.. :: : .. : ..
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs- Chamaecy (419 aa)

initn: 39 initl: 39 opt: 64 Z-score: 86.8 bits: 22.7 E(): 7.4
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (4-62:89-149)

AAD-12 SNVKADGT-VRQHSAPAEWDDMMKVIVGNMAWHA
..... : : : :
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
60 70 80 90 100 110

AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
: . : . : : : : : : : :
gi+AHw-114 DFNLMGTGVIDGQGQWAGQCKVNGRVTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
120 130 140 150 160 170

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
180 190 200 210 220 230

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)

initn: 36 initl: 36 opt: 59 Z-score: 86.0 bits: 21.4 E(): 8.1
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (5-66:31-86)

AAD-12 SNVKADGTVRQHSAPAEWDDMMKVIVGNMAWHADS
.. :: : : : : : :
gi+AHw-109 EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS

```

                10          20          30          40          50
AAD-12      40      50      60      70      80
TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
      :.  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-109  DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAAASASRRRSSEVFQF
      60          70          80          90          100          110

gi+AHw-109  LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
      120          130          140          150          160          170

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
Full+AD0-Poly (514 aa)
initn: 39 initl: 39 opt: 64 Z-score: 85.1 bits: 22.6 E(): 9.2
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (4-62:119-179)

```

                                10          20          30
AAD-12                        SNVKADGT-VRQHSPAEWDDMMKVIVGNMAWHA
                                :.:.:.:  .:  .:  .:  .:  .:  .:
gi+AHw-476  ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
      90          100          110          120          130          140

```

```

                40          50          60          70          80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
      :.  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-476  DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
      150          160          170          180          190          200

```

```

gi+AHw-476  FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
      210          220          230          240          250          260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 initl: 55 opt: 57 Z-score: 84.9 bits: 20.9 E(): 9.4
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (28-56:23-50)

```

                10          20          30          40          50          60
AAD-12  SNVKADGTVRQHSPAEWDDMMKVIVGNMAWHAADSTYMPVMAQGAVFSAEVVPAVGGRTCF
      ..  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-444  MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTI
      10          20          30          40          50

```

```

                70          80
AAD-12  ADMRAAYDALDEATRALVHQ

gi+AHw-444  KKISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSI
      60          70          80          90          100          110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences

```
Scomplib +AFs-34t26+AF0-
start: Fri Feb  5 12:55:50 2010 done: Fri Feb  5 12:55:50 2010
Total Scan time:  0.090 Total Display time:  0.000
```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 80 - 159 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

64      15      32:+AD0APQA9AD0-      +ACo-
66      39      25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68      25      20:+AD0APQA9AD0AKgA9AD0-
70      23      16:+AD0APQA9ACoAPQA9-
72      10      12:+AD0APQAq-
74      3       10:+AD0-      +ACo-
76      14      7:+AD0AKgA9AD0-
78      10      6:+AD0AKgA9-
80      4       4:+ACo-
82      3       3:+ACo-
84      3       3:+ACo-
86      2       2:+ACo-
88      5       2:+ACoAPQ-      inset +AD0- represents 1 library
sequences
90      1       1:+ACo-
92      0       1:+ACo-      :+ACo-
94      0       1:+ACo-      :+ACo-
96      0       1:+ACo-      :+ACo-
98      0       0:      +ACo-
100     1       0:+AD0-      +ACoAPQ-
102     1       0:+AD0-      +ACoAPQ-
104     0       0:      +ACo-
106     0       0:      +ACo-
108     0       0:      +ACo-
110     0       0:      +ACo-
112     0       0:      +ACo-
114     0       0:      +ACo-
116     0       0:      +ACo-
118     0       0:      +ACo-
+AD4-120      0       0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.83440.0033+ADs- mu+AD0- 3.1543
0.170
mean+AF8-var+AD0-48.265516.785, 0's: 2 Z-trim: 2 B-trim: 10 in 1/42
Lambda+AD0- 0.184610
Kolmogorov-Smirnov statistic: 0.0479 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 67 23.7 0.87
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 65 23.1 1.2
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 60 21.7 4.8
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 21.0 5.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 58 21.2 5.8
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
58 21.2 5.8

```

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 58 21.2 5.8
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 58 21.2 5.8
 gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
 64 22.7 7.3
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 59 21.4 8.1
 gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0- (514)
 64 22.7 9.1
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 20.9 9.4

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Pollen (97 aa)
 initn: 59 initl: 59 opt: 67 Z-score: 103.5 bits: 23.7 E(): 0.87
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (4-33:30-56)

		10	20	30
AAD-12		NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST		
		:	:	:
gi+AHw-126	TKVDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQH
	10	20	30	40
				50
	40	50	60	70
AAD-12	YMPVMAQGA	VFSAEVVP	AVGGRTCF	ADMRAAYD
				80
gi+AHw-126	KPLTGPMN	FRFLSKG	GGMKNVF	DEVIPTAFT
	60	70	80	90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-Poll (96 aa)
 initn: 55 initl: 55 opt: 65 Z-score: 100.7 bits: 23.1 E(): 1.2
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (4-34:30-57)

		10	20	30
AAD-12		NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADST		
		:	:	:
gi+AHw-144	VKVTFKVEK	GS	DPKKLVLD	IKYTRPGD
	10	20	30	40
				50
	40	50	60	70
AAD-12	YMPVMAQGA	VFSAEVVP	AVGGRTCF	ADMRAAYD
				80
gi+AHw-144	KPLTGPFN	FRFMSK	GGMNRNV	FDEVIPTAF
	60	70	80	90

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 60 Z-score: 90.1 bits: 21.7 E(): 4.8
 Smith-Waterman score: 60+ADs- 27.083+ACU- identity (58.333+ACU- similar)
 in 48 aa overlap (33-80:5-51)

```

          10          20          30          40          50          60
AAD-12  KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
          .. ... .. .. .. ..
gi+AHw-189  MASKSSITPLLLAAVLASVF AAAAATGQYCYAGM
          10          20          30
```

```

          70          80
AAD-12  RAA YDALDEATRALVHQR
          . : . : . :
gi+AHw-189  GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFI
          40          50          60          70          80          90
```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 89.1 bits: 21.0 E(): 5.5
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (4-65:31-86)

```

          10          20          30
AAD-12  NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
          .. .... :: . : . : . :
gi+AHw-126  AAPVEFTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
          10          20          30          40          50
```

```

          40          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR
          .. .: .: .: .: .: .: .:
gi+AHw-126  DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
          60          70          80          90
```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (4-62:55-107)

```

          10          20          30
AAD-12  NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
          .. .... :: : : : : . :
gi+AHw-117  WCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
          30          40          50          60          70          80
```

```

          40          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR
          .. :: .: .: .: .: .: .:
gi+AHw-117  EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPKYTIGATYAPEE
          90          100          110          120
```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (4-62:55-107)


```

                                10      20      30
AAD-12                        NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYA PEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (4-62:55-107)

```

                                10      20      30
AAD-12                        NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYA PEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 88.6 bits: 21.2 E(): 5.8
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (4-62:55-107)

```

                                10      20      30
AAD-12                        NVKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQR
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYA PEE
                                90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)
 initn: 39 initl: 39 opt: 64 Z-score: 86.9 bits: 22.7 E(): 7.3
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (3-61:89-149)

```

                                10      20      30
AAD-12                        NVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : : : :
gi+AHw-114 ASAVLVVPANKKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                60      70      80      90     100     110

```

```

                                40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR
                                : . : . : : : : : : : :
gi+AHw-114 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                120     130     140     150     160     170

```

```

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                180     190     200     210     220     230

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)
initn: 36 init1: 36 opt: 59 Z-score: 86.1 bits: 21.4 E(): 8.1
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (4-65:31-86)

```

                                10      20      30
AAD-12                        NVKADGTVRQHSPA EWDDMMKVIVGNMAWHAADS
                                : . : : : : : : : : : : :
gi+AHw-109 EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR
                                : . : : : : : : : : : :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAASASRRRSSEVFQF
                                60      70      80      90     100     110

```

```

gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
                                120     130     140     150     160     170

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
Full+AD0-Poly (514 aa)
initn: 39 init1: 39 opt: 64 Z-score: 85.2 bits: 22.7 E(): 9.1
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (3-61:119-179)

```

                                10      20      30
AAD-12                        NVKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                : : : : : : : : : : : :
gi+AHw-476 ASAVLLVPANKKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                90      100     110     120     130     140

```

```

                                40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQR
                                : . : . : : : : : : : :
gi+AHw-476 DFNLMGTGVIDGQGQWWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                150     160     170     180     190     200

```

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
 210 220 230 240 250 260

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 84.9 bits: 20.9 E(): 9.4
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (27-55:23-50)

10 20 30 40 50 60
 AAD-12 NVKADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFA
 .. .:: : .: .: .: :::: . ::
 gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIK
 10 20 30 40 50

70 80
 AAD-12 DMRAAYDALDEATRALVHQR

gi+AHw-444 KISFGEESHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSII
 60 70 80 90 100 110

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:50 2010 done: Fri Feb 5 12:55:50 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 81 - 160 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	1	0:+AD0-	
26	0	0:	
28	1	0:+AD0-	
30	8	2:+ACo-+AD0-	
32	6	8:+AD0AKg-	
34	18	21:+AD0APQA9AD0APQAq-	

inset +AD0- represents 1 library

AAD-12
 VKADGTVRQHS¹⁰PAEWDDMMKVIVGNMAWHADST³⁰
 :. :. :. :. :. :. :. :.
 gi+AHw-126 TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSA
 10 20 30 40 50
 40 50 60 70 80

AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRS

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
60 70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 100.5 bits: 23.1 E(): 1.3
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (3-33:30-57)

AAD-12 VKADGTVRQHSPAEWDDMMKVIVGNMAWHADST
10 20 30
:. .:. .:. .: .: .:. .:. .:
gi+AHw-144 VKVTFKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEWEPLTKK--GNL-WEVKSS
10 20 30 40 50

AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRS

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
60 70 80 90

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 62 Z-score: 92.8 bits: 22.2 E(): 3.4
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (32-80:5-52)

AAD-12 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
10 20 30 40 50 60
:. .:. .:. .: .: .:. .:. .:
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGM
10 20 30

AAD-12 RAAVDALDEATRALVHQRS
70 80
.: .: .: .: .:
gi+AHw-189 GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRVRYFI
40 50 60 70 80 90

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 89.0 bits: 21.0 E(): 5.5
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (3-64:31-86)

AAD-12 VKADGTVRQHSPAEWDDMMKVIVGNMAWHADS
10 20 30
:. .:. .:. .: .: .:. .:. .:
gi+AHw-126 AAPVEFTVEKGSDEKNLALSISKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
10 20 30 40 50
40 50 60 70 80

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRS

.. .. : : : : : : : : :

gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGGTTYKPE
60 70 80 90

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:

Full+AD0-Polle (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 88.5 bits: 21.2 E(): 5.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (3-61:55-107)

AAD-12 VKADGTVRQHSPAEDDMMKVIVGNMAWHADS
.. : : : : : : : : :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
30 40 50 60 70 80

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRS
.. .. : : : : : : : : :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 88.5 bits: 21.2 E(): 5.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (3-61:55-107)

AAD-12 VKADGTVRQHSPAEDDMMKVIVGNMAWHADS
.. : : : : : : : : :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
30 40 50 60 70 80

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRS
.. .. : : : : : : : : :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 88.5 bits: 21.2 E(): 5.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (3-61:55-107)

AAD-12 VKADGTVRQHSPAEDDMMKVIVGNMAWHADS
.. : : : : : : : : :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
30 40 50 60 70 80

40 50 60 70 80

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRS

.. :: : .. : ..

gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 88.5 bits: 21.2 E(): 5.9
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (3-61:55-107)

AAD-12 VKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
.. :: : : : .. ::
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
30 40 50 60 70 80

AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRS
.. :: : .. : ..
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDVVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs- Chamaecy (419 aa)

initn: 39 initl: 39 opt: 64 Z-score: 86.6 bits: 22.6 E(): 7.5
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (2-60:89-149)

AAD-12 VKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
..... : : : : .
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
60 70 80 90 100 110

AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRS
: . : . . :: . : . : : : :
gi+AHw-114 DFNLMGTGVIDGQGQWQWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
120 130 140 150 160 170

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
180 190 200 210 220 230

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)

initn: 36 initl: 36 opt: 59 Z-score: 85.9 bits: 21.4 E(): 8.3
Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (3-64:31-86)

AAD-12 VKADGTVRQHSPA EWDDMMKVIVGNMAWHADS
.. :: : : : :
gi+AHw-109 EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS


```

                10          20          30          40          50
          40          50          60          70          80
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRS
      .. .. :. . : :. :. :. :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAASASRRRSSEVFQF
          60          70          80          90          100          110

gi+AHw-109 LILSCQGRIVNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQ
          120          130          140          150          160          170

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 85.6 bits: 20.9 E(): 8.6
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (32-80:5-52)

```

                10          20          30          40          50          60
AAD-12  KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
      .. ... .. :. . . . :. :. :
gi+AHw-439 MASKSSITPLLLAAVLASVF AAATATGQYCYAGM
          10          20          30

```

```

                70          80
AAD-12  RAA YDALDEATRVLHQRS
      . : . : : : :. :
gi+AHw-439 GLPSNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYF
          40          50          60          70          80          90

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName:
 Full+AD0-Poly (514 aa)
 initn: 39 initl: 39 opt: 64 Z-score: 84.9 bits: 22.6 E(): 9.4
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (2-60:119-179)

```

                                10          20          30
AAD-12                                VKADGT-VRQHSPA EWDDMMKVIVGNMAWHA
      .. :. : : :. :. :. :. :. :. :
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
          90          100          110          120          130          140

```

```

                40          50          60          70          80
AAD-12  DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRS
      : . : . :. : : :. :. :. :
gi+AHw-476 DFNLMGTGVIDGQGQWWAGQCKVNVGRITVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
          150          160          170          180          190          200

```

```

gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
          210          220          230          240          250          260

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 84.8 bits: 20.9 E(): 9.6

Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (26-54:23-50)

```

                10         20         30         40         50         60
AAD-12 VKADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFAD
                .. ... : .. : .. : .. : .. :
gi+AHw-444   MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKK
                10         20         30         40         50

                70         80
AAD-12 MRAAYDALDEATRALVHQRS

gi+AHw-444 ISFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIK
                60         70         80         90        100        110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:51 2010 done: Fri Feb 5 12:55:51 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 82 - 161 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      1      0:+AD0-
      26      0      0:
      28      1      0:+AD0-
      30      4      2:+ACo-
      32      6      8:+AD0AKg-
      34     10     21:+AD0APQA9- +ACo-
      36     31     44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      38     32     72:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      40     72    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42     76    123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-

```

```
mean+AF8-var+AD0-38.2288 9.989, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
```

Lambda+AD0- 0.207433

Kolmogorov-Smirnov statistic: 0.1025 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
 (97) 67 25.4 0.26

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 65 24.8 0.39

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
 144) 62 23.8 1.2

gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
 (97) 57 22.4 2.1

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
 (122) 58 22.6 2.3

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 58 22.6 2.3

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 58 22.6 2.3

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 58 22.6 2.3

gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
 419) 64 24.0 2.9

gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 59 22.8 3.2

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145)
 57 22.3 3.4

gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-
 (514) 64 24.0 3.7

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.2 3.8

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
 160) 56 21.9 4.7

gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
 (158) 55 21.6 5.7

gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
 (379) 60 22.9 5.8

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
 301) 58 22.3 6.7

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.3 7.2

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
 145) 53 21.1 7.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)

initn: 59 init1: 59 opt: 67 Z-score: 112.8 bits: 25.4 E(): 0.26

Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (2-31:30-56)

```

AAD-12                                KADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  ....  ...  :  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGS DAKTLVLN IKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAE VVPAVGGR TCFADMRAAYDALDEATRALVHQRSA

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 55 initl: 55 opt: 65 Z-score: 109.6 bits: 24.8 E(): 0.39
Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
in 31 aa overlap (2-32:30-57)

```

                                10      20      30
AAD-12                                KADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEP LTKK--GNL-WEVKSS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAE VVPAVGGR TCFADMRAAYDALDEATRALVHQRSA

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                                60      70      80      90

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 62 Z-score: 100.9 bits: 23.8 E(): 1.2
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (31-79:5-52)

```

                                10      20      30      40      50      60
AAD-12 KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGR TCFADM
                                ..  ...  ...  :.  .  :.  :.  :..  :
gi+AHw-189 MASKSSITPLLLAAVLASVF AAAAATGQYCYAGM
                                10      20      30

```

```

                                70      80
AAD-12 RAA YDALDEATRALVHQRSA
                                .  :  :.  :  :  :..
gi+AHw-189 GLPSNPL-EGCREYVAQQTCGV TIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFI
                                40      50      60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 57 Z-score: 96.6 bits: 22.4 E(): 2.1
Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
in 62 aa overlap (2-63:31-86)

```

                                10      20      30

```

```

AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-126 AAPVEFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
                                ..  ..  ..  .  :  :  :  :  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
                                60      70      80      90

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (2-60:55-107)

```

                                10      20      30
AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
                                ..  ..  ..  .  :  :  :  :  :
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100      110      120

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (2-60:55-107)

```

                                10      20      30
AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
                                ..  ..  ..  .  :  :  :  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100      110      120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
in 59 aa overlap (2-60:55-107)

10 20 30

```

AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                     ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                     30      40      50      60      70      80

```

```

                                     40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
                                     ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                     90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 init1: 46 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (2-60:55-107)

```

                                     10      20      30
AAD-12                                KADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                     ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                     30      40      50      60      70      80

```

```

                                     40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
                                     ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                     90      100     110     120

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)

initn: 39 init1: 39 opt: 64 Z-score: 94.1 bits: 24.0 E(): 2.9
 Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
 in 63 aa overlap (1-59:89-149)

```

                                     10      20
AAD-12                                KADGT-VRQHS PAEWDDMMKVIVGNMAWHA
                                     :  :  :  :  :  :  :  :  :  :  :
gi+AHw-114 ASAVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                     60      70      80      90      100     110

```

```

                                     30      40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
                                     :  .  :  .  :  :  :  :  :  :
gi+AHw-114 DFNLMGTGVIDGQGQWQWAGQCKVVNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                     120     130     140     150     160     170

```

```

gi+AHw-114 FHLVFGECEGVKIQGLKIKAPRDSPTNDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
                                     180     190     200     210     220     230

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)

initn: 36 init1: 36 opt: 59 Z-score: 93.2 bits: 22.8 E(): 3.2

Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
in 62 aa overlap (2-63:31-86)

```

                                10      20      30
AAD-12                        KADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-109 EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
                                ..  .:  ..  .  :  :  ::  ....  :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGM RNVFVDVVPADFKVGT TYKPEEAAAASASRRRSSEVFQF
                                60      70      80      90      100     110

gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTDRFFFDGLEIIYKIFKMMFQ
                                120     130     140     150     160     170

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetrameric (145 aa)

initn: 50 initl: 50 opt: 57 Z-score: 92.8 bits: 22.3 E(): 3.4
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (31-79:5-52)

```

                                10      20      30      40      50      60
AAD-12 KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
                                ..  ...  ...  :  .  .  .  :  ::  :
gi+AHw-439 MASKSSITPLLLAAVLASVF AAATATGQYCYAGM
                                10      20      30

                                70      80
AAD-12 RAA YDALDEATR ALVHQRSA
                                .  :  .  :  :  :  ...
gi+AHw-439 GLPSNPL-EGCREYVAQQTCGV TIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYF
                                40      50      60      70      80      90

```

+AD4APg-gi+AHw-47606004+AHw-sp+AHw-Q7M1E7.1+AHw-PGLR2+AF8-CHAOB RecName: Full+AD0-Poly (514 aa)

initn: 39 initl: 39 opt: 64 Z-score: 92.2 bits: 24.0 E(): 3.7
Smith-Waterman score: 64+ADs- 33.333+ACU- identity (57.143+ACU- similar)
in 63 aa overlap (1-59:119-179)

```

                                10      20
AAD-12                        KADGT-VRQHSPA EWDDMMKVIVGNMAWHA
                                .....  :  :  .....  .  ..  .  ...  .
gi+AHw-476 ASAVLLVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLT
                                90      100     110     120     130     140

                                30      40      50      60      70      80
AAD-12 DSTYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSA
                                :  .  :  .  ...  .  :  .....  :
gi+AHw-476 DFNLMGTGVIDGQGQW WAGQCKV VNGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPE
                                150     160     170     180     190     200

```


gi+AHw-476 FHLVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSN
210 220 230 240 250 260

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 91.9 bits: 22.2 E(): 3.8
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (25-53:23-50)

10 20 30 40 50 60
AAD-12 KADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
.. .:: : .: .: .: :::: . ::
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKKI
10 20 30 40 50

70 80
AAD-12 RAAVDALDEATRALVHQRSA

gi+AHw-444 SFGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKS
60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 90.3 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (29-53:27-50)

10 20 30 40 50 60
AAD-12 KADGTVRQHSPAEDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM
::: .: .: .: :::: . ::
gi+AHw-165 MGVFTHENEITSAPPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKI
10 20 30 40 50

70 80
AAD-12 RAAVDALDEATRALVHQRSA

gi+AHw-165 TFGEQSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKN
60 70 80 90 100 110

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 initl: 39 opt: 55 Z-score: 88.8 bits: 21.6 E(): 5.7
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (10-37:114-147)

10 20 30
AAD-12 KADGTVRQHSPAEDDMMKVIV----GNMAWHA--DSTY
:::: .: .: .: : : . : .
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
90 100 110 120 130 140

40 50 60 70 80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
:::

gi+AHw-250 APVLDFVFSTLKNEL
150

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 init1: 48 opt: 60 Z-score: 88.6 bits: 22.9 E(): 5.8
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (9-70:134-194)

	10	20	30
AAD-12	KADGTVRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM		
	:	:	:
gi+AHw-309	SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGSGWAFS		
	110	120	130

	40	50	60	70	80
AAD-12	AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA				
	:	:	:	:	:
gi+AHw-309	ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSF EWVLEHGGIATDDDDY				
	170	180	190	200	210

gi+AHw-309	PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISV SIDAKDFH
	230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 49 init1: 49 opt: 58 Z-score: 87.5 bits: 22.3 E(): 6.7
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (26-75:23-71)

	10	20	30	40	50	60
AAD-12	KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM					
	:	:	:	:	:	:
gi+AHw-663	MAVQKYTV ALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDE					
	10	20	30	40	50	

	70	80
AAD-12	RAAYDALDEATRALVHQRSA	
	:	:
gi+AHw-663	QKLLLEDVNAGFKA AVAADANAPPADKFKIFEAAFSE SCKG LLATSDAKAPGLILKLD TDY	
	60	70

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 init1: 52 opt: 54 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (25-53:23-50)

	10	20	30	40	50	60
AAD-12	KADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADM					
	:	:	:	:	:	:
gi+AHw-444	MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTA EIVEGDGGVGTIKKI					
	10	20	30	40	50	

```

              70          80
AAD-12 RAAVDALDEATRALVHQRSA

gi+AHw-444 SFGEESHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVSADGGSIKS
              60          70          80          90          100          110

```

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
  initn: 46 initl: 46 opt: 53 Z-score: 86.3 bits: 21.1 E(): 7.8
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (31-79:5-52)

```

```

              10          20          30          40          50          60
AAD-12 KADGTVRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADM
              .. ... .. .. : ... :
gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGM
              10          20          30

```

```

              70          80
AAD-12 RAAVDALDEATRALVHQRSA
              . : . : : ...
gi+AHw-217 GLPINPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCEAVRYF
              40          50          60          70          80          90

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:51 2010 done: Fri Feb 5 12:55:51 2010
Total Scan time: 0.090 Total Display time: 0.000

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 83 - 162 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      1      0:+AD0-
      26      0      0:
      28      1      0:+AD0-
      30      4      2:+ACo-

```

```

32      6      8:+AD0AKg-
34     12     21:+AD0APQA9- +ACo-
36     30     44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
38     34     72:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
40     69    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42     78    123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
44    124    136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
46    166
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
48    183
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
50     96
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
52    103
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9-
54     69     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
56     75     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
58     42     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60     50     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62     48     40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
64     64     32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
66     40     25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68     23     20:+AD0APQA9AD0AKgA9-
70     42     16:+AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
72     17     12:+AD0APQA9AD0APQ-
74     19     10:+AD0APQA9AD0APQ-
76     20      7:+AD0AKgA9AD0APQ-
78     10      6:+AD0AKgA9-
80      4      4:+ACo-
82      8      3:+ACoAPQ-
84     14      3:+ACoAPQA9AD0-
86      3      2:+ACo-
88      2      2:+ACo- inset +AD0- represents 1 library sequences
90      1      1:+ACo-
92      3      1:+ACo- :+ACoAPQA9-
94      0      1:+ACo- :+ACo-
96      5      1:+ACoAPQ- :+ACoAPQA9AD0APQ-
98      0      0: +ACo-
100     1      0:+AD0- +ACoAPQ-
102     0      0: +ACo-
104     0      0: +ACo-
106     0      0: +ACo-
108     0      0: +ACo-
110     1      0:+AD0- +ACoAPQ-
112     1      0:+AD0- +ACoAPQ-
114     0      0: +ACo-

```

```

116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.84990.00316+ADs- mu+AD0- 1.4245
0.163
mean+AF8-var+AD0-38.022910.019, 0's: 2 Z-trim: 3 B-trim: 222 in 2/41
Lambda+AD0- 0.207994
Kolmogorov-Smirnov statistic: 0.1004 (N+AD0-29) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  67 25.4    0.26
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  65 24.8    0.39
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  62 23.8    1.2
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)  57 22.4    2.1
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122)  58 22.6    2.2
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
58 22.6    2.2
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
58 22.6    2.2
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
58 22.6    2.2
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
59 22.8    3.2
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145)
57 22.3    3.4
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.2    3.8
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  56 21.9    4.7
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
(158)  55 21.6    5.7
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
(379)  60 22.9    5.8
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301)  58 22.3    6.6
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.3    7.1
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145)  53 21.1    7.7
gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (
419)  58 22.2    9.9

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)

```

initn: 59 initl: 59 opt: 67 Z-score: 112.9 bits: 25.4 E(): 0.26
 Smith-Waterman score: 67+ADs- 40.000+ACU- identity (63.333+ACU- similar)
 in 30 aa overlap (1-30:30-56)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  ....  ...  :  ...  ...  :
gi+AHw-126 TKVDLTVEKGS DAKTLVLN IKYTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSA
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR

```

```

gi+AHw-126 KPLTGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                60      70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)

initn: 55 initl: 55 opt: 65 Z-score: 109.8 bits: 24.8 E(): 0.39
 Smith-Waterman score: 65+ADs- 35.484+ACU- identity (64.516+ACU- similar)
 in 31 aa overlap (1-31:30-57)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADST
                                ..  ....  ...  .  :  ...  ...  ..
gi+AHw-144 VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEP LTKK--GNL-WEVKSS
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YMPVMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR

```

```

gi+AHw-144 KPLTGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
                                60      70      80      90

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)

initn: 55 initl: 55 opt: 62 Z-score: 101.1 bits: 23.8 E(): 1.2
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (30-78:5-52)

```

                                10      20      30      40      50      60
AAD-12 ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMR
                                ..  ...  ...  ..  ..  ..  ...  :
gi+AHw-189                        MASKSSITPLLLA AVLASVFAAAAATGQYCYAGMG
                                10      20      30

```

```

                                70      80
AAD-12 AAYDALDEATRALVHQRSAR

```

```

.  :  :  :  :  :  :
gi+AHw-189 LPSNPL-EGCREYVAQQTCGV TIAGSPVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFIG
                                40      50      60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)

initn: 36 initl: 36 opt: 57 Z-score: 96.7 bits: 22.4 E(): 2.1
 Smith-Waterman score: 57+ADs- 27.419+ACU- identity (51.613+ACU- similar)
 in 62 aa overlap (1-62:31-86)

```

                                10      20      30
AAD-12                      ADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  ..  ...  :
gi+AHw-126 AAPVEFTVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                        10      20      30      40      50

                        40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                        ..  .:  ..  .  :  :  ::  :  ..  :
gi+AHw-126 DK-PL--KGP-FNFRFVSEKGM RNVFDDVVPADFKVGT TYKPE
                        60      70      80      90

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.2 bits: 22.6 E(): 2.2
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (1-59:55-107)

```

                                10      20      30
AAD-12                      ADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  ..  ::
gi+AHw-117 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                        30      40      50      60      70      80

                        40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                        ..  ::  ..  .  .  :  ..  :  ..
gi+AHw-117 EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATY APEE
                        90      100     110     120

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
 II) (122 aa)
 initn: 46 initl: 46 opt: 58 Z-score: 96.2 bits: 22.6 E(): 2.2
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (1-59:55-107)

```

                                10      20      30
AAD-12                      ADGTVRQHS PAEWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  ..  ::
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                        30      40      50      60      70      80

                        40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR ALVHQRSAR
                        ..  ::  ..  .  .  :  ..  :  ..
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNV FDDVVPEKYTIGATY APEE
                        90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
 II) (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 96.2 bits: 22.6 E(): 2.2
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (1-59:55-107)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 46 initl: 46 opt: 58 Z-score: 96.2 bits: 22.6 E(): 2.2
 Smith-Waterman score: 58+ADs- 30.508+ACU- identity (50.847+ACU- similar)
 in 59 aa overlap (1-59:55-107)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  :  :  :  :  :  :
gi+AHw-400 WCVPKVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDS
                                30      40      50      60      70      80

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                ..  ::  ..  .  .  :  ..  :  :
gi+AHw-400 EE-PL--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100     110     120

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)

initn: 36 initl: 36 opt: 59 Z-score: 93.3 bits: 22.8 E(): 3.2
 Smith-Waterman score: 59+ADs- 27.419+ACU- identity (53.226+ACU- similar)
 in 62 aa overlap (1-62:31-86)

```

                                10      20      30
AAD-12                        ADGTVRQHSPA EWDDMMKVIVGNMAWHADS
                                ..  ....  ::  .  :  :  ..  ...  :
gi+AHw-109 EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKS
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12 TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                ..  ..  ..  .  :  :  :  :  :
gi+AHw-109 DK-PL--KGP-FNFRFVSEKGMKNVFDDVVPADFKVGT TYKPEEAAAASASRRRSSEVFQF
                                60      70      80      90      100     110

gi+AHw-109 LILSCQGRIVNNCEVLICVMRRGNAMCLIASISMHHILTDRFFFDGLEIIYKIFKMMFQ
                                120     130     140     150     160     170

```


+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 92.9 bits: 22.3 E(): 3.4
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (30-78:5-52)

	10	20	30	40	50	60
AAD-12	ADGTVRQHSPA	EWDDMMKVIVGN	MAWHADSTYMP	VMAQGAVFSAE	VVPAVGGRTCF	ADMR
				:	:	:
gi+AHw-439				MASSITPLLLA	AVLASVF	AAATATGQYCYAGMG
				10	20	30

	70	80
AAD-12	AAYDALDEATRALVH	QRSAR
	:	:
gi+AHw-439	LPSNPL-EGCREYVA	QQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFI
	40	50

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 92.0 bits: 22.2 E(): 3.8
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (24-52:23-50)

	10	20	30	40	50	60
AAD-12	ADGTVRQHSPA	EWDDMMKVIVGN	MAWHADSTYMP	VMAQGAVFSAE	VVPAVGGRTCF	ADMR
				:	:	:
gi+AHw-444	MGVFTYADESTSV	IPPPRLFKALVLEAD-TLIPK	IA PQSVKSAEIVE	GDGGVGTIKKIS		
	10	20	30	40	50	

	70	80
AAD-12	AAYDALDEATRALVH	QRSAR
gi+AHw-444	FGEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKL	VASADGGSIIKST
	60	70

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 90.4 bits: 21.9 E(): 4.7
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (28-52:27-50)

	10	20	30	40	50	60
AAD-12	ADGTVRQHSPA	EWDDMMKVIVGN	MAWHADSTYMP	VMAQGAVFSAE	VVPAVGGRTCF	ADMR
				:	:	:
gi+AHw-165	MGVFTHENEITSA	IPPGRLFKAFVL	DADNL-IPKLAPHA	IKSAEIIIEGNGG	PGTIKKIT	
	10	20	30	40	50	

	70	80
AAD-12	AAYDALDEATRALVH	QRSAR
gi+AHw-165	FGEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNT	
	60	70

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 initl: 39 opt: 55 Z-score: 88.9 bits: 21.6 E(): 5.7
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (9-36:114-147)

```

                                10      20      30
AAD-12      ADGTVRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
                                .... : : : : : : : :
gi+AHw-250  EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
              90      100      110      120      130      140

              40      50      60      70      80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
              ...
gi+AHw-250  APVLDFVFSTLKNEL
              150

```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 initl: 48 opt: 60 Z-score: 88.7 bits: 22.9 E(): 5.8
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (8-69:134-194)

```

                                10      20      30
AAD-12      ADGTVRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM
                                : : : : : : : :
gi+AHw-309  SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
              110      120      130      140      150      160

              40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
              : : : : : : : :
gi+AHw-309  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFWEVLEHGGIATDDDDY
              170      180      190      200      210      220

gi+AHw-309  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
              230      240      250      260      270      280

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 49 initl: 49 opt: 58 Z-score: 87.6 bits: 22.3 E(): 6.6
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (25-74:23-71)

```

              10      20      30      40      50      60
AAD-12  ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
              .. : : : : : : : :
gi+AHw-663  MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQ
              10      20      30      40      50

              70      80
AAD-12  AAYDALDEATRALVHQRSAR

```

```

      . . . . . : :
gi+AHw-663 KLEEDVNAGFKAAVAADANAPPADKFKIFEAAFSESCKGLLATSDAKAPGLILKLDTDYD
      60          70          80          90         100         110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 87.1 bits: 21.3 E(): 7.1
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (24-52:23-50)

```

      10          20          30          40          50          60
AAD-12 ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
      .. . : : : : : : : : : : : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKIS
      10          20          30          40          50

```

```

      70          80
AAD-12 AAYDALDEATRALVHQRSAR

```

```

gi+AHw-444 FGEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKST
      60          70          80          90         100         110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 86.4 bits: 21.1 E(): 7.7
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (30-78:5-52)

```

      10          20          30          40          50          60
AAD-12 ADGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMR
      : : : : : : : : : : : :
gi+AHw-217 MASKSSISPLLLLATV LVS VF AAATATGPYCYAGMG
      10          20          30

```

```

      70          80
AAD-12 AAYDALDEATRALVHQRSAR

```

```

      . : : : : : :
gi+AHw-217 LPINPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCCKEYLDASQHCRCEAVRYFI
      40          50          60          70          80          90

```

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Chamaecy (419 aa)

initn: 39 initl: 39 opt: 58 Z-score: 84.5 bits: 22.2 E(): 9.9
 Smith-Waterman score: 58+ADs- 32.787+ACU- identity (55.738+ACU- similar)
 in 61 aa overlap (2-58:91-149)

```

      10          20          30
AAD-12 ADGT-VRQHSPA EWDDMMKVIVGNMAWHADS
      : : : : : : : : : : : :
gi+AHw-114 AVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLTDF
      70          80          90         100         110

```

```

      40          50          60          70          80
AAD-12 TYMP---VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR

```

```

      . :      . .:: . :      .::: :      :
gi+AHw-114 NLMGTGVIDGQGGQWWAGQCKVVGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPEFH
      120      130      140      150      160      170

gi+AHw-114 LVFGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSNIT
      180      190      200      210      220      230

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:51 2010 done: Fri Feb 5 12:55:51 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 84 - 163 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:      one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      6      2:+ACoAPQ-
      32      4      8:+AD0AKg-
      34      14     21:+AD0APQA9AD0- +ACo-
      36      31     44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      38      36     72:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      40      65    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      42      79    123:+AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      44      116
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-
      46      169
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
      48      183
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-

```

```

50      98
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
52      103
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAq-
54      68      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
56      74      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
58      44      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
60      49      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      49      40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
64      66      32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-+AD0-
66      33      25:+AD0APQA9AD0APQA9ACoAPQA9-
68      29      20:+AD0APQA9AD0AKgA9AD0APQ-
70      38      16:+AD0APQA9ACoAPQA9AD0APQA9AD0-
72      21      12:+AD0APQAqAD0APQA9-
74      19      10:+AD0APQAqAD0APQ-
76      21      7:+AD0AKgA9AD0APQA9-
78      9      6:+AD0AKgA9-
80      5      4:+ACoAPQ-
82      8      3:+ACoAPQ-
84      14      3:+ACoAPQA9AD0-
86      2      2:+ACo-
88      2      2:+ACo-      inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      7      1:+ACoAPQ-      :+ACoAPQA9AD0APQA9AD0-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:      +ACo-
106     1      0:+AD0-      +ACoAPQ-
108     0      0:      +ACo-
110     1      0:+AD0-      +ACoAPQ-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120     0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.87230.00303+ADs- mu+AD0- 1.2936
0.157
mean+AF8-var+AD0-37.6036 9.920, 0's: 2 Z-trim: 2 B-trim: 223 in 2/41
Lambda+AD0- 0.209151
Kolmogorov-Smirnov statistic: 0.1052 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
 (97) 65 24.9 0.37
 gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
 (96) 63 24.3 0.56
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
 62 23.8 1.1
 gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
 (97) 55 21.9 3
 gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
 (122) 56 22.1 3.2
 gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
 56 22.1 3.2
 gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
 56 22.1 3.2
 gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
 56 22.1 3.2
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145)
 57 22.3 3.2
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.3 3.7
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 56 22.0 4.5
 gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
 57 22.2 4.7
 gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
 (158) 55 21.7 5.5
 gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
 (379) 60 22.9 5.6
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
 58 22.4 6.5
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.4 6.9
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
 53 21.1 7.5
 gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-Cham (419)
 58 22.3 9.7
 gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
 (91) 49 20.1 9.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 57 initl: 57 opt: 65 Z-score: 110.1 bits: 24.9 E(): 0.37
 Smith-Waterman score: 65+ADs- 42.308+ACU- identity (65.385+ACU- similar)
 in 26 aa overlap (4-29:34-56)

		10	20	30	
AAD-12		DGTVRQHSPEAWDDMMKVIVGNMAWHADSTYMP			
		:	:
gi+AHw-126	DLTVEKGS	DAKTLVL	NIKYTR	PGDTLAE	VELRQHGSEEW
	10	20	30	40	50
	40	50	60	70	80
AAD-12	VMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH				

40 50 60 70 80
 AAD-12 VMAQGVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH
 * * * * * * * *

gi+AHw-126 L--KGP-FNFRFVSEKGMKNVFDVVPAEDFKVGTTRYKPE
70 80 90

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 93.2 bits: 22.1 E(): 3.2
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (4-58:59-107)

AAD-12 DGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMP
..... :: :: : .: :: :
gi+AHw-117 KVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
30 40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARH
. :: :. . . : .: :: :.
gi+AHw-117 L--QGP-FNFRFLTEKGMKNVFDVVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 93.2 bits: 22.1 E(): 3.2
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (4-58:59-107)

AAD-12 DGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMP
..... :: :: : .: :: :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
30 40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARH
. :: :. . . : .: :: :.
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDVVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group
II) (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 93.2 bits: 22.1 E(): 3.2
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (4-58:59-107)

AAD-12 DGTVRQHSPAEDDDMMKVIVGNMAWHADSTYMP
..... :: :: : .: :: :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
30 40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALLVHQRSARH
. :: :. . . : .: :: :.

70 80
AAD-12 AYDALDEATRALVHQRSARH

```

                                10      20      30
AAD-12      DGTVRQHSPA EWDDMMKVIV----GNMAWHA--DSTY
                                :::: :. :. :. :. :. :. :. :.
gi+AHw-250  EVMDLLGNDANTPTILAKAKDFGKSHKSRSPAQLDNFRKSLVVYLKGATKWDSAVESSW
           90      100      110      120      130      140

           40      50      60      70      80
AAD-12  MPVMAQGAVFSAE VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARH
           ::.

```

gi+AHw-250 APVLDFVFSTLKNEL
150

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 init1: 48 opt: 60 Z-score: 88.9 bits: 22.9 E(): 5.6
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (7-68:134-194)

		10	20	30	
AAD-12		DGTVRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM			
		:	:	:	:
gi+AHw-309	SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS				
	110 120 130 140 150 160				

	40	50	60	70	80
AAD-12	AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR LVHQRSARH				
	:	:	:	:	:
gi+AHw-309	ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSF EWVLEHGGIATDDDDY				
	170 180 190 200 210 220				

gi+AHw-309	PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
	230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 49 init1: 49 opt: 58 Z-score: 87.8 bits: 22.4 E(): 6.5
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (24-73:23-71)

	10	20	30	40	50	60
AAD-12	DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA					
	:	:	:	:	:	:
gi+AHw-663	MAVQKYTV ALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQK					
	10 20 30 40 50					

	70	80
AAD-12	AYDALDEATR LVHQRSARH	
	:	:
gi+AHw-663	LLEDVNAGFKA AVAADANAPPADKFKIFEAAFS ESCKGLLATSDAKAPGLILKLDTDYDV	
	60 70 80 90 100 110	

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 init1: 52 opt: 54 Z-score: 87.3 bits: 21.4 E(): 6.9
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (23-51:23-50)

	10	20	30	40	50	60
AAD-12	DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA					
	:	:	:	:	:	:
gi+AHw-444	MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDGGVGTIKKISF					
	10 20 30 40 50					

70 80
AAD-12 AYDALDEATRALVHQRSARH

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 86.7 bits: 21.1 E(): 7.5
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (29-77:5-52)

10 20 30 40 50 60
AAD-12 DGTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAE VVPAVGGRTCFADMRA
gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGMGL
10 20 30

70 80
AAD-12 AYDALDEATRALVHQRSARH
gi+AHw-217 PINPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIG
40 50 60 70 80 90

+AD4APg-gi+AHw-114841683+AHw-dbj+AHw-BAF32143.1+AHw- pollen allergen +AFs-
Chamaecy (419 aa)

initn: 39 initl: 39 opt: 58 Z-score: 84.7 bits: 22.3 E(): 9.7
Smith-Waterman score: 58+ADs- 32.787+ACU- identity (55.738+ACU- similar)
in 61 aa overlap (1-57:91-149)

10 20
AAD-12 DGT-VRQHSPA EWDDMMKVIVGNMAWHADS
gi+AHw-114 AVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKNS-KIWL-QFAQLTDF
70 80 90 100 110

30 40 50 60 70 80
AAD-12 TYMP---VMAQGAVFSAE VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH
gi+AHw-114 NLMGTGVIDGQGQWWAGQCKVVGRTVCNDRNRPTAIKIDYSKSVTVKELTLMNSPEFH
120 130 140 150 160 170

gi+AHw-114 LVFGECEGVKIQGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSNIT
180 190 200 210 220 230

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)

initn: 37 initl: 37 opt: 49 Z-score: 84.6 bits: 20.1 E(): 9.8
Smith-Waterman score: 49+ADs- 32.258+ACU- identity (58.065+ACU- similar)
in 31 aa overlap (3-31:35-64)

10 20 30
AAD-12 DGTVRQHSPA E--WDDMMKVIVGNMAWHADST
: : : . : . : : . .

```

gi+AHw-323 QTCAGNICCSQYGYCGTTADYCSFDNNCQATYHYYNPAQNNWD-LRAVSAYCSTWDADKP
           10          20          30          40          50          60
           40          50          60          70          80
AAD-12  YMPVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARH
      :
gi+AHw-323 YSWRYGWTAFCGPAGPRCLRTNAAVTVR
           70          80          90

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:51 2010 done: Fri Feb 5 12:55:51 2010
Total Scan time: 0.090 Total Display time: 0.000

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 85 - 164 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      3      2:+ACo-
      32      4      8:+AD0AKg-
      34      12     21:+AD0APQA9- +ACo-
      36      28     44:+AD0APQA9AD0APQA9AD0- +ACo-
      38      39     72:+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      40      72    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42      72    123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      44      127
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ- +ACo-
      46      113
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-

```

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
  join: 42, opt: 30, open/ext: -10/-2, width: 32
```

Scan time: 0.090

The best scores are:

opt bits E(1471)

```

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 65 25.1 0.31
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 63 24.5 0.47
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.0 0.98
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 55 22.1 2.6
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122) 56 22.3 2.8
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
56 22.3 2.8
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
56 22.3 2.8
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
56 22.3 2.8
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.5 2.8
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.5 3.2
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.2 4
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
57 22.4 4.2
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-GL
( 158) 55 21.9 4.8
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 60 23.0 5.2
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.5 5.9
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.6 6.1
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.3 6.6
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 49 20.3 8.5
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.2
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.2
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.2
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.0 9.2
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.0 9.2
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.2
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.2
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.2

```

gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9.2
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9.2
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.0 9.3
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
 (379) 57 22.1 9.8
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 57 22.1 9.8

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 57 initl: 57 opt: 65 Z-score: 111.5 bits: 25.1 E(): 0.31
 Smith-Waterman score: 65+ADs- 42.308+ACU- identity (65.385+ACU- similar)
 in 26 aa overlap (3-28:34-56)

			10	20	30
AAD-12			GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP		
		 : :	... : .. :
gi+AHw-126	DLTVEKGS	DAKTLVL	NIKYTRPG	DTLAEVEL	RQHGSEEW
	10	20	30	40	50
					60

	40	50	60	70	80
AAD-12	VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS				

gi+AHw-126	TGPMNFRFL	SKGGMKNV	FDEVIPTA	FTVGKTYT	PEYN
	70	80	90		

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 53 initl: 53 opt: 63 Z-score: 108.3 bits: 24.5 E(): 0.47
 Smith-Waterman score: 63+ADs- 37.037+ACU- identity (66.667+ACU- similar)
 in 27 aa overlap (3-29:34-57)

			10	20	30
AAD-12			GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP		
		 :	... : .. :
gi+AHw-144	TFKVEKGS	DPKKLVLD	IKYTRPGD	TLAEVELR	QHGSEEW
	10	20	30	40	50
					60

	40	50	60	70	80
AAD-12	VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS				

gi+AHw-144	TGPFNFRF	MSKGGMRN	VFDEVIPT	AFKIGTTY	TPEE
	70	80	90		

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 102.6 bits: 24.0 E(): 0.98
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (28-76:5-52)

10	20	30	40	50	60
----	----	----	----	----	----

AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLP
10 20 30

AAD-12 YDALDEATRALVHQRSARHS
gi+AHw-189 SNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRR
40 50 60 70 80 90

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 55 Z-score: 95.0 bits: 22.1 E(): 2.6
Smith-Waterman score: 55+ADs- 27.586+ACU- identity (51.724+ACU- similar)
in 58 aa overlap (3-60:35-86)

AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
gi+AHw-126 EFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P
10 20 30 40 50 60

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
gi+AHw-126 L--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
40 50 60 70 80 90

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
Full+AD0-Polle (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 94.3 bits: 22.3 E(): 2.8
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (3-57:59-107)

AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
gi+AHw-117 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
30 40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
gi+AHw-117 L--QGP-FNFRFLTEKGMKNVFDDVVP EKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 94.3 bits: 22.3 E(): 2.8
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (3-57:59-107)

10 20 30

```

AAD-12                                GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  :  :  :  :  :  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30          40          50          60          70          80

```

```

              40          50          60          70          80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
      .  ::  ..  .  .  :  ..  :  :
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90          100          110          120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 44 init1: 44 opt: 56 Z-score: 94.3 bits: 22.3 E(): 2.8
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (3-57:59-107)

```

                                10          20          30
AAD-12                                GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  :  :  :  :  :  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30          40          50          60          70          80

```

```

              40          50          60          70          80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
      .  ::  ..  .  .  :  ..  :  :
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90          100          110          120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 44 init1: 44 opt: 56 Z-score: 94.3 bits: 22.3 E(): 2.8
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (3-57:59-107)

```

                                10          20          30
AAD-12                                GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  :  :  :  :  :  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30          40          50          60          70          80

```

```

              40          50          60          70          80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
      .  ::  ..  .  .  :  ..  :  :
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90          100          110          120

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetrameric (145 aa)
 initn: 50 init1: 50 opt: 57 Z-score: 94.2 bits: 22.5 E(): 2.8
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (28-76:5-52)

```

              10          20          30          40          50          60

```

```

AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
              ... ..
gi+AHw-439  MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLP
              10      20      30

```

```

              70      80
AAD-12  YDALDEATRALVHQRSARHS
              . : . : . : . : . :
gi+AHw-439 SNPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGR
              40      50      60      70      80      90

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 93.3 bits: 22.5 E(): 3.2
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (22-50:23-50)

```

              10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              .. ... : : : : : : : : : :
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
              10      20      30      40      50

```

```

              60      70      80
AAD-12  AYDALDEATRALVHQRSARHS
              60      70      80      90      100      110
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 91.6 bits: 22.2 E(): 4
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (26-50:27-50)

```

              10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ... : : : : : : : :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
              10      20      30      40      50

```

```

              60      70      80
AAD-12  AYDALDEATRALVHQRSARHS
              60      70      80      90      100      110
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196 aa)
 initn: 36 initl: 36 opt: 57 Z-score: 91.2 bits: 22.4 E(): 4.2
 Smith-Waterman score: 57+ADs- 27.586+ACU- identity (53.448+ACU- similar)
 in 58 aa overlap (3-60:35-86)

AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
 :: . : : :
 gi+AHw-109 TFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
 . .: .. . : : .. :... :
 gi+AHw-109 L--KGP-FNFRFVSEKGMNVFVDVVPADFKVGTITYKPEEAAAASASRRRSSEVFQFLILS
 70 80 90 100 110

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
 Full+AD0-Globin (158 aa)
 initn: 39 initl: 39 opt: 55 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
 in 34 aa overlap (7-34:114-147)

10 20 30
 AAD-12 GTVRQHSPA EWDDMMKVIV---GNMAWHA--DSTY
 :::. ... : : : : . :...
 gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
 90 100 110 120 130 140

40 50 60 70 80
 AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
 :..
 gi+AHw-250 APVLDFVFSTLKNEL
 150

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
 max+AF0- (379 aa)
 initn: 48 initl: 48 opt: 60 Z-score: 89.5 bits: 23.0 E(): 5.2
 Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
 in 63 aa overlap (6-67:134-194)

10 20 30
 AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM
 : :: : : :
 gi+AHw-309 SKKYLQAPKDVSQQIKMANKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
 110 120 130 140 150 160

40 50 60 70 80
 AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
 : ::. ::. : :..
 gi+AHw-309 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFEWVLEHGGIATDDDDY
 170 180 190 200 210 220

gi+AHw-309 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
 230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 88.6 bits: 22.5 E(): 5.9

Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (23-72:23-71)

```

      10      20      30      40      50      60
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
      .. ::: : : : . : ..... : .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
      10      20      30      40      50

```

```

      70      80
AAD-12  YDALDEATRALVHQRSARHS
      . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAFSECKGLLATSDAKAPGLILKLDTDYDVA
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.3 bits: 21.6 E(): 6.1
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (22-50:23-50)

```

      10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      .. ::: : : : . : ..... : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
      10      20      30      40      50

```

```

      60      70      80
AAD-12  AYDALDEATRALVHQRSARHS
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 87.6 bits: 21.3 E(): 6.6
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (28-76:5-52)

```

      10      20      30      40      50      60
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
      .. ... .. : : : : : :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLP
      10      20      30

```

```

      70      80
AAD-12  YDALDEATRALVHQRSARHS
      . : : : : :
gi+AHw-217 INPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGR
      40      50      60      70      80      90

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)

initn: 37 initl: 37 opt: 49 Z-score: 85.7 bits: 20.3 E(): 8.5

Smith-Waterman score: 49+ADs- 32.258+ACU- identity (58.065+ACU- similar)
in 31 aa overlap (2-30:35-64)

```

                                10      20
AAD-12                        GTVRQHSPAEE--WDDMMKVIVGNMAWHADST
                                : . . . . . : : . . . : :
gi+AHw-323 QTCAGNICCSQYGYCGTTADYCS PDNNCQATYHYYNPAQNNWD-LRAVSAYCSTWDADKP
                                10      20      30      40      50      60

```

```

        30      40      50      60      70      80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
        :
gi+AHw-323 YSWRYGWTAFCGPAGPRCLRTNAAVTVR
        70      80      90

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

        10      20      30      40      50
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                : : . : : : : : : : : :
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
        10      20      30      40      50

```

```

        60      70      80
AAD-12 AYDALDEATRALVHQRSARHS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

        10      20      30      40      50
AAD-12 GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                : : . : : : : : : : : :
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
        10      20      30      40      50

```

```

        60      70      80
AAD-12 AYDALDEATRALVHQRSARHS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

          60          70          80          90          100          110
gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

          60          70          80          90          100          110
gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-131  MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

          60          70          80          90          100          110
gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

      10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10      20      30      40      50
```

```

      60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
      60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

      10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10      20      30      40      50
```

```

      60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

      10      20      30      40      50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10      20      30      40      50
```

```

      60      70      80
AAD-12  AYDALDEATRALVHQRSARHS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFITYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (26-50:27-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFITYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 50 initl: 50 opt: 52 Z-score: 85.0 bits: 21.0 E(): 9.3
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (22-50:23-50)

```

          10          20          30          40          50
AAD-12  GTVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          ..  ::.  .:  .:  .:  ::.  .:  ::
gi+AHw-444  MGVFITYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEG DGGVGTIKKISF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHS

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)
initn: 48 initl: 48 opt: 57 Z-score: 84.6 bits: 22.1 E(): 9.8

Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (6-67:134-194)

```

                                10      20      30
AAD-12      GTVRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
              : :: :: : .. .. ...
gi+AHw-129 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
              110      120      130      140      150      160

              40      50      60      70      80
AAD-12 AQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
              : ::. .... ::. . .... . : ....
gi+AHw-129 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFEWVLEHGGIATDDDDY
              170      180      190      200      210      220

gi+AHw-129 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
              230      240      250      260      270      280

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
initn: 48 initl: 48 opt: 57 Z-score: 84.6 bits: 22.1 E(): 9.8
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (6-67:134-194)

```

                                10      20      30
AAD-12      GTVRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
              : :: :: : .. .. ...
gi+AHw-119 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
              110      120      130      140      150      160

              40      50      60      70      80
AAD-12 AQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
              : ::. .... ::. . .... . : ....
gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFEWVLEHGGIATDDDDY
              170      180      190      200      210      220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
              230      240      250      260      270      280

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:51 2010 done: Fri Feb 5 12:55:52 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

[illegible]

```

82      2      3:+ACo-
84     17     3:+ACoAPQA9AD0APQ-
86      1     2:+ACo-
88      4     2:+ACo-          inset +AD0- represents 1 library sequences
90      2     1:+ACo-
92      2     1:+ACo-          :+ACoAPQ-
94      6     1:+ACoAPQ-       :+ACoAPQA9AD0APQA9-
96      0     1:+ACo-          :+ACo-
98      0     0:              +ACo-
100     0     0:              +ACo-
102     1     0:+AD0-         +ACoAPQ-
104     0     0:              +ACo-
106     0     0:              +ACo-
108     1     0:+AD0-         +ACoAPQ-
110     1     0:+AD0-         +ACoAPQ-
112     0     0:              +ACo-
114     0     0:              +ACo-
116     0     0:              +ACo-
118     0     0:              +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.05020.00293+ADs- mu+AD0- -
0.0733 0.152
mean+AF8-var+AD0-36.8188 9.860, 0's: 2 Z-trim: 2 B-trim: 223 in 2/41
Lambda+AD0- 0.211368
Kolmogorov-Smirnov statistic: 0.1278 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  65 25.2      0.3
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  63 24.6      0.46
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  62 24.1      0.95
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)  55 22.1      2.5
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  56 22.3      2.7
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
56 22.3      2.7
gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
56 22.3      2.7
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
56 22.3      2.7
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.6      2.8
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.5      3.1
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  56 22.2      3.9

```

```

gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
57 22.4 4.1
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-G1
( 158) 55 21.9 4.7
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 60 23.1 5
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.6 5.7
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.6 5.9
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.3 6.4
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 49 20.3 8.3
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.0 9
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.0 9
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.0 9
gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
( 379) 57 22.2 9.4
gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac ( 379)
57 22.2 9.4

```

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 57 init1: 57 opt: 65 Z-score: 111.6 bits: 25.2 E(): 0.3
Smith-Waterman score: 65+ADs- 42.308+ACU- identity (65.385+ACU- similar)
in 26 aa overlap (2-27:34-56)

```

```

AAD-12 TVRQHSPEAWDDMMKVIVGNMAWHADSTYMP
      10 20 30
      .... : : : : :
gi+AHw-126 DLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEEWEPMTK--KGNL-WEVKSAPKL
      10 20 30 40 50 60
      40 50 60 70 80

```

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL

gi+AHw-126 TGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
70 80 90

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 53 initl: 53 opt: 63 Z-score: 108.4 bits: 24.6 E(): 0.46
Smith-Waterman score: 63+ADs- 37.037+ACU- identity (66.667+ACU- similar)
in 27 aa overlap (2-28:34-57)

AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
..... :. . : :. :. :.
gi+AHw-144 TFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQH GSEWEPLTK--KGNL-WEVKSSKPL
10 20 30 40 50 60

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL

gi+AHw-144 TGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
70 80 90

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 62 Z-score: 102.7 bits: 24.1 E(): 0.95
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (27-75:5-52)

AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY
:. :. :. :. :. :. :. :.
gi+AHw-189 MASKSSITPLLLAAVLASVF AAAAATGQYCYAGMGLPS
10 20 30

AAD-12 DALDEATRALVHQRSARHSL
. : :. : :.
gi+AHw-189 NPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRS
40 50 60 70 80 90

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 36 initl: 36 opt: 55 Z-score: 95.1 bits: 22.1 E(): 2.5
Smith-Waterman score: 55+ADs- 27.586+ACU- identity (51.724+ACU- similar)
in 58 aa overlap (2-59:35-86)

AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMP
..... :. . : :. :. :.
gi+AHw-126 EFTVEKGSDEKLNLA LSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P
10 20 30 40 50 60
40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL

. .: . . : : . . : . :
gi+AHw-126 L--KGP-FNFRFVSEKGMKNVFDVVPADFKVGTTYKPE
70 80 90

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:

Full+AD0-Polle (122 aa)

initn: 44 initl: 44 opt: 56 Z-score: 94.5 bits: 22.3 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (2-56:59-107)

AAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMP
. . . . : : : : :
gi+AHw-117 KVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
30 40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL
. .: . . : : . . : . :
gi+AHw-117 L--QGP-FNFRFLTEKGMKNVFDVVPPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)

initn: 44 initl: 44 opt: 56 Z-score: 94.5 bits: 22.3 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (2-56:59-107)

AAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMP
. . . . : : : : :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
30 40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL
. .: . . : : . . : . :
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDVVPPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)

initn: 44 initl: 44 opt: 56 Z-score: 94.5 bits: 22.3 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (2-56:59-107)

AAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMP
. . . . : : : : :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
30 40 50 60 70 80

40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL

. :: .. . : .. ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)

initn: 44 initl: 44 opt: 56 Z-score: 94.5 bits: 22.3 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (2-56:59-107)

AAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMP
..... :: : : : : : : :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYEGLTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
30 40 50 60 70 80

AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
. :: .. . : .. ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
90 100 110 120

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetrameric (145 aa)

initn: 50 initl: 50 opt: 57 Z-score: 94.4 bits: 22.6 E(): 2.8
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (27-75:5-52)

AAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY
:. :. . :. :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPS
10 20 30

AAD-12 DALDEATRALVHQRSARHSL
. : : : :
gi+AHw-439 NPL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRR
40 50 60 70 80 90

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 93.5 bits: 22.5 E(): 3.1
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (21-49:23-50)

AAD-12 TVRQHSPAEDDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.. ... : : : : : : : :
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKKISF
10 20 30 40 50
60 70 80

30 40 50 60 70 80

AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRSARHSL

:::

gi+AHw-250 APVLDFVFSTLKNEL
150

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)

initn: 48 initl: 48 opt: 60 Z-score: 89.8 bits: 23.1 E(): 5
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (5-66:134-194)

	10	20	30
AAD-12	TVRQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM		
	:	:	:
gi+AHw-309	SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS		
	110	120	130
		140	150
			160

	40	50	60	70	80
AAD-12	AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRSARHSL				
	:	:	:	:	:
gi+AHw-309	ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFEWVLEHGGIATDDDDY				
	170	180	190	200	210
					220

gi+AHw-309	PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
	230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 88.8 bits: 22.6 E(): 5.7
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (22-71:23-71)

	10	20	30	40	50
AAD-12	TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA				
	:	:	:	:	:
gi+AHw-663	MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL				
	10	20	30	40	50

	60	70	80
AAD-12	YDALDEATRVLHQRSARHSL		
	:	:	:
gi+AHw-663	LEDVNAGFKAAVAADANAPPADKFKIFEAAFSESCKGLLATSDAKAPGLILKLDTDYDVA		
	60	70	80
			90
			100
			110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.5 bits: 21.6 E(): 5.9
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (21-49:23-50)

	10	20	30	40	50
AAD-12	TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA				
	:	:	:	:	:
gi+AHw-444	MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDGGVGTIKKISF				

```

                10          20          30          40          50
        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
        60          70          80          90          100          110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
  initn: 46 initl: 46 opt: 53 Z-score: 87.8 bits: 21.3 E(): 6.4
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (27-75:5-52)

                10          20          30          40          50          60
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAY
        :. :.. :. :. :. :. :. :. :
gi+AHw-217 MASKSSISPLLLATVIVSVFAAATATGPYCYAGMGLPI
                10          20          30

                70          80
AAD-12 DALDEATRALVHQRSARHSL
        . : :. : : :. :
gi+AHw-217 NPL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRR
        40          50          60          70          80          90

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
  initn: 37 initl: 37 opt: 49 Z-score: 85.9 bits: 20.3 E(): 8.3
Smith-Waterman score: 49+ADs- 32.258+ACU- identity (58.065+ACU- similar)
in 31 aa overlap (1-29:35-64)

                10          20
AAD-12 TVRQHSPA E--WDDMMKVIVGNMAWHADST
        : . :. :. :. :. :. :. :. :
gi+AHw-323 QTCAGNICCSQYGYCGTTADYCS PDNNCQATYHYYNPAQNNWD-LRAVSAYCSTWDADKP
        10          20          30          40          50          60

        30          40          50          60          70          80
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
        :
gi+AHw-323 YSWRYGWTAFCGPAGPRCLRTNAAVTVR
        70          80          90

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10          20          30          40          50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
        :.. :. :. :. :. :. :. :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF

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```

                10         20         30         40         50
      60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
      60         70         80         90        100        110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. . ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10         20         30         40         50

      60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60         70         80         90        100        110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. . ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10         20         30         40         50

      60         70         80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSNGSVIKSTSH
      60         70         80         90        100        110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10         20         30         40         50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. . ::
gi+AHw-279 MGVF TYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
```

```

        10          20          30          40          50
      60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60          70          80          90         100         110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

        10          20          30          40          50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. . ::
gi+AHw-131 MGVFN YETEF TSVIP PARLFNAFVL DADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
      10          20          30          40          50

      60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60          70          80          90         100         110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

        10          20          30          40          50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. . ::
gi+AHw-602 MGVFTY ESEFT SVIP PARLFNAFVL DADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
      10          20          30          40          50

      60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
      60          70          80          90         100         110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

        10          20          30          40          50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. . ::
gi+AHw-602 MGVFTY ESEFT SVIP PARLFNAFVL DADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
```

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                10          20          30          40          50
        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10          20          30          40          50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVF TYESEFTSIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10          20          30          40          50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (25-49:27-50)

                10          20          30          40          50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
```

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                10          20          30          40          50
        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
  initn: 50 initl: 50 opt: 52 Z-score: 85.2 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (21-49:23-50)

                10          20          30          40          50
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. .:: : .: .: .: .::: . .::
gi+AHw-444 MGVFTYADESTSVITPPRLFALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSL

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
        60          70          80          90          100          110

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)
  initn: 48 initl: 48 opt: 57 Z-score: 84.9 bits: 22.2 E(): 9.4
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (5-66:134-194)

                10          20          30
AAD-12 TVRQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
                : :: : : . . . .
gi+AHw-129 SKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
        110          120          130          140          150          160

        40          50          60          70          80
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
        : :: . . . . .:: . . . . . : .::
gi+AHw-129 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFEWVLEHGGIATDDDDY
        170          180          190          200          210          220

gi+AHw-129 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
        230          240          250          260          270          280

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
vacuola (379 aa)
  initn: 48 initl: 48 opt: 57 Z-score: 84.9 bits: 22.2 E(): 9.4
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (5-66:134-194)

```

```

AAD-12                      TVRQHSPAEWDDMMKVIVGNMAWHADSTY-MPVM
                        :  ::  ::  :  ..  ..  ...
gi+AHw-119 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
                110          120          130          140          150          160

                40          50          60          70          80
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSL
                :  ::.  .....  ::.  .  .....  .  :  .....
gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFEWVLEHGGIATDDDDY
                170          180          190          200          210          220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
                230          240          250          260          270          280

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:52 2010 done: Fri Feb 5 12:55:52 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 87 - 166 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      4      2:+ACo-
      32      3      8:+AD0AKg-
      34      6      21:+AD0APQ- +ACo-
      36      35      44:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      39      72:+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      40      98
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AK
g-
      42      53      123:+AD0APQ-+AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-

```



```
mean+AF8-var+AD0-36.6097 9.849, 0's: 2 Z-trim: 2 B-trim: 223 in 2/41
```

Lambda+AD0- 0.211971

Kolmogorov-Smirnov statistic: 0.1257 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
(97) 65 25.2 0.29

gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
(96) 63 24.6 0.44

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144)
62 24.1 0.92

gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
(97) 55 22.2 2.5

gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
(122) 56 22.4 2.7

gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group (122)
56 22.4 2.7

gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group (122)
56 22.4 2.7

gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group (122)
56 22.4 2.7

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145)
57 22.6 2.7

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.6 3

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
56 22.3 3.8

gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II (196)
57 22.5 3.9

gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
(158) 55 22.0 4.6

gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
(379) 60 23.1 4.8

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
58 22.6 5.5

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.6 5.7

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
53 21.4 6.3

gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
53 21.3 7.1

gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.0 8.7

gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7

gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7

gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
52 21.0 8.7

gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.0 8.7
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.0 8.7
 gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 21.0 8.7
 gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.0 8.7
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.0 8.7
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.0 8.8
 gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
 (379) 57 22.2 9.1
 gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac (379)
 57 22.2 9.1

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 57 initl: 57 opt: 65 Z-score: 111.9 bits: 25.2 E(): 0.29
 Smith-Waterman score: 65+ADs- 42.308+ACU- identity (65.385+ACU- similar)
 in 26 aa overlap (1-26:34-56)

			10	20	30
AAD-12			VRQHSPA	EWDDMMKV	IVGNMAWHADSTYMP
		 : :	... : :
gi+AHw-126	DLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEVELRQ	HGSEEWEPMTK--KGNL-WEVKS
	10	20	30	40	50 60
	40	50	60	70	80
AAD-12	VMAQGAVF	SAEVVPAV	GGRTCFAD	MRAAYDAL	DEATRALVHQRSARHSLV
gi+AHw-126	TGPMNFR	FLSKGGM	KNVFDEVI	PTAFTVGK	TYTPEYN
	70	80	90		

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
 Full+AD0-Poll (96 aa)
 initn: 53 initl: 53 opt: 63 Z-score: 108.7 bits: 24.6 E(): 0.44
 Smith-Waterman score: 63+ADs- 37.037+ACU- identity (66.667+ACU- similar)
 in 27 aa overlap (1-27:34-57)

			10	20	30
AAD-12			VRQHSPA	EWDDMMKV	IVGNMAWHADSTYMP
		 : :	... : :
gi+AHw-144	TFKVEKGS	DPKKLVLD	IKYTRPGD	TLAEVELRQ	HGSEEWEPMTK--KGNL-WEVKS
	10	20	30	40	50 60
	40	50	60	70	80
AAD-12	VMAQGAVF	SAEVVPAV	GGRTCFAD	MRAAYDAL	DEATRALVHQRSARHSLV
gi+AHw-144	TGPFNFR	FMKGGMR	NVFDEVI	PTAFKIGT	TYTPEE
	70	80	90		

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 103.0 bits: 24.1 E(): 0.92
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (26-74:5-52)

```

                10         20         30         40         50         60
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
                ::   ...   ...   ..   ..   ..   ::   ::   ::   :
gi+AHw-189                MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSN
                        10         20         30

```

```

                70         80
AAD-12 ALDEATRALVHQRSARHSLV
                :  ::  :  :  ::
gi+AHw-189 PL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSH
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)
 initn: 36 initl: 36 opt: 55 Z-score: 95.4 bits: 22.2 E(): 2.5
 Smith-Waterman score: 55+ADs- 27.586+ACU- identity (51.724+ACU- similar)
 in 58 aa overlap (1-58:35-86)

```

                                10         20         30
AAD-12                                VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::   .  :   :  ....  :   :
gi+AHw-126 EFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P
                10         20         30         40         50         60

```

```

                40         50         60         70         80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
                .  .:  :  .  :   :  ::  :  ::  :
gi+AHw-126 L--KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTTYKPE
                70         80         90

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 44 initl: 44 opt: 56 Z-score: 94.7 bits: 22.4 E(): 2.7
 Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
 in 55 aa overlap (1-55:59-107)

```

                                10         20         30
AAD-12                                VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::   :  :   :  .:  ::  :
gi+AHw-117 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
                30         40         50         60         70         80

```

```

                40         50         60         70         80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
                .  ::  :  .  .  :  ..  :  ::
gi+AHw-117 L--QGP-FNFRFLTEKGMKNVFDDVVP EKYTIGATYAPEE
                90         100        110        120

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group II) (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 94.7 bits: 22.4 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (1-55:59-107)

```

                                10      20      30
AAD-12                        VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  ::  :  ::  ::  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30      40      50      60      70      80

              40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
.  ::  ..  .  .  :  ..  ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90      100     110     120
```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 94.7 bits: 22.4 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (1-55:59-107)

```

                                10      20      30
AAD-12                        VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  ::  :  ::  ::  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30      40      50      60      70      80

              40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
.  ::  ..  .  .  :  ..  ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90      100     110     120
```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
initn: 44 initl: 44 opt: 56 Z-score: 94.7 bits: 22.4 E(): 2.7
Smith-Waterman score: 56+ADs- 30.909+ACU- identity (50.909+ACU- similar)
in 55 aa overlap (1-55:59-107)

```

                                10      20      30
AAD-12                        VRQHSPA EWDDMMKVIVGNMAWHADSTYMP
                                .....  ::  ::  :  ::  ::  :
gi+AHw-400 KVTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-P
              30      40      50      60      70      80

              40      50      60      70      80
AAD-12 VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
.  ::  ..  .  .  :  ..  ::
gi+AHw-400 L--QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90      100     110     120
```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 94.7 bits: 22.6 E(): 2.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (26-74:5-52)

```

                10      20      30      40      50      60
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
                .. ... .. .. .. .. ..
gi+AHw-439                MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSN
                        10      20      30

```

```

                70      80
AAD-12 ALDEATRALVHQRSARHSLV
                : .. : : ...
gi+AHw-439 PL-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRS
                40      50      60      70      80      90

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 93.7 bits: 22.6 E(): 3
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (20-48:23-50)

```

                10      20      30      40      50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. ... : .. : .. : .. : .. : ..
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

                60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLV
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 92.1 bits: 22.3 E(): 3.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (24-48:27-50)

```

                10      20      30      40      50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... .. : .. : .. : .. : .. : ..
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10      20      30      40      50

```

```

                60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLV
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)

initn: 36 init1: 36 opt: 57 Z-score: 91.7 bits: 22.5 E(): 3.9
Smith-Waterman score: 57+ADs- 27.586+ACU- identity (53.448+ACU- similar)
in 58 aa overlap (1-58:35-86)

			10	20	30
AAD-12			VRQHSPA	EWDDMMKVIVGNMAWHADSTYMP	
			:: . :	:: . . :
gi+AHw-109	TFTVEKGSDEKNLALS	SIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-P			
	10	20	30	40	50
					60

	40	50	60	70	80
AAD-12	VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV				
	. .:	:: . :	: :: . . . :		
gi+AHw-109	L--KGP-FNFRFVSEKGM	RNVFVDVVPADFKVGT	TTYKPEEAAAASASRRRSSEVFQFLILS		
	70	80	90	100	110

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
Full+AD0-Globin (158 aa)
initn: 39 init1: 39 opt: 55 Z-score: 90.5 bits: 22.0 E(): 4.6
Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
in 34 aa overlap (5-32:114-147)

			10	20	
AAD-12			VRQHSPA	EWDDMMKVIV----	GNMAWHA--DSTY
			::::	... :	: :
gi+AHw-250	EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW				
	90	100	110	120	130
					140

	30	40	50	60	70	80
AAD-12	MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV					
	:::					
gi+AHw-250	APVLDFVFSTLKNEL					
	150					

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine
max+AF0- (379 aa)
initn: 48 init1: 48 opt: 60 Z-score: 90.1 bits: 23.1 E(): 4.8
Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
in 63 aa overlap (4-65:134-194)

			10	20	30
AAD-12			VRQHSPA	EWDDMMKVIVGNMAWHAD-STYMPVM	
			:	:: ::	:
gi+AHw-309	SKKYLQAPKDVSQQIKMANKMKKEQYSCDHPPASWDWRKKG	VITQVKYQGGCGSGWAFS			
	110	120	130	140	150
					160

	40	50	60	70	80
AAD-12	AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV				
	: ::	::	:		
gi+AHw-309	ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSF	EWVLEHGGIATDDDY			
	170	180	190	200	210
					220

gi+AHw-309 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 89.1 bits: 22.6 E(): 5.5
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (21-70:23-71)

10 20 30 40 50
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
.. :. : . : . : :.
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
10 20 30 40 50

60 70 80
AAD-12 YDALDEATRALLVHQRSARHSLV
. . . . :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.7 bits: 21.6 E(): 5.7
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (20-48:23-50)

10 20 30 40 50
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.. :. : . : . : :.
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIPQSVKTAEIVEGDDGGVGTIKKISF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALLVHQRSARHSLV
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 88.1 bits: 21.4 E(): 6.3
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (26-74:5-52)

10 20 30 40 50 60
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYD
:. :. . . : . : : :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPIN
10 20 30

70 80
AAD-12 ALDEATRALLVHQRSARHSLV
: . : : : .

gi+AHw-217 PL-EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCCCKELYDASQHCRCEAVRYFIGRRS
40 50 60 70 80 90

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)

initn: 47 initl: 47 opt: 53 Z-score: 87.1 bits: 21.3 E(): 7.1
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (29-80:31-87)

10 20 30 40 50
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
.: .: .: .: .: .: .: .:
gi+AHw-132 MGVFNYYETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
10 20 30 40 50

60 70 80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLV
: : : : :
gi+AHw-132 DEGSPFNYYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.: .: .: .: .: .: .: .:
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV
gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.: .: .: .: .: .: .: .:
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-131 MGVFN YETFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-131 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTY ESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (24-48:27-50)

10 20 30 40 50
AAD-12 VRQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTY ESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLV

60 70 80
AAD-12 AYDALDEATRALVHORSARHSLV

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
 Full+AD0-P34 prob (379 aa)
 initn: 48 initl: 48 opt: 57 Z-score: 85.1 bits: 22.2 E(): 9.1
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (4-65:134-194)

AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTY-MPVM
 : :: :: :
 gi+AHw-129 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
 110 120 130 140 150 160

AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
 : :: : : : : : :
 gi+AHw-129 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFVLEHGGIATDDDDY
 170 180 190 200 210 220

gi+AHw-129 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
 230 240 250 260 270 280

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
 vacuola (379 aa)
 initn: 48 initl: 48 opt: 57 Z-score: 85.1 bits: 22.2 E(): 9.1
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (4-65:134-194)

AAD-12 VRQHSPAEWDDMMKVIVGNMAWHADSTY-MPVM
 : :: :: :
 gi+AHw-119 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
 110 120 130 140 150 160

AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
 : :: : : : : : :
 gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFVLEHGGIATDDDDY
 170 180 190 200 210 220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
 230 240 250 260 270 280

80 residues in 1 query sequences
 331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:52 2010 done: Fri Feb 5 12:55:52 2010

Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 88 - 167 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      1      0: +AD0-
      30      4      2: +ACo-
      32      3      8: +AD0AKg-
      34      7      21: +AD0APQ- +ACo-
      36      35      44: +AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      38      72: +AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      40      95
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42      60      123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      44      112
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0- +ACo-
      46      107
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9- +ACo-
      48      196      132: +AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      50      125
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQ-
      52      100
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      54      75      91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      56      82
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
      58      50      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      60      51      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      62      37      40: +AD0APQA9AD0APQA9AD0APQA9ACo-
      64      57      32: +AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
      66      42      25: +AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
```

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68      41      20:+AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
70      19      16:+AD0APQA9ACoAPQ-
72      34      12:+AD0APQAqAD0APQA9AD0APQA9-
74      19      10:+AD0APQAqAD0APQ-
76      26      7:+AD0AKgA9-+AD0APQA9AD0-
78      8        6:+AD0AKg-
80      8        4:+ACoAPQ-
82      1        3:+ACo-
84      17      3:+ACoAPQA9AD0APQ-
86      2        2:+ACo-
88      3        2:+ACo-          inset +AD0- represents 1 library sequences
90      3        1:+ACo-
92      6        1:+ACoAPQ-          :+ACoAPQA9AD0APQA9-
94      2        1:+ACo-          :+ACoAPQ-
96      0        1:+ACo-          :+ACo-
98      0        0:          +ACo-
100     0        0:          +ACo-
102     1        0:+AD0-          +ACoAPQ-
104     0        0:          +ACo-
106     1        0:+AD0-          +ACoAPQ-
108     0        0:          +ACo-
110     1        0:+AD0-          +ACoAPQ-
112     0        0:          +ACo-
114     0        0:          +ACo-
116     0        0:          +ACo-
118     0        0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.00820.00294+ADs- mu+AD0- 0.1418
0.153
mean+AF8-var+AD0-36.4107 9.920, 0's: 2 Z-trim: 2 B-trim: 223 in 2/41
Lambda+AD0- 0.212549
Kolmogorov-Smirnov statistic: 0.1244 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97)  64 24.9    0.36
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96)  62 24.3    0.55
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  62 24.1    0.92
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.6    2.7
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97)  54 21.8    3
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.6    3
gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group ( 122)
55 22.1    3.3

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gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group ( 122)
55 22.1      3.3
gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName: Full+AD0-P
( 122)  55 22.1      3.3
gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group ( 122)
55 22.1      3.3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  56 22.3      3.8
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
( 158)  55 22.0      4.6
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379)  60 23.1      4.8
gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II ( 196)
56 22.2      4.9
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301)  58 22.6      5.5
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.6      5.8
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145)  53 21.4      6.3
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.3      7.1
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.0      8.7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.7
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.7
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.7
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.7
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.0      8.7
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.7
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.7
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.7
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.7
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.0      8.8
gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName: Full+AD0-P34
( 379)  57 22.2      9.2
gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed vac ( 379)
57 22.2      9.2

```

+AD4APg-gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName:

Full+AD0-Pollen (97 aa)

initn: 56 initl: 56 opt: 64 Z-score: 110.3 bits: 24.9 E(): 0.36

Smith-Waterman score: 64+ADs- 44.000+ACU- identity (64.000+ACU- similar)

in 25 aa overlap (1-25:35-56)


```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                .... : : : : : :
gi+AHw-126  LTVEKGSDAKTLVLNLIK YTRPGDTLAEVELRQH GSEEWEPMTK--KGNL-WEVKSAKPLT
                                10      20      30      40      50      60

```

```

                                40      50      60      70      80
AAD-12  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY

gi+AHw-126  GPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN
                                70      80      90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:
Full+AD0-Poll (96 aa)
initn: 52 init1: 52 opt: 62 Z-score: 107.1 bits: 24.3 E(): 0.55
Smith-Waterman score: 62+ADs- 38.462+ACU- identity (65.385+ACU- similar)
in 26 aa overlap (1-26:35-57)

```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                .... : : : : : :
gi+AHw-144  FKVEKGSDPKKLVLDIKYTRPGDTLAEVELRQH GSEEWEPMTK--GNL-WEVKSSKPLT
                                10      20      30      40      50      60

```

```

                                40      50      60      70      80
AAD-12  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY

gi+AHw-144  GPFNFRFMSKGGMRNVFDEVIPTAFKIGT TYTPEE
                                70      80      90

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 103.0 bits: 24.1 E(): 0.92
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (25-73:5-52)

```

                                10      20      30      40      50      60
AAD-12  RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDA
                                :. :.. ... :. .. :. :. :. :.
gi+AHw-189  MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNP
                                10      20      30      40

```

```

                                70      80
AAD-12  LDEATRALVHQRSARHSLVY
                                : :. : : :.
gi+AHw-189  L-EGCREYVAQQTCGVVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHP
                                50      60      70      80      90

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
initn: 50 init1: 50 opt: 57 Z-score: 94.7 bits: 22.6 E(): 2.7
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (25-73:5-52)

```

                10      20      30      40      50      60
AAD-12  RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDA
                .. ... .. .. .. .. .. ..
gi+AHw-439                MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNP
                        10      20      30      40

```

```

                70      80
AAD-12  LDEATRVLVHQRSARHSLVY
                : .. : : ...
gi+AHw-439 L-EGCREYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSH
                50      60      70      80      90

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
initn: 35 init1: 35 opt: 54 Z-score: 93.7 bits: 21.8 E(): 3
Smith-Waterman score: 54+ADs- 28.070+ACU- identity (50.877+ACU- similar)
in 57 aa overlap (1-57:36-86)

```

                                10      20      30
AAD-12                                RQHSPAEWDDMMKVIVGNMAWHADSTYMPV
                                .... .. : : .. ... : ..
gi+AHw-126 FTVEKGSDEKNLALSIIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-PL
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLVHQRSARHSLVY
                .. :. . : : .. : .. :
gi+AHw-126 --KGP-FNFRFVSEKGMNRNVFDDVVPADFKVGTITYKPE
                70      80      90

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 init1: 55 opt: 57 Z-score: 93.7 bits: 22.6 E(): 3
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (19-47:23-50)

```

                10      20      30      40      50
AAD-12  RQHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. ... : : : : : .. ... : ..
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRVLVHQRSARHSLVY
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-4007040+AHw-emb+AHw-CAA10345.1+AHw- pollen allergen (group
II) (122 aa)
initn: 43 init1: 43 opt: 55 Z-score: 93.1 bits: 22.1 E(): 3.3
Smith-Waterman score: 55+ADs- 31.481+ACU- identity (50.000+ACU- similar)
in 54 aa overlap (1-54:60-107)

```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                :...  ::  ::  :  ::  ::
gi+AHw-400  VTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-PL
              30      40      50      60      70      80

```

```

              40      50      60      70      80
AAD-12  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
              ::  ::  .  .  .  :  .  .  :  ::
gi+AHw-400  --QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90      100     110     120

```

+AD4APg-gi+AHw-4007636+AHw-emb+AHw-CAA10350.1+AHw- pollen allergen (group II) (122 aa)
 initn: 43 init1: 43 opt: 55 Z-score: 93.1 bits: 22.1 E(): 3.3
 Smith-Waterman score: 55+ADs- 31.481+ACU- identity (50.000+ACU- similar)
 in 54 aa overlap (1-54:60-107)

```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                :...  ::  ::  :  ::  ::
gi+AHw-400  VTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-PL
              30      40      50      60      70      80

```

```

              40      50      60      70      80
AAD-12  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
              ::  ::  .  .  .  :  .  .  :  ::
gi+AHw-400  --QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90      100     110     120

```

+AD4APg-gi+AHw-1171009+AHw-sp+AHw-P43214.1+AHw-MPAP2+AF8-PHLPR RecName:
 Full+AD0-Polle (122 aa)
 initn: 43 init1: 43 opt: 55 Z-score: 93.1 bits: 22.1 E(): 3.3
 Smith-Waterman score: 55+ADs- 31.481+ACU- identity (50.000+ACU- similar)
 in 54 aa overlap (1-54:60-107)

```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                :...  ::  ::  :  ::  ::
gi+AHw-117  VTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-PL
              30      40      50      60      70      80

```

```

              40      50      60      70      80
AAD-12  MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
              ::  ::  .  .  .  :  .  .  :  ::
gi+AHw-117  --QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
              90      100     110     120

```

+AD4APg-gi+AHw-4007655+AHw-emb+AHw-CAA10348.1+AHw- pollen allergen (group II) (122 aa)
 initn: 43 init1: 43 opt: 55 Z-score: 93.1 bits: 22.1 E(): 3.3
 Smith-Waterman score: 55+ADs- 31.481+ACU- identity (50.000+ACU- similar)
 in 54 aa overlap (1-54:60-107)

```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
                                :...  ::  :  :  :  :  :  :
gi+AHw-400 VTFTVEKGSNEKHLAVLVKYE GDTMAEVELREHGSDEWVAMTKGEGG--VWTFDSEE-PL
                                30      40      50      60      70      80

```

```

                                40      50      60      70      80
AAD-12 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                                ::  ::  .  .  :  ..  :  ::
gi+AHw-400 --QGP-FNFRFLTEKGMKNVFDDVVPEKYTIGATYAPEE
                                90      100      110      120

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 92.0 bits: 22.3 E(): 3.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                                10      20      30      40      50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  .:  ::...  .  ::
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLADADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
 Full+AD0-Globin (158 aa)
 initn: 39 init1: 39 opt: 55 Z-score: 90.5 bits: 22.0 E(): 4.6
 Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
 in 34 aa overlap (4-31:114-147)

```

                                10      20
AAD-12      RQHSPA EWDDMMKVIV----GNMAWHA--DSTY
                                :...  ...  :  .:  :  :  .  ....
gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
                                90      100      110      120      130      140

```

```

                                30      40      50      60      70      80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                                ::.
gi+AHw-250 APVLDFVFSTLKNEL
                                150

```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0- (379 aa)
 initn: 48 init1: 48 opt: 60 Z-score: 90.1 bits: 23.1 E(): 4.8
 Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
 in 63 aa overlap (3-64:134-194)

```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHAD-STYMPVM
              :  ::  ::      :  ..  ..  ..  ..
gi+AHw-309  SKKYLQAPKDV SQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
              110      120      130      140      150      160

```

```

                40      50      60      70      80
AAD-12  AQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
              :  ::  ..  ..  ::  .  ..  ..  .  :  ::  .
gi+AHw-309  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFEWVLEHGGIATDDDDY
              170      180      190      200      210      220

```

```

gi+AHw-309  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
              230      240      250      260      270      280

```

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
(196 aa)
initn: 35 init1: 35 opt: 56 Z-score: 90.0 bits: 22.2 E(): 4.9
Smith-Waterman score: 56+ADs- 28.070+ACU- identity (52.632+ACU- similar)
in 57 aa overlap (1-57:36-86)

```

                                10      20      30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPV
              ....  ::  .  :  :  ..  :  :  ..
gi+AHw-109  FTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKN--GDGVWEIKSDK-PL
              10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12  MAQQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
              :  :  .  .  :  :  :  :  :  :
gi+AHw-109  --KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTTYKPEEAAAASARRRSSEVFQFLILSC
              70      80      90      100      110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 49 init1: 49 opt: 58 Z-score: 89.1 bits: 22.6 E(): 5.5
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (20-69:23-71)

```

                10      20      30      40      50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQQGAVFSAEVVPAVGGRTCFADMRAA
              ..  ::  :  :  :  .  :  :  :  :  :  :  :
gi+AHw-663  MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
              10      20      30      40      50

```

```

                60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVY
              .  .  .  .  :  :
gi+AHw-663  LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.7 bits: 21.6 E(): 5.8
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (19-47:23-50)

```

                10      20      30      40      50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :::  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVF TYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 88.0 bits: 21.4 E(): 6.3
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (25-73:5-52)

```

                10      20      30      40      50      60
AAD-12  RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDA
                :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-217                MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINP
                10      20      30      40

```

```

                70      80
AAD-12  LDEATRALVHQRSARHSLVY
                :  :  :  :  :  :
gi+AHw-217  L-EGCREYVAQQTCGISISGSASVSTEPGNTPRDRCCCKELYDASQHCRCEAVRYFIGRRSD
                50      60      70      80      90

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)

initn: 47 initl: 47 opt: 53 Z-score: 87.1 bits: 21.3 E(): 7.1
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (28-79:31-87)

```

                10      20      30      40      50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
                :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-132  MGVFNYETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
                10      20      30      40      50

```

```

                60      70      80
AAD-12  DMRAAYDALDEATRALVHQRSARHSLVY
                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-132  DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
 +AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-279 MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSNGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-602 MGVF TYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-602 MGVF TYESEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-131 MGVF NYETEFTSVIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (23-47:27-50)

```
          10          20          30          40          50
AAD-12    RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .: .:  :: :...  .  ::
gi+AHw-602 MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
              10          20          30          40          50
```

```
          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (23-47:27-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVL DADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.4 bits: 21.0 E(): 8.8
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (19-47:23-50)

```

                10         20         30         40         50
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ::  :  .:  .:  .:  ::  ::::.  .  ::
gi+AHw-444  MGVF TYADESTSVITPPRLFKALVLEAD-TLIPK IAPQSVKGAEIVEG DGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
 Full+AD0-P34 prob (379 aa)

initn: 48 initl: 48 opt: 57 Z-score: 85.1 bits: 22.2 E(): 9.2
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (3-64:134-194)

```

                10         20         30
AAD-12      RQHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
                :  ::  ::  :  ..  .  ...
gi+AHw-129  SKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
                110        120        130        140        150        160

```

```

                40         50         60         70         80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                :  ::.  ::::.  :::  .  ::::.  .  :  ::::.
gi+AHw-129  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFVLEHGGIATDDDY
                170        180        190        200        210        220

```

```

gi+AHw-129  PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
                230        240        250        260        270        280

```

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
 vacuola (379 aa)
 initn: 48 initl: 48 opt: 57 Z-score: 85.1 bits: 22.2 E(): 9.2
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (3-64:134-194)

```

                                10      20      30
AAD-12                        RQHSPAEWDDMMKVIVGNMAWHADSTY-MPVM
                                :  ::  ::  :  ..  ..  ...
gi+AHw-119 SKKYLQAPKDVSQQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
              110      120      130      140      150      160

              40      50      60      70      80
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
              :  ::  ..  ....  ::  .  ....  .  :  ....
gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFEWVLEHGGIATDDDY
              170      180      190      200      210      220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
              230      240      250      260      270      280

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:52 2010 done: Fri Feb 5 12:55:52 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 89 - 168 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      2      0:+AD0-
      30      2      2:+ACo-
      32      9      8:+AD0AKgA9-
      34      4      21:+AD0-      +ACo-

```

sequences

```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.96080.00297+ADs- mu+AD0- 0.3733
0.155
mean+AF8-var+AD0-37.4504 9.925, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.209578
Kolmogorov-Smirnov statistic: 0.1244 (N+AD0-29) at 46

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.0 1
gi+AHw-126387+AHw-sp+AHw-P14948.1+AHw-MPAL3+AF8-LOLPR RecName: Full+AD0-Po
( 97) 57 22.6 1.8
gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName: Full+AD0-
( 96) 55 22.0 2.6
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.5 2.9
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.5 3.3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.1 4
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-GL
( 158) 55 21.9 4.9
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 60 23.0 5.1
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.5 5.9
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.5 6.2
gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName: Full+AD0-Po
( 97) 51 20.8 6.2
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.3 6.7
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.2 7.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.0 8.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.3
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 20.9 9.3
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.3
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.3
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.3

```

```

                                10           20           30
AAD-12                QHSPA EWDDMMKVIVGNMAWHDSTYMPVM
                        ...   ... : :   ... .. :
gi+AHw-126 TVEKGS DAKTLVLN IKYTRPGDTLAEVELRQH GSEEWEPMTKK--GNL-WEVKSA KPLTG
              10            20             30          40           50           60

                    40         50        60       70      80
AAD-12 AQGAVFS AEVVP AVGGRTCFADMRAAYDALDEATRALVHQRSARHS L VYS
gi+AHw-126 PMNFRFLSKGGMKNVFDEV IPTAFTVGKT YTP EYN
               70            80           90

```

+AD4APg-gi+AHw-14423759+AHw-sp+AHw-P93124.1+AHw-MPAG3+AF8-DACGL RecName:

Full+AD0-Poll (96 aa)

initn: 45 initl: 45 opt: 55 Z-score: 94.8 bits: 22.0 E(): 2.6

Smith-Waterman score: 55+ADs- 36.000+ACU- identity (64.000+ACU- similar)

in 25 aa overlap (1-25:36-57)

```

                                10      20      30
AAD-12                        QHSPA EWDDMMKVIVGNMAWHADSTYMPVM
                                ...  ...  .  :  ...  ...  ..
gi+AHw-144 KVEKGSDPKKLVLDIKYTRPGDTLAEVELRQHGSEEWEP LTKK--GNL-WEVKSSKPLTG
              10      20      30      40      50      60

```

```

              40      50      60      70      80
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-144 PFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTP EE
              70      80      90

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)

initn: 50 initl: 50 opt: 57 Z-score: 94.1 bits: 22.5 E(): 2.9

Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)

in 49 aa overlap (24-72:5-52)

```

              10      20      30      40      50      60
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL
              ..  ...  ...  .  .  .  .  :  ...  :  .  :
gi+AHw-439 MASKSSITPLLLA AVLASFVFAAATATGQYCYAGMGLPSNPL
              10      20      30      40

```

```

              70      80
AAD-12 DEATRALVHQRSARHSLVYS
              ..  :  :  ...
gi+AHw-439 -EGCREYVAQQTCGVVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHP
              50      60      70      80      90      100

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 93.1 bits: 22.5 E(): 3.3

Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)

in 29 aa overlap (18-46:23-50)

```

              10      20      30      40      50
AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ..  ...  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444 MGVTYADESTSVIPPR LFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKKISF
              10      20      30      40      50

```

```

              60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 91.5 bits: 22.1 E(): 4
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                :::  .:  .:  .:  ::::  .  ::
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
 Full+AD0-Globin (158 aa)
 initn: 39 initl: 39 opt: 55 Z-score: 90.0 bits: 21.9 E(): 4.9
 Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
 in 34 aa overlap (3-30:114-147)

```

                        10      20
AAD-12                        QHSPA EWDDMMKVIV----GNMAWHA--DSTY
                        ::::  .:  .:  .:  :  :  .  ....
gi+AHw-250  EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
                        90      100      110      120      130      140

```

```

                30      40      50      60      70      80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
                ::.
gi+AHw-250  APVLDFVFSTLKNEL
                150

```

+AD4APg-gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0- (379 aa)
 initn: 48 initl: 48 opt: 60 Z-score: 89.6 bits: 23.0 E(): 5.1
 Smith-Waterman score: 60+ADs- 22.222+ACU- identity (61.905+ACU- similar)
 in 63 aa overlap (2-63:134-194)

```

                        10      20      30
AAD-12                        QHSPA EWDDMMKVIVGNMAWHAD-STYMPVM
                        :  ::  ::  :  .  .  .  .  .
gi+AHw-309  SKKYLQAPKDVSQQIKMANKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGSGWAFS
                        110      120      130      140      150      160

```

```

                40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
                :  ::.  .....  ::.  .  .....  .  :  ....
gi+AHw-309  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFVLEHGGIATDDDY
                170      180      190      200      210      220

```


gi+AHw-309 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
 230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 88.6 bits: 22.5 E(): 5.9
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (19-68:23-71)

AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .. :: : : : . : : :
 gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
 10 20 30 40 50

AAD-12 YDALDEATRALVHQRSARHSLVYS
 : :
 gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.2 bits: 21.5 E(): 6.2
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (18-46:23-50)

AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. :: : : : . : : :
 gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDDGGVGTIKKISF
 10 20 30 40 50

AAD-12 AYDALDEATRALVHQRSARHSLVYS
 60 70 80 90 100 110
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
 Full+AD0-Pollen (97 aa)

initn: 32 initl: 32 opt: 51 Z-score: 88.2 bits: 20.8 E(): 6.2
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (50.000+ACU- similar)
 in 56 aa overlap (1-56:37-86)

AAD-12 QHSPA EWDDMMKVIVGNMAWHADSTYMPVM
 ... :: . : : . : : : : :
 gi+AHw-126 TVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKK--NGDGVWEIKSDK-PL-
 10 20 30 40 50 60

AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
 40 50 60 70 80

```

      .:  .:  .:  .:  .:  .:  .:
gi+AHw-126 -KGP-FNFRFVSEKGMARNVFDDVVPADFKVGTTRYKPE
              70              80              90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 87.5 bits: 21.3 E(): 6.7
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (24-72:5-52)

```

              10              20              30              40              50              60
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL
              .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-217              MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL
                      10              20              30              40

```

```

              70              80
AAD-12 DEATRALVHQRSARHSLVYS
              .:  .:  .:  .:
gi+AHw-217 -EGCREYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCEAVRYFIGRRSDP
              50              60              70              80              90              100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (27-78:31-87)

```

              10              20              30              40              50
AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCF
              .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-132 MGVFNYYETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
              10              20              30              40              50

```

```

              60              70              80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYS
              :  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-132 DEGSPFNYYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
              60              70              80              90              100              110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 85.4 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (57-80:29-52)

```

              30              40              50              60              70              80
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
              :  .:  .:  .:  .:  .:  .:  .:  .:  .:  .:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAEARISAKNALESYAYSRLRNTLS
              10              20              30              40              50

```

```

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAG
              60              70              80              90              100              110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVF TYESEFTSIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  :: :...  .  ::
gi+AHw-279  MGVF TYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10         20         30         40         50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... ..: .: :: ::::: . ::
gi+AHw-602  MGVF TYE SEFTSVIPPARLFNAFVL DADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
                60         70         80         90         100         110
```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10         20         30         40         50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... ..: .: :: ::::: . ::
gi+AHw-602  MGVF TYE SEFTSVIPPARLFNAFVL DADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSGSVIKSTSH
                60         70         80         90         100         110
```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10         20         30         40         50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... ..: .: :: ::::: . ::
gi+AHw-602  MGVF TYE SEFTSVIPPARLFNAFVL DADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSGSVIKSTSH
                60         70         80         90         100         110
```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... ..: .: :: ::::. . ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                60      70      80      90      100      110
```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... ..: .: :: ::::. . ::
gi+AHw-131  MGVF NYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... ..: .: :: ::::. . ::
gi+AHw-602  MGVF TYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (22-46:27-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVF TYE SEFTSVIPPARLFNAFVL DADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
                10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 84.9 bits: 20.9 E(): 9.4
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (18-46:23-50)

```

                10      20      30      40      50
AAD-12      QHSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ::  :  .:  .:  .:  ::::.  .  ::
gi+AHw-444  MGVF TYA DESTSVITPPRLFKALVLEAD-TLIPK IAPQSVKGAEIVEG DGGVGTIKKISF
                10      20      30      40      50

```

```

        60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYS

```

```

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-129353+AHw-sp+AHw-P22895.1+AHw-P34+AF8-SOYBN RecName:
Full+AD0-P34 prob (379 aa)

initn: 48 initl: 48 opt: 57 Z-score: 84.7 bits: 22.1 E(): 9.6
Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
in 63 aa overlap (2-63:134-194)

```

                        10      20      30
AAD-12                        QHSPA EWDDMMKVIVGNMAWHADSTY-MPVM
                        :  ::  ::  :  ..  ..  ...
gi+AHw-129  SKKYLQAPKDVSQQIKMANKMKKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGRGWAFS
                110      120      130      140      150      160

```

```

        40      50      60      70      80
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
        :  ::.  .....  :::  .  .....  .  :  ....

```

```

gi+AHw-129  ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSF EWVLEHGGIATDDDY
                170      180      190      200      210      220

```

gi+AHw-129 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
 230 240 250 260 270 280

+AD4APg-gi+AHw-1199563+AHw-gb+AHw-AAB09252.1+AHw- 34 kDa maturing seed
 vacuola (379 aa)

initn: 48 initl: 48 opt: 57 Z-score: 84.7 bits: 22.1 E(): 9.6
 Smith-Waterman score: 57+ADs- 22.222+ACU- identity (58.730+ACU- similar)
 in 63 aa overlap (2-63:134-194)

AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTY-MPVM
 : :: :: :
 gi+AHw-119 SKKYLQAPKDVSSQIKMANKKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFS
 110 120 130 140 150 160

AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
 : :: .. : : .. : :
 gi+AHw-119 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGSYNGWQYQSFEWVLEHGGIATDDDDY
 170 180 190 200 210 220

gi+AHw-119 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
 230 240 250 260 270 280

+AD4APg-gi+AHw-1093120+AHw-prf+AHwAfA-2103117A allergen Dac g II
 (196 aa)

initn: 34 initl: 34 opt: 53 Z-score: 84.6 bits: 21.2 E(): 9.8
 Smith-Waterman score: 53+ADs- 28.571+ACU- identity (51.786+ACU- similar)
 in 56 aa overlap (1-56:37-86)

AAD-12 QHSPAEWDDMMKVIVGNMAWHADSTYMPVM
 : : : : : : : :
 gi+AHw-109 TVEKGSDEKNLALSIIKYNKEGDSMAEVELKEHGSNEWLALKK--NGDGVWEIKSDK-PL-
 10 20 30 40 50 60

AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
 : : : : : : : :
 gi+AHw-109 -KGP-FNFRFVSEKGMNRNVFVDVVPADFKVGTITYKPEEAAAASASRRRSSEVFQFLILSCQ
 70 80 90 100 110 120

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:53 2010 done: Fri Feb 5 12:55:54 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 90 - 169 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]


```

66      56      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
68      48      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
70      13      16:+AD0APQA9AD0APQAq-
72      38      12:+AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
74      17      10:+AD0APQA9ACoAPQA9-
76      17      7:+AD0APQAqAD0APQA9-
78      22      6:+AD0AKgA9AD0APQA9AD0APQ-
80      7       4:+AD0AKgA9-
82      3       3:+ACo-
84      10      3:+ACoAPQA9AD0-
86      12      2:+ACoAPQA9AD0-
88      3       2:+ACo-          inset +AD0- represents 1 library sequences
90      3       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      2       1:+ACo-          :+ACoAPQ-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     1       0:+AD0-          +ACoAPQ-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.09580.00295+ADs- mu+AD0- -
0.5339 0.154
mean+AF8-var+AD0-36.5168 9.708, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.212240
Kolmogorov-Smirnov statistic: 0.1298 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.2 0.88
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.7 2.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.6 2.9
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.3 3.6
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 54 21.8 4.4
gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-Gl
( 158) 55 22.0 4.4
gi+AHw-3097321+AHw-dbj+AHw-BAA25899.1+AHw- Bd 30K +AFs-Glycine max+AF0-
( 379) 60 23.2 4.7

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 62 Z-score: 103.4 bits: 24.2 E(): 0.88
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (23-71:5-52)

70 80

60 70 80

AAD-12
 HSPA EWDDMMKVIVGNMAWHAD-STYPMV
 : : : : : : : : : :
 gi+AHw-309 SKKYLQAPKDVSQQIKMANKMKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGSGWAFS
 110 120 130 140 150 160
 30 40 50 60 70 80

AAD-12 A QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ

: ::. ::. : ::.

gi+AHw-309 ATGAIEAAHAI-ATGDLVSLSEQELV-DCVEESEGCYNGWHYQSFEWVLEHGGIATDDDDY
170 180 190 200 210 220

gi+AHw-309 PYRAKEGRCKANKIQDKVTIDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFH
230 240 250 260 270 280

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 89.3 bits: 22.7 E(): 5.3
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (18-67:23-71)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
.. ::. : : : . : : :
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
10 20 30 40 50

60 70 80
AAD-12 YDALDEATRALVHQRSARHSLVYSQ
. . . . : :
gi+AHw-663 LEDVNAGFKA AVAADANAPPADKFKIFEAFSECKGLLATSDAKAPGLILKLDTDYDVA
60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 89.0 bits: 21.7 E(): 5.5
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (17-45:23-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.. ::. : : : . : : :
gi+AHw-444 MGVTYSDESTSVIPPRLFKALVLEAD-TLIPKIAPQSVKTA EIVEGDGGVGTIKKISF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 88.4 bits: 21.4 E(): 6
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (23-71:5-52)

10 20 30 40 50 60
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
:. :.. . : : : : : : : : : : : :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-

AAD-12 MPVMAQGAVFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSRLRNTLS

```

                10          20          30          40          50
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAG
           60          70          80          90         100         110

```

```

+AD4APg-gi+AHw-126386+AHw-sp+AHw-P14947.1+AHw-MPAL2+AF8-LOLPR RecName:
Full+AD0-Pollen (97 aa)
  initn: 32 initl: 32 opt: 49 Z-score: 85.8 bits: 20.4 E(): 8.3
Smith-Waterman score: 49+ADs- 29.091+ACU- identity (49.091+ACU- similar)
in 55 aa overlap (1-55:38-86)

```

```

                                10          20          30
AAD-12                        HSPA EWDDMMKVIVGNMAWHADSTYMPVMA
                                ..  ::  .  :  ::  ...  :  ::
gi+AHw-126 VEKGSDEKNLALSIIKYNKEGDSMAEVELKEHGSNEWLALKK--NGDGVWEIKSDK-PL--
           10          20          30          40          50          60

```

```

                40          50          60          70          80
AAD-12 QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
           ..  ::  .  :  :  ::  :  ::  :
gi+AHw-126 KGP-FNFRFVSEKGM RNVFDDVVPADFKVGT TYKPE
           70          80          90

```

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

```

```

                10          20          30          40          50
AAD-12      HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  ::  .  :  ::  ::...  .  ::
gi+AHw-602 MGVTYSEFTSIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
           10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-602 GEGSTYSYVKHRIDGV DKNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
           60          70          80          90         100         110

```

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

```

```

                10          20          30          40          50
AAD-12      HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  ::  .  :  ::  ::...  .  ::
gi+AHw-602 MGVTYSEFTSVIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEG DGGVGTIKKINF
           10          20          30          40          50

```

```

           60          70          80

```

AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :: :::: . :
gi+AHw-279 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-279 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :: :::: . :
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :: :::: . :
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80

AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :: :::: . : ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :: :::: . : ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :: :::: . : ::
gi+AHw-131 MGVTNYETEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80

AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :: :::: . : ::
gi+AHw-602 MG VFTY ESEFTSVIPPARLFNAFVLADNL-IPK IAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (21-45:27-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :: :::: . : ::
gi+AHw-602 MG VFTY ESEFTSVIPPARLFNAFVLADNL-IPK IAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.7 bits: 21.1 E(): 8.4
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (17-45:23-50)

10 20 30 40 50
AAD-12 HSPA EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.. :: : : : : : : :::: . : ::
gi+AHw-444 MG VFTY ADESTSVITPPRLFKALVLEAD-TLIPK IAPQSVKGAEIVEGDGGVGTIKKISF
10 20 30 40 50

60 70 80

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:54 2010 done: Fri Feb 5 12:55:54 2010
Total Scan time: 0.080 Total Display time: 0.010

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APg-+AD4-AAD-12: 91 - 170 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

58      19
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
   60    46    50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9-+AD0APQA9AD0AKg-
   62    38    40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
   64    35    32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
   66    60    25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQ-
   68    26    20:+AD0APQA9AD0APQA9ACoAPQA9-
   70    35    16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
   72    28    12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
   74    29    10:+AD0APQA9ACoAPQA9AD0APQA9AD0-
   76    20     7:+AD0APQAqAD0APQA9AD0-
   78    19     6:+AD0AKgA9AD0APQA9AD0-
   80     7     4:+AD0AKgA9-
   82     6     3:+ACoAPQ-
   84     1     3:+ACo-
   86    14     2:+ACoAPQA9AD0APQ-
   88     3     2:+ACo-                inset +AD0- represents 1 library sequences
   90     3     1:+ACo-
   92     2     1:+ACo-                :+ACoAPQ-
   94     1     1:+ACo-                :+ACo-
   96     2     1:+ACo-                :+ACoAPQ-
   98     0     0:                    +ACo-
  100     0     0:                    +ACo-
  102     0     0:                    +ACo-
  104     0     0:                    +ACo-
  106     1     0:+AD0-                +ACoAPQ-
  108     0     0:                    +ACo-
  110     0     0:                    +ACo-
  112     0     0:                    +ACo-
  114     0     0:                    +ACo-
  116     0     0:                    +ACo-
  118     0     0:                    +ACo-
+AD4-120      0      0:                    +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.05660.00294+ADs- mu+AD0- -
0.3656 0.153
mean+AF8-var+AD0-33.5864 9.201, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.221306
Kolmogorov-Smirnov statistic: 0.1224 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)    62 24.6        0.65
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 23.0            2
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 23.0            2.3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)    56 22.7        2.8

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gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName: Full+AD0-GL
( 158)  55 22.3      3.5
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  54 22.1      3.5
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301)  58 23.0      4.3
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 22.0      4.4
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145)  53 21.7      4.8
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.7      5.5
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.4      6.4
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.4      6.8
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.4      6.8
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.4      6.8
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.4      6.8
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.4      6.8
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.4      6.8
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.4      6.8
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.4      6.8
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.4      6.8
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.4      6.8
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.4      6.9
gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA ( 301)
55 22.0      8.3
gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P
( 133)  50 20.8      8.4
gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - be ( 26)
40 18.4      8.6
gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sw ( 26)
40 18.4      8.6
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  55 22.0      9.7

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```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
  initn: 55 initl: 55 opt: 62 Z-score: 105.7 bits: 24.6 E(): 0.65
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (22-70:5-52)

```

10

20

30

40

50

60

AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
 : : : : : : : : : :
 gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-E
 10 20 30 40

70 80
 AAD-12 ATRALVHQRSARHSLVYSQS
 . : : :..
 gi+AHw-189 GCREYVAQQTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWR
 50 60 70 80 90 100

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 97.0 bits: 23.0 E(): 2
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (22-70:5-52)

10 20 30 40 50 60
 AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
 : : : : : : : : : :
 gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-E
 10 20 30 40

70 80
 AAD-12 ATRALVHQRSARHSLVYSQS
 . : : :..
 gi+AHw-439 GCREYVAQQTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDW
 50 60 70 80 90 100

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 95.9 bits: 23.0 E(): 2.3
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (16-44:23-50)

10 20 30 40 50
 AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 : : : : : : : : : :
 gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKSAEIVEGDGGVGTIKKISF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQS
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 94.2 bits: 22.7 E(): 2.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (20-44:27-50)

10 20 30 40 50

AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: .: .: .: .: .: .:
 gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQS
 gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-2506460+AHw-sp+AHw-P02221.2+AHw-GLB1+AF8-CHITH RecName:
 Full+AD0-Globin (158 aa)
 initn: 39 initl: 39 opt: 55 Z-score: 92.6 bits: 22.3 E(): 3.5
 Smith-Waterman score: 55+ADs- 32.353+ACU- identity (58.824+ACU- similar)
 in 34 aa overlap (1-28:114-147)

10 20
 AAD-12 SPAEWDDMMKVIV----GNMAWHA--DSTY
 ::. .: .: .: .: .: .: .: .:
 gi+AHw-250 EVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDNFRKSLVVYLKGATKWDSAVESSW
 90 100 110 120 130 140

30 40 50 60 70 80
 AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS
 ::.
 gi+AHw-250 APVLDFVFSTLKNEL
 150

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 32 initl: 32 opt: 54 Z-score: 92.6 bits: 22.1 E(): 3.5
 Smith-Waterman score: 54+ADs- 32.000+ACU- identity (64.000+ACU- similar)
 in 50 aa overlap (32-79:9-54)

10 20 30 40 50
 AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--D
 : ::. .: .: .: .: .: .: .: .:
 gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIE
 10 20 30

60 70 80
 AAD-12 EATRALVHQRSARHSLVYSQS
 :
 gi+AHw-111 QANHAI--EKGEHQLLYLQHQLDLENENKSKELQEKIIRELDVVCAMIEGAQGALEREL
 40 50 60 70 80 90

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 91.1 bits: 23.0 E(): 4.3
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (17-66:23-71)

10 20 30 40 50

AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .. :. : : : : : : : : : : : : : : :
 gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
 10 20 30 40 50

60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQS
 : : :
 gi+AHw-663 LEDVNAGFKAABAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 90.8 bits: 22.0 E(): 4.4
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (16-44:23-50)

10 20 30 40 50
 AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. :. : : : : : : : : : : : : : : :
 gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQS
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 90.1 bits: 21.7 E(): 4.8
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (22-70:5-52)

10 20 30 40 50 60
 AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
 :. :. . :. . . : : : : : : : : : :
 gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-E
 10 20 30 40

70 80
 AAD-12 ATRALVHQRSARHSLVYSQS
 . : : : .
 gi+AHw-217 GCREYVAQQTCGISISGSVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNS
 50 60 70 80 90 100

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 89.0 bits: 21.7 E(): 5.5
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (25-76:31-87)

10 20 30 40

50 60 70 80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQS
:
gi+AHw-132 DEGSPFN~~Y~~IKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
60 70 80 90 100 110

AAD-12 MPVMAQGAVFSAEVPVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSRLRNTLS

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAx18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQS
 gi+AHw-602 GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

10
20
30
40
50

AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMR

::
::
::
::
::
::
::
::

qi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADADNL-IPKIAPOAVKSAEILEGDDGGVGTIKKINF

10 20 30 40 50
60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

10 20 30 40 50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

10 20 30 40 50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

10 20 30 40 50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF

```

                10          20          30          40          50
        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

                10          20          30          40          50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-279 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
        10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

                10          20          30          40          50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
        10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

                10          20          30          40          50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-131 MGVFNYETEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
```

```

                10          20          30          40          50
      60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60          70          80          90          100          110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

                10          20          30          40          50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10          20          30          40          50

      60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
      60          70          80          90          100          110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.4 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (20-44:27-50)

                10          20          30          40          50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10          20          30          40          50

      60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60          70          80          90          100          110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
  initn: 50 initl: 50 opt: 52 Z-score: 87.3 bits: 21.4 E(): 6.9
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (16-44:23-50)

                10          20          30          40          50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        .. ::. : .: .: .: ::::. . ::
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIAPQSVKGAEIVEGDDGGVGTIKKISF
```

```

                10          20          30          40          50
      60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQS

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
      60          70          80          90          100          110

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
pre (301 aa)
  initn: 53 init1: 53 opt: 55 Z-score: 85.9 bits: 22.0 E(): 8.3
Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (11-56:16-62)

                10          20          30          40          50
AAD-12 SPAEWDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
      ...: : . :: : : : . : . :.....
gi+AHw-441 MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
      10          20          30          40          50          60

      60          70          80
AAD-12 YDALDEATRALVHQRSARHSLVYSQS
      :
gi+AHw-441 EDVNAGFKA AVAAAAANAPPADKFKIFEAFSESSKGLLATSAAKAPGLIPKLDTAYDVAY
      70          80          90          100          110          120

+AD4APg-gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName:
Full+AD0-Proba (133 aa)
  initn: 50 init1: 50 opt: 50 Z-score: 85.8 bits: 20.8 E(): 8.4
Smith-Waterman score: 50+ADs- 28.125+ACU- identity (59.375+ACU- similar)
in 32 aa overlap (11-42:11-42)

                10          20          30          40          50          60
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
      :... :: ... : : : :...
gi+AHw-249 MRTVSMAALVVIAAALAWTSSAEPAPAPAGEEACGKVVDIMPCLHFKVKGEEKEPSKEC
      10          20          30          40          50          60

      70          80
AAD-12 ATRALVHQRSARHSLVYSQS

gi+AHw-249 CSGTKKLSEEVKTTEQKREACKCIVRATKGISGIKNELVAEVPKKCDIKTTLPITADFD
      70          80          90          100          110          120

+AD4APg-gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - bent
g (26 aa)
  initn: 40 init1: 40 opt: 40 Z-score: 85.6 bits: 18.4 E(): 8.6
Smith-Waterman score: 40+ADs- 57.143+ACU- identity (100.000+ACU- similar)
in 7 aa overlap (18-24:19-25)

                10          20          30          40          50
AAD-12 SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
      :.....
gi+AHw-320 YTTEGGTKAEADVIPEGWKADTSYE
```

10 20

+AD4APg-gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I -
 sweet (26 aa)
 initn: 40 initl: 40 opt: 40 Z-score: 85.6 bits: 18.4 E(): 8.6
 Smith-Waterman score: 40+ADs- 57.143+ACU- identity (100.000+ACU- similar)
 in 7 aa overlap (18-24:19-25)

```

                10      20      30      40      50
AAD-12  SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
                .....:
gi+AHw-320 YTTEGGKKVEAEDVIPEGWKADTSYE
                10      20

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 55 initl: 55 opt: 55 Z-score: 84.6 bits: 22.0 E(): 9.7
 Smith-Waterman score: 55+ADs- 30.556+ACU- identity (58.333+ACU- similar)
 in 36 aa overlap (3-38:155-190)

```

                                10      20      30
AAD-12                                SPAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                                : . . . . . : . . . . . :
gi+AHw-249 QLTSKLDAALKLAYEAAQGATPEAKYDAYVATLLEALRVIAGTLEVHAVKPAAEVVKVGA
                130      140      150      160      170      180

                40      50      60      70      80
AAD-12  VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS
                . . . . .
gi+AHw-249 IPAAEVQLIDKVDAAAYRTAATAANAAPANDKFTVFENTFNNAIKVS LGAAAYDSYKFIPTL
                190      200      210      220      230      240

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:54 2010 done: Fri Feb 5 12:55:54 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 92 - 171 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

88      1      2: +ACo-      inset +AD0- represents 1 library sequences
90      3      1: +ACo-
92      0      1: +ACo-      : +ACo-
94      2      1: +ACo-      : +ACoAPQ-
96      2      1: +ACo-      : +ACoAPQ-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     1      0: +AD0-      +ACoAPQ-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.02820.00296+ADs- mu+AD0- -
0.2039 0.155
mean+AF8-var+AD0-33.9199 9.303, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.220215
Kolmogorov-Smirnov statistic: 0.1244 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.6 0.68
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 23.0 2.1
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.9 2.4
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 55 22.4 2.9
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.6 2.9
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.9 4.4
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 22.0 4.6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.7 5
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.7 5.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.4 6.6
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7

```

10 20 30 40 50 60

AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEA
 :. :. :. :. :. :. :. :. :. :.
 gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EG
 10 20 30 40

70 80
 AAD-12 TRALVHQRSARHSLVYSQSK
 : : :.
 gi+AHw-439 CREYVAQQTTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWS
 50 60 70 80 90 100

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 95.7 bits: 22.9 E(): 2.4
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (15-43:23-50)

10 20 30 40 50
 AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. :. :. :. :. :. :. :.
 gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 32 initl: 32 opt: 55 Z-score: 94.1 bits: 22.4 E(): 2.9
 Smith-Waterman score: 55+ADs- 30.769+ACU- identity (63.462+ACU- similar)
 in 52 aa overlap (31-80:9-56)

10 20 30 40 50
 AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--D
 : :. :. :. :. :. :.
 gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIE
 10 20 30

60 70 80
 AAD-12 EATRALVHQRSARHSLVYSQSK
 :.
 gi+AHw-111 QANHAI---EKGEHQLLYLQHQLDLENENKSKELQEKIIRELDVVCAMIEGAQGALEREL
 40 50 60 70 80 90

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 94.0 bits: 22.6 E(): 2.9
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (19-43:27-50)

10 20 30 40 50

AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: .: .: .: .: .: .:
 gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
 gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 90.9 bits: 22.9 E(): 4.4
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (16-65:23-71)

10 20 30 40 50
 AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .. ::. : .: .: .: .: .: .: .:
 gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
 10 20 30 40 50

60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSK
 : .:
 gi+AHw-663 LEDVNAGFKAABAADANAPPADKFKIFEAAFSSECKGLLATSDAKAPGLILKLDTDYDVA
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 90.5 bits: 22.0 E(): 4.6
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (15-43:23-50)

10 20 30 40 50
 AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. ::. : .: .: .: .: .: .: .:
 gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDGGVGTIKKISF
 10 20 30 40 50

60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 89.8 bits: 21.7 E(): 5
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (21-69:5-52)

10 20 30 40 50 60

10
20
30
40
50

AAD-12
 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMR

::
::
::
::
::
::
::
::

gi+AHw-602
 MGVFTYESEFTSIIPPARLFNAFVLADNL-IPKIAPOAVKSAEILEGDDGGVGTIKKINF

10 20 30 40 50
60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF

10 20 30 40 50
60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK
gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

10 20 30 40 50
AAD-12 PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF

```

                10          20          30          40          50
        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-131 MGVFNYTEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.2 bits: 21.3 E(): 7
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (19-43:27-50)

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
```



```

                10          20          30          40          50
        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
        60          70          80          90          100          110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
  initn: 50 initl: 50 opt: 52 Z-score: 87.1 bits: 21.3 E(): 7.1
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (15-43:23-50)

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        .. .:: : .: .: .: .::: . :
gi+AHw-444 MGVFTYADESTSVITPPRLFKA LVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                10          20          30          40          50

        60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSK

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
        60          70          80          90          100          110

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
pre (301 aa)
  initn: 53 initl: 53 opt: 55 Z-score: 85.7 bits: 22.0 E(): 8.5
Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (10-55:16-62)

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        ...: : . :: : : . : . : .::: . ...
gi+AHw-441 MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
                10          20          30          40          50          60

        60          70          80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSK
:
gi+AHw-441 EDVNAGFKA AVAAAAANAPPADKFKIFEAFSESSKGLLATSAAKAPGLIPKLDTAYDVAY
                70          80          90          100          110          120

+AD4APg-gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName:
Full+AD0-Proba (133 aa)
  initn: 50 initl: 50 opt: 50 Z-score: 85.6 bits: 20.8 E(): 8.6
Smith-Waterman score: 50+ADs- 28.125+ACU- identity (59.375+ACU- similar)
in 32 aa overlap (10-41:11-42)

                10          20          30          40          50
AAD-12          PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDE
                        .... .:: ... : : : .::: .
gi+AHw-249 MRTVSMAALVVIAAALAWTSSAEPAPAPAPGEEACGKVVDIMPCLHFKVKGEEKEPSKEC

```

```

                10         20         30         40         50         60
60      70      80
AAD-12  ATRALVHQRSARHSLVYSQSK

gi+AHw-249  CSGTKKLSEEVKTTEQKREACKCIVRATKGISGIKNELVAEVPKKCDIKTTLPITADFD
                70         80         90        100        110        120

+AD4APg-gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - bent
g (26 aa)
  initn:  40 initl:  40 opt:  40 Z-score: 85.3 bits: 18.4 E():  8.9
Smith-Waterman score: 40+ADs-  57.143+ACU- identity (100.000+ACU- similar)
in 7 aa overlap (17-23:19-25)
```

```

                10         20         30         40         50
AAD-12  PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
                :.:.:.:.:
gi+AHw-320  YTTEGGTKAEAEVDVIPEGWKADTSYE
                10         20
```

```

+AD4APg-gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I -
sweet (26 aa)
  initn:  40 initl:  40 opt:  40 Z-score: 85.3 bits: 18.4 E():  8.9
Smith-Waterman score: 40+ADs-  57.143+ACU- identity (100.000+ACU- similar)
in 7 aa overlap (17-23:19-25)
```

```

                10         20         30         40         50
AAD-12  PAEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
                :.:.:.:.:
gi+AHw-320  YTTEGGKKVEAEVDVIPEGWKADTSYE
                10         20
```

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
  initn:  55 initl:  55 opt:  55 Z-score: 84.5 bits: 21.9 E():  9.9
Smith-Waterman score: 55+ADs-  30.556+ACU- identity (58.333+ACU- similar)
in 36 aa overlap (2-37:155-190)
```

```

                                10         20         30
AAD-12                                PAEWDDMMKVIVGNMAWHADSTYMPVMAQGA
                                : . . . . . :. . . . :
gi+AHw-249  QLTSKLDAALKLAYEAAQGATPEAKYDAYVATLLEALRVIAGTLEVHAVKPAAEEVKVGA
                130         140         150         160         170         180

                40         50         60         70         80
AAD-12  VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSK
                . . . . .
gi+AHw-249  IPAAEVQLIDKVDAAAYRTAATAANAAPANDKFTVFENTFNNAIKVS LGAA YDSYKFIPTL
                190         200         210         220         230         240
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences

```
Scomplib +AFs-34t26+AF0-
start: Fri Feb  5 12:55:54 2010 done: Fri Feb  5 12:55:54 2010
Total Scan time:  0.090 Total Display time:  0.000
```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 93 - 172 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

54      83
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0- +ACo-
56      74
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58      66      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQAqAD0-
60      46      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62      44      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      30      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      55      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
68      40      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
70      21      16:+AD0APQA9AD0APQAqAD0-
72      41      12:+AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQ-
74      17      10:+AD0APQA9-+ACoAPQA9-
76      16      7:+AD0APQAqAD0APQA9-
78      20      6:+AD0AKgA9AD0APQA9AD0-
80      7      4:+AD0AKgA9-
82      5      3:+ACoAPQ-
84      5      3:+ACoAPQ-
86      13      2:+ACoAPQA9AD0APQ-
88      1      2:+ACo- inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      0      1:+ACo- :+ACo-
94      2      1:+ACo- :+ACoAPQ-
96      1      1:+ACo- :+ACo-
98      0      0: +ACo-
100     0      0: +ACo-
102     1      0:+AD0- +ACoAPQ-
104     1      0:+AD0- +ACoAPQ-
106     0      0: +ACo-
108     0      0: +ACo-
110     0      0: +ACo-
112     0      0: +ACo-
114     0      0: +ACo-
116     0      0: +ACo-
118     0      0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.88880.0028+ADs- mu+AD0- 0.6239
0.147
mean+AF8-var+AD0-34.2067 9.660, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.219290
Kolmogorov-Smirnov statistic: 0.1101 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are: opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.5 0.72

```

```

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 60 23.9 1
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.9 2.2
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.9 2.5
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.5 3.1
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.9 4.5
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.9 4.8
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.6 5.2
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.6 6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.3 6.9
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.4
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.4
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.4
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.4
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.4
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.4
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.3 7.4
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.4
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.3 7.4
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.4
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.3 7.4
gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA ( 301)
55 22.0 8.7
gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P
( 133) 50 20.7 9.1
gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - be ( 26)
40 18.2 9.9
gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sw ( 26)
40 18.2 9.9

```

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)

```

```

initn: 55 initl: 55 opt: 62 Z-score: 104.9 bits: 24.5 E(): 0.72
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (20-68:5-52)

```

```

          10          20          30          40          50          60
AAD-12  AEWDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
          :.  ...  ...  :.  ...  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-189      MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGC
                  10          20          30          40

```

```

          70          80
AAD-12  RALVHQRSARHSLVYSQSKL
          :  :  :..
gi+AHw-189  REYVAQQTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCRVRYFIGRRSHPDWRVL
          50          60          70          80          90          100

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 34 init1: 34 opt: 60 Z-score: 102.2 bits: 23.9 E(): 1
Smith-Waterman score: 60+ADs- 32.075+ACU- identity (64.151+ACU- similar)
in 53 aa overlap (30-80:9-57)

```

          10          20          30          40          50
AAD-12  AEWDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DE
          :  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-111      MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQ
                  10          20          30

```

```

          60          70          80
AAD-12  ATRALVHQRSARHSLVYSQSKL
          :...:  .....: : :
gi+AHw-111  ANHAI---EKGEHQLLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELK
          40          50          60          70          80          90

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of
tetrameric (145 aa)
initn: 50 init1: 50 opt: 57 Z-score: 96.3 bits: 22.9 E(): 2.2
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (20-68:5-52)

```

          10          20          30          40          50          60
AAD-12  AEWDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
          :.  ...  ...  :.  ...  :.  :.  :.  :.  :.  :.  :.  :.
gi+AHw-439      MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGC
                  10          20          30          40

```

```

          70          80
AAD-12  RALVHQRSARHSLVYSQSKL
          :  :  :..
gi+AHw-439  REYVAQQTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSV
          50          60          70          80          90          100

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 init1: 55 opt: 57 Z-score: 95.3 bits: 22.9 E(): 2.5
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (14-42:23-50)

```

                10      20      30      40      50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :::  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 init1: 55 opt: 56 Z-score: 93.6 bits: 22.5 E(): 3.1
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10      20      30      40      50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                :::  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium per (301 aa)
 initn: 49 init1: 49 opt: 58 Z-score: 90.6 bits: 22.9 E(): 4.5
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (15-64:23-71)

```

                10      20      30      40      50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ..  :::  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-663  MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10      20      30      40      50

```

```

                60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKL
                .  .  .  .  :  :  :
gi+AHw-663  LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 52 init1: 52 opt: 54 Z-score: 90.2 bits: 21.9 E(): 4.8
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (14-42:23-50)

```

                10      20      30      40      50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ...  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 89.4 bits: 21.6 E(): 5.2
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (20-68:5-52)

```

                10      20      30      40      50      60
AAD-12  AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEAT
                :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-217  MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGC
                10      20      30      40

```

```

                70      80
AAD-12  RALVHQRSARHSLVYSQSKL
                :  :  :
gi+AHw-217  REYVAQQTCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSV
                50      60      70      80      90      100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 88.5 bits: 21.6 E(): 6
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (23-74:31-87)

```

                10      20      30      40
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-132  MGVFN YETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  DMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                :  :  :  :  :  :  :  :  :  :
gi+AHw-132  DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 87.3 bits: 21.3 E(): 6.9
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (53-76:29-52)


```

          30          40          50          60          70          80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
          : : : : : : : : : : : :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
          10          20          30          40          50
```

```

gi+AHw-144  DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAG
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          : : : : : : : : : : : :
gi+AHw-602  MGVFTYESEFTSIIPPAPLAFVLDADNL-IPKIAQAVKSAEILEGDDGGVGTIKKINF
          10          20          30          40          50
```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          : : : : : : : : : : : :
gi+AHw-602  MGVFTYESEFTSVIPPAPLAFVLDADNL-IPKIAQAVKSAEILEGDDGGVGTIKKINF
          10          20          30          40          50
```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
```

```

                ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

                10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                ... .. : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

                10          20          30          40          50
AAD-12 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... .. : : : : : :
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

                10          20          30          40          50
AAD-12 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... .. : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (18-42:27-50)

```

                10          20          30          40          50
AAD-12 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

:::  .: .:  :: :... .  ::
gi+AHw-131 MGVFN YET EFTSVIP PARLFNAFVLDADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

        60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90         100         110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.8 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (18-42:27-50)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          :::  .: .:  :: :... .  ::
gi+AHw-602 MGVFTY ESEFTSVIP PARLFNAFVLDADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

        60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
        60          70          80          90         100         110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 86.7 bits: 21.3 E(): 7.4
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (14-42:23-50)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          .. :... : .: .:  .: :... :  ::
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPK IAPQSVKGA EIVEG DGGVGTIKKISF
          10          20          30          40          50

```

```

        60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKL

```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
        60          70          80          90         100         110

```

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA pre (301 aa)

initn: 53 initl: 53 opt: 55 Z-score: 85.5 bits: 22.0 E(): 8.7
 Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (9-54:16-62)

```

          10          20          30          40          50
AAD-12      AEWDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA

```

10
20
30
40
50

AAD-12 AEWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD
: : : : :

gi+AHw-320 YTTEGGKKVEAEDVIPEGWKADTSYE
10
20

	opt	E ()	
+ADw-	20	2	0:+AD0-
22	1		one +AD0- represents 3 library sequences
24	1		0:+AD0-
26	2		0:+AD0-
28	1		0:+AD0-
30	3		2:+ACo-
32	3		8:+AD0- +ACo-
34	10		21:+AD0APQA9AD0- +ACo-
36	33		44:+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
38	43		72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
40	100		
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-			
42	59		123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-			
44	115		136:+AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-			
D0APQA9AD0- +ACo-			
46	111		
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-			
QA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-			
48	163		
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0-			
9AD0-			
50	147		
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-			
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-			
52	82		
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-			
QA9AD0- +ACo-			

```

54      80
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9-   +ACo-
56      80
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9-
58      66
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60      42      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
62      41      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      37      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66      55      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
68      34      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
70      32      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      31      12:+AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
74      22      10:+AD0APQA9ACoAPQA9AD0APQ-
76      16      7:+AD0APQAqAD0APQA9-
78      20      6:+AD0AKgA9AD0APQA9AD0-
80      7      4:+AD0AKgA9-
82      5      3:+ACoAPQ-
84      5      3:+ACoAPQ-
86      13      2:+ACoAPQA9AD0APQ-
88      1      2:+ACo-               inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      0      1:+ACo-               :+ACo-
94      2      1:+ACo-               :+ACoAPQ-
96      1      1:+ACo-               :+ACo-
98      0      0:                   +ACo-
100     0      0:                   +ACo-
102     1      0:+AD0-               +ACoAPQ-
104     1      0:+AD0-               +ACoAPQ-
106     0      0:                   +ACo-
108     0      0:                   +ACo-
110     0      0:                   +ACo-
112     0      0:                   +ACo-
114     0      0:                   +ACo-
116     0      0:                   +ACo-
118     0      0:                   +ACo-
+AD4-120    0      0:                   +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.93370.00278+ADs- mu+AD0- 0.3618
0.146
mean+AF8-var+AD0-34.0260 9.566, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.219872
Kolmogorov-Smirnov statistic: 0.1107 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                               opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)    62 24.5      0.7

```

```

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 60 23.9 0.99
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.9 2.1
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.9 2.4
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.6 3
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.9 4.4
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.9 4.7
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.7 5.1
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.6 5.8
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.3 6.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.2
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.2
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.2
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.2
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.2
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.2
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.3 7.2
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.2
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.3 7.2
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.3 7.2
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.3 7.3
gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA ( 301)
55 22.0 8.6
gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P
( 133) 50 20.8 8.9
gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - be ( 26)
40 18.3 9.5
gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sw ( 26)
40 18.3 9.5

```

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)

```

```

initn: 55 initl: 55 opt: 62 Z-score: 105.1 bits: 24.5 E(): 0.7
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (19-67:5-52)

```


70
80
 AAD-12 ALVHQRSARHSLVYSQSKLG
:
...
 gi+AHw-189 EYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRVRVYFIGRRSHPDWRVLK
50
60
70
80
90
100

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 34 initl: 34 opt: 60 Z-score: 102.4 bits: 23.9 E(): 0.99
Smith-Waterman score: 60+ADs- 32.075+ACU- identity (64.151+ACU- similar)
in 53 aa overlap (29-79:9-57)

AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEA
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQA

60 70 80
AAD-12 TRALVHQRSARHSLVYSQSKLG
... .. : :
gi+AHw-111 NHAI---EKGEHQLLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKR
40 50 60 70 80 90

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 96.5 bits: 22.9 E(): 2.1
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (19-67:5-52)

10 20 30 40 50 60
 AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
 : . . . : : : . : :
 gi+AHw-439 MASKSSITPLLLAASVFAAATATGQYCYAGMGLPSNPL-EGCR
 10 20 30 40

70 80
 AAD-12 ALVHQRSARHSLVYSQSKLG
 : ...
 gi+AHw-439 EYVAQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVL
 50 60 70 80 90 100

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 init1: 55 opt: 57 Z-score: 95.5 bits: 22.9 E(): 2.4
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (13-41;23-50)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ... :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
initn: 55 init1: 55 opt: 56 Z-score: 93.8 bits: 22.6 E(): 3
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (17-41:27-50)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

                60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs- Lolium per (301 aa)
initn: 49 init1: 49 opt: 58 Z-score: 90.8 bits: 22.9 E(): 4.4
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (14-63:23-71)

```

                10         20         30         40         50
AAD-12          EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ..  ... :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-663  MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10         20         30         40         50

```

```

                60         70         80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLG
                .  .  .  .  :  :  :
gi+AHw-663  LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
initn: 52 init1: 52 opt: 54 Z-score: 90.3 bits: 21.9 E(): 4.7
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (13-41:23-50)

```

                10      20      30      40      50
AAD-12      EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ... :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

                60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 89.6 bits: 21.7 E(): 5.1
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (19-67:5-52)

```

                10      20      30      40      50      60
AAD-12  EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATR
                :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-217  MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCR
                10      20      30      40

```

```

                70      80
AAD-12  ALVHQRSARHSLVYSQSKLG
                :  :  :
gi+AHw-217  EYVAQQTGCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVL
                50      60      70      80      90      100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 88.6 bits: 21.6 E(): 5.8
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (22-73:31-87)

```

                10      20      30      40
AAD-12      EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
                :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-132  MGVFNYETETTSVIPPARLFKRFVLDSNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLG
                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-132  DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 87.4 bits: 21.3 E(): 6.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (52-75:29-52)

```

          30          40          50          60          70          80
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLG
          : : : : : : : : : :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
          10          20          30          40          50

```

```

gi+AHw-144  DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAG
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

          10          20          30          40          50
AAD-12      EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          : : : : : : : : : :
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
 1.03D (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

          10          20          30          40          50
AAD-12      EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          : : : : : : : : : :
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
          10          20          30          40          50

```

```

          60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

          10          20          30          40          50
AAD-12      EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

```

                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                10          20          30          40          50
AAD-12      EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                10          20          30          40          50
AAD-12      EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10          20          30          40          50

```

```

                60          70          80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                10          20          30          40          50
AAD-12      EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (17-41:27-50)

10 20 30 40 50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (17-41:27-50)

10 20 30 40 50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (17-41:27-50)

10 20 30 40 50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

```

                ... .. : : : : : :
gi+AHw-131 MGVFNYETFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (17-41:27-50)

```

                10         20         30         40         50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ... .. : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 86.9 bits: 21.3 E(): 7.3
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (13-41:23-50)

```

                10         20         30         40         50
AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. : : : : : : : : : : : :
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEG DGGVGTIKKISF
                10         20         30         40         50

```

```

                60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLG

```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA pre (301 aa)

initn: 53 init1: 53 opt: 55 Z-score: 85.6 bits: 22.0 E(): 8.6
 Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (8-53:16-62)

```

                10         20         30         40         50
AAD-12 EWDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA

```

10
20
30
40
50

AAD-12 EWDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALD

: : : : :

gi+AHw-320 YTTEGGKKVEAEDVIPEGWKADTSYE

10
20

[illegible]

```

54      80      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
56      72
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
58      61
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
60      50      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62      44      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      31      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      55      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
68      35      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      33      16:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
72      30      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      20      10:+AD0APQA9ACoAPQA9AD0-
76      16      7:+AD0APQA9AD0APQA9-
78      20      6:+AD0AKgA9AD0APQA9AD0-
80      7      4:+AD0AKgA9-
82      5      3:+ACoAPQ-
84      5      3:+ACoAPQ-
86      13      2:+ACoAPQA9AD0APQ-
88      1      2:+ACo- inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      0      1:+ACo- :+ACo-
94      2      1:+ACo- :+ACoAPQ-
96      1      1:+ACo- :+ACo-
98      0      0: +ACo-
100     0      0: +ACo-
102     1      0:+AD0- +ACoAPQ-
104     1      0:+AD0- +ACoAPQ-
106     0      0: +ACo-
108     0      0: +ACo-
110     0      0: +ACo-
112     0      0: +ACo-
114     0      0: +ACo-
116     0      0: +ACo-
118     0      0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.88690.00284+ADs- mu+AD0- 0.6342
0.149
mean+AF8-var+AD0-33.9298 9.626, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.220183
Kolmogorov-Smirnov statistic: 0.1053 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are: opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.5 0.7
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 60 23.9 0.99

```

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145)
57 22.9 2.1
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
57 22.9 2.4
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
160) 56 22.6 3
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
301) 58 22.9 4.4
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
54 21.9 4.7
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
145) 53 21.7 5.1
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
53 21.6 5.8
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152)
(152) 52 21.3 6.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
52 21.3 7.2
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
52 21.3 7.2
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
52 21.3 7.2
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
52 21.3 7.3
gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
55 22.0 8.5
gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P (133)
(133) 50 20.7 8.9
gi+AHw-320606+AHw-pir+AHwAfA-E37396 pollen allergen Agr a I - be (26)
40 18.3 9.7
gi+AHw-320607+AHw-pir+AHwAfA-G37396 pollen allergen Ant o I - sw (26)
40 18.3 9.7

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
initn: 55 init1: 55 opt: 62 Z-score: 105.1 bits: 24.5 E(): 0.7
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (18-66:5-52)

10

20

30

40

50

60

```

AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
      .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCRE
      10      20      30      40

```

```

      70      80
AAD-12 LVHQRSARHSLVYSQSKLGH
      : ...
gi+AHw-189 YVAQQTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKD
      50      60      70      80      90      100

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 34 initl: 34 opt: 60 Z-score: 102.4 bits: 23.9 E(): 0.99
Smith-Waterman score: 60+ADs- 32.075+ACU- identity (64.151+ACU- similar)
in 53 aa overlap (28-78:9-57)

```

      10      20      30      40      50
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEAT
      : ... .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQAN
      10      20      30      40

```

```

      60      70      80
AAD-12 RALVHQRSARHSLVYSQSKLGH
      ... .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-111 HAI---EKGEHQLLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRT
      50      60      70      80      90

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of
tetrameric (145 aa)
initn: 50 initl: 50 opt: 57 Z-score: 96.5 bits: 22.9 E(): 2.1
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (18-66:5-52)

```

      10      20      30      40      50      60
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
      .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCRE
      10      20      30      40

```

```

      70      80
AAD-12 LVHQRSARHSLVYSQSKLGH
      : ...
gi+AHw-439 YVAQQTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLK
      50      60      70      80      90      100

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 initl: 55 opt: 57 Z-score: 95.5 bits: 22.9 E(): 2.4
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (12-40:23-50)

```

      10      20      30      40

```

```

AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. .:: : .: .: .: ::::: . ::
gi+AHw-444 MGVFYYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                10          20          30          40          50

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                60          70          80          90          100          110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0-      (160 aa)
  initn: 55 initl: 55 opt: 56 Z-score: 93.8 bits: 22.6 E(): 3
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

                10          20          30          40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ::. .: .: .: ::::. . ::
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10          20          30          40          50

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60          70          80          90          100          110

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per      (301 aa)
  initn: 49 initl: 49 opt: 58 Z-score: 90.8 bits: 22.9 E(): 4.4
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (13-62:23-71)

                10          20          30          40          50
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                .. .:: : .: .: .: : ::::: .: .
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10          20          30          40          50

                60          70          80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGH
  . . . . .: :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60          70          80          90          100          110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a      (160 aa)
  initn: 52 initl: 52 opt: 54 Z-score: 90.3 bits: 21.9 E(): 4.7
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (12-40:23-50)

                10          20          30          40

```

AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. .:: : .: .: .: .::: . :
 gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 89.6 bits: 21.7 E(): 5.1
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (18-66:5-52)

10 20 30 40 50 60
 AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRA
 :. :.. .: .: .: .: : ::: : . : : :
 gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCRE
 10 20 30 40

70 80
 AAD-12 LVHQRSARHSLVYSQSKLGH
 : :..
 gi+AHw-217 YVAQQTCGISISGSASVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLK
 50 60 70 80 90 100

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 88.6 bits: 21.6 E(): 5.8
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (21-72:31-87)

10 20 30 40
 AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
 .: .: .: .: .: .: .: .: :
 gi+AHw-132 MGVFN YETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
 10 20 30 40 50

50 60 70 80
 AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGH
 : : : : :
 gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
 60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 87.4 bits: 21.3 E(): 6.8
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (51-74:29-52)

30 40 50 60 70 80

AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH

: : : : : . . . : : :

gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
10 20 30 40 50

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAG
60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40

: : . : : : : . : :

gi+AHw-602 MGVTYSEFTSIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40

: : . : : : : . : :

gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40

: : . : : : : . : :

gi+AHw-602 MGVTYSEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF

10 20 30 40 50
50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

10 20 30 40
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

10 20 30 40
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

10 20 30 40
AAD-12 WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF


```

                10         20         30         40         50
      50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60         70         80         90        100        110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. .  ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10         20         30         40         50

      50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60         70         80         90        100        110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. .  ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10         20         30         40         50

      50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60         70         80         90        100        110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
  initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

                10         20         30         40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: ::::. .  ::
gi+AHw-131 MGVFNYETEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
```

```

                10          20          30          40          50
50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (16-40:27-50)

```

                10          20          30          40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::. .: .: :: ::::. . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10          20          30          40          50

```

```

50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 50 initl: 50 opt: 52 Z-score: 86.9 bits: 21.3 E(): 7.3
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (12-40:23-50)

```

                10          20          30          40
AAD-12          WDDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        .. ::. : .: .: .: ::::. . ::
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIAPQSVKGAEIVEGDDGGVGTIKKISF
                10          20          30          40          50

```

```

50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGH

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
pre (301 aa)
initn: 53 initl: 53 opt: 55 Z-score: 85.7 bits: 22.0 E(): 8.5
Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (7-52:16-62)

```

                10          20          30          40          50
AAD-12          WDDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        ...: : . ::. : .: : . : . : ::::. ...
gi+AHw-441 MAVQKYTVLFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL

```

```
80 residues in 1 query sequences
331323 residues in 1471 library sequences
```

```
Scomplib +AFs-34t26+AF0-
start: Fri Feb  5 12:55:54 2010 done: Fri Feb  5 12:55:54 2010
Total Scan time:  0.080 Total Display time:  0.000
```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 96 - 175 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

56      79
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9-
58      54      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
60      53      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
62      39      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      29      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66      57      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
68      49      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
70      22      16:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
72      34      12:+AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
74      14      10:+AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
76      17      7:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
78      23      6:+AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
80      7      4:+AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
82      5      3:+ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
84      4      3:+ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
86      12      2:+ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
88      2      2:+ACo- inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      0      1:+ACo- :+ACo-
94      2      1:+ACo- :+ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
96      1      1:+ACo- :+ACo-
98      0      0: +ACo-
100     0      0: +ACo-
102     1      0:+AD0- +ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
104     1      0:+AD0- +ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
106     0      0: +ACo-
108     0      0: +ACo-
110     0      0: +ACo-
112     0      0: +ACo-
114     0      0: +ACo-
116     0      0: +ACo-
118     0      0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.89150.0031+ADs- mu+AD0- 0.5955
0.163
mean+AF8-var+AD0-34.7186 9.748, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.217667
Kolmogorov-Smirnov statistic: 0.1073 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are: opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.4 0.76
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 60 23.8 1.1
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.8 2.3

```

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)
 57 22.8 2.6
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 56 22.5 3.2
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301)
 58 22.9 4.7
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)
 54 21.9 5
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145)
 53 21.6 5.4
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)
 53 21.5 6.2
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152)
 52 21.3 7.2
 gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
 52 21.2 7.6
 gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.2 7.6
 gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.2 7.6
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.2 7.7
 gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
 55 21.9 9
 gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName: Full+AD0-P (133)
 50 20.7 9.3

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 104.5 bits: 24.4 E(): 0.76
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (17-65:5-52)

	10	20	30	40	50	60
AAD-12	DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRAL					
	
gi+AHw-189	MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREY					
		10	20	30	40	

70

80

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVSADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)

initn: 55 initl: 55 opt: 56 Z-score: 93.3 bits: 22.5 E(): 3.2
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: .: :::: . ::
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
10 20 30 40 50

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
60 70 80 90 100 110

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 90.4 bits: 22.9 E(): 4.7
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (12-61:23-71)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
.. ::. : .: . : . : ::::: . : .
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
10 20 30 40 50

AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHV

. . . . : :
gi+AHw-663 LEDVNAGFKAABAADANAPPADKFKIFEAAAFSECKGLLATSDAKAPGLILKLDTDYDVA
60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 89.9 bits: 21.9 E(): 5
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (11-39:23-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.. ::. : .: . : . : ::::. . ::
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAIEIVEGDGGVGTIKKISF
10 20 30 40 50

50 60 70 80

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 89.2 bits: 21.6 E(): 5.4
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (17-65:5-52)

10 20 30 40 50 60
AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRAL
:. :.. .. :. . . . : :. : . : :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREY
10 20 30 40

70 80
AAD-12 VHQRSARHSLVYSQSKLGHV
: :..
gi+AHw-217 VAQQTGCGISISGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKD
50 60 70 80 90 100

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)

initn: 47 initl: 47 opt: 53 Z-score: 88.2 bits: 21.5 E(): 6.2
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (20-71:31-87)

10 20 30 40
AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
.: :. :. :. :. :. :.
gi+AHw-132 MGVFNJETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
10 20 30 40 50

50 60 70 80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHV
: : : : :
gi+AHw-132 DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)

initn: 52 initl: 52 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.2
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (50-73:29-52)

20 30 40 50 60 70
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
: : : : : . . : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSLRNTLS
10 20 30 40 50

AAD-12 V

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

10 20 30 40
AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSIIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

10 20 30 40
AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
60 70 80 90 100 110

+AD4-+AD4-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

10 20 30 40
AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

10 20 30 40
AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

10 20 30 40
AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

10 20 30 40
AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
10 20 30 40 50

50 60 70 80

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40
::: .: .: :: :... . ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV
50 60 70 80

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV
50 60 70 80

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40
::: .: .: :: :... . ::
gi+AHw-131 MGVFNYTEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (15-39:27-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
60 70 80 90 100 110

+AD4-+AD4-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 init1: 50 opt: 52 Z-score: 86.5 bits: 21.2 E(): 7.7
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (11-39:23-50)

AAD-12 DDMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
10 20 30 40
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIPQSVKGAEIVEGDGGVGTIKKISF
10 20 30 40 50

AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHV

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
pre (301 aa)

initn: 53 init1: 53 opt: 55 Z-score: 85.3 bits: 21.9 E(): 9
Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (6-51:16-62)

AAD-12 DDMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
10 20 30 40
gi+AHw-441 MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
10 20 30 40 50 60

50 60 70 80

AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHV

```

      :
gi+AHw-441 EDVNAGFKA AVAAAANAPPADKFKIFEAAFSESSKGLLATSAAKAPGLIPKLD TAYDVAY
              70          80          90          100          110          120

```

+AD4APg-gi+AHw-2497750+AHw-sp+AHw-P55958.1+AHw-NLT21+AF8-PARJU RecName:

Full+AD0-Proba (133 aa)

initn: 50 initl: 50 opt: 50 Z-score: 84.9 bits: 20.7 E(): 9.3

Smith-Waterman score: 50+ADs- 28.125+ACU- identity (59.375+ACU- similar)

in 32 aa overlap (6-37:11-42)

```

              10          20          30          40          50
AAD-12      DDMKVIVGNMAWHADSTYMPVMAQGA VFSAE VVPAVGGRTCFADMRAAYDALDE
              :... :... :... :... :... :... :... :... :... :... :...
gi+AHw-249 MRTVSMAALVVIAAALAWTSSAEPAPAPAGEEACGKV VQDIMPCLH FVKGEEKEPSKEC
              10          20          30          40          50          60

```

```

              60          70          80
AAD-12      ATRALVHQRSARHSLVYSQSKLGHV

```

```

gi+AHw-249 CSGTKKLSEEVKTTEQKREACKCIVRATKGISGIKNELVAEVPKKCDIKTTLPITADFD
              70          80          90          100          110          120

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:54 2010 done: Fri Feb 5 12:55:55 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 97 - 176 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      1      0:+AD0-
      24      1      0:+AD0-
      26      1      0:+AD0-
      28      2      0:+AD0-
      30      3      2:+ACo-
      32      5      8:+AD0APQAq-

```

one +AD0- represents 3 library sequences

[illegible]

```

102      0      0:      +ACo-
104      1      0:+AD0-      +ACoAPQ-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.06190.00318+ADs- mu+AD0- -
0.2586 0.167
mean+AF8-var+AD0-35.9651 9.815, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.213862
Kolmogorov-Smirnov statistic: 0.1148 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.2 0.86
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 60 23.7 1.2
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.7 2.5
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.7 2.9
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.3 3.5
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.7 5.2
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.7 5.4
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.5 5.9
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.4 6.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.1 7.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.3

```


gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)
 52 21.1 8.3
 gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.3
 gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)
 52 21.1 8.3
 gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.3
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.1 8.3
 gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
 55 21.8 9.9

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 init1: 55 opt: 62 Z-score: 103.6 bits: 24.2 E(): 0.86
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (16-64:5-52)

	10	20	30	40	50	60
AAD-12	DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV					
	
gi+AHw-189		MASKSSITPLLLAAVLASVF	AAAAAATGQYCYAGMGLPSNPL-EGCREYV			
		10	20	30	40	

	70	80
AAD-12	HQRSARHSLVYSQSKLGHVQ	
	...	
gi+AHw-189	AQQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSPDWRVLKDLP	
	50	60

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 34 init1: 34 opt: 60 Z-score: 101.0 bits: 23.7 E(): 1.2
 Smith-Waterman score: 60+ADs- 32.075+ACU- identity (64.151+ACU- similar)
 in 53 aa overlap (26-76:9-57)

	10	20	30	40	50
AAD-12	DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRA				
		:	:::	:	:
gi+AHw-111		MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHA			
		10	20	30	40

	60	70	80
AAD-12	LVHQRSARHSLVYSQSKLGHVQ		
	:
gi+AHw-111	I---EKGEHQLLYLQHQLDLENENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDL		
	50	60	70

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 init1: 50 opt: 57 Z-score: 95.2 bits: 22.7 E(): 2.5
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (16-64:5-52)

```

          10          20          30          40          50          60
AAD-12 DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
          :. :.. ... :. . . . :. : : : :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYV
          10          20          30          40

```

```

          70          80
AAD-12 HQRSARHSLVYSQSKLGHVQ
          :..
gi+AHw-439 AQQTCGVTTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDL
          50          60          70          80          90          100

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 94.2 bits: 22.7 E(): 2.9
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (10-38:23-50)

```

          10          20          30          40
AAD-12 DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          .. :. : : : : : : : : : : :
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIAFQSVKSAEIVEGDGGVGTIKKISF
          10          20          30          40          50

```

```

          50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 92.5 bits: 22.3 E(): 3.5
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (14-38:27-50)

```

          10          20          30          40
AAD-12 DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
          :.. :. : : : : : : : : :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
          10          20          30          40          50

```

```

          50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs- Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 89.5 bits: 22.7 E(): 5.2
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (11-60:23-71)

```

                10         20         30         40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                .. ::: : : : . : ..... : :
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12          YDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 89.2 bits: 21.7 E(): 5.4
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (10-38:23-50)

```

                10         20         30         40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. ::: : : : . : ..... : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12          AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 88.5 bits: 21.5 E(): 5.9
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (16-64:5-52)

```

                10         20         30         40         50         60
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV
                :. :.. .. :. . . . : :. : . : : :
gi+AHw-217      MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYV
                10         20         30         40

```

```

                70         80
AAD-12          HQRSARHSLVYSQSKLGHVQ
                :..
gi+AHw-217 AQQTCGISISGSVSTPGNTPRDRCKELYDASQHCRCEAVRYFIGRRSDPNSSVLKDL
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 87.5 bits: 21.4 E(): 6.7
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (19-70:31-87)

```

                10         20         30         40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                .: .: .: .: .: .: .: .:
gi+AHw-132  MGVFN YETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12  DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQ
                : . . . . . : : : :
gi+AHw-132  DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.4 bits: 21.1 E(): 7.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (49-72:29-52)

```

                20         30         40         50         60         70
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
                : : : : : : . . . : : :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
                10         20         30         40         50

```

```

                80
AAD-12  VQ
gi+AHw-144  DSKVDEKLDAGDKQKLTAIEDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAG
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10         20         30         40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : .: .: .: : : : : .:
gi+AHw-602  MGVFTYSEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
gi+AHw-602  GEGSTYSYVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::::. .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50
```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::::. .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50
```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::::. .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50
```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50
```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50
```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100     110
```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::...  .  ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10      20      30      40      50
```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::::. .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::::. .  ::
gi+AHw-131  MGVFNYTEFTSVIPPARLFNAFVLADADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (14-38:27-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...  .: .:  ::  ::::. .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 50 init1: 50 opt: 52 Z-score: 85.8 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (10-38:23-50)

```

                10      20      30      40
AAD-12          DMMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  ... :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQ

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
pre (301 aa)
initn: 53 initl: 53 opt: 55 Z-score: 84.5 bits: 21.8 E(): 9.9
Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (5-50:16-62)

```

                10      20      30      40
AAD-12          DMMKVIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                ...:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-441  MAVQKYTVLFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
                10      20      30      40      50      60

```

```

                50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                :
gi+AHw-441  EDVNAGFKA AVAAAAANAPPADKFKIFEAFSESSKGLLATSAAKAPGLIPKLD TAYDVAY
                70      80      90      100     110     120

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:55 2010 done: Fri Feb 5 12:55:55 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 98 - 177 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

inset +AD0- represents 1 library sequences

```

 98      0      0:      +ACo-
100      0      0:      +ACo-
102      1      0:+AD0-      +ACoAPQ-
104      1      0:+AD0-      +ACoAPQ-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.98190.00321+ADs- mu+AD0- 0.4037
0.169
mean+AF8-var+AD0-36.010810.064, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.213726
Kolmogorov-Smirnov statistic: 0.1053 (N+AD0-28) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
                                opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  62 24.2      0.83
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  62 24.2      0.91
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.6      2.7
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.6      3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  56 22.3      3.8
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301)  58 22.6      5.5
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.6      5.8
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145)  53 21.4      6.3
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.3      7.1
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.0      8.3
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  51 20.8      8.7
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
51 20.8      8.7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.8
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.0      8.8

```

70 80
 AAD-12 QRSARHSLVYSQSKLGHVQQ
 ...
 gi+AHw-189 QQTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPG
 50 60 70 80 90 100

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 94.7 bits: 22.6 E(): 2.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (15-63:5-52)

	10	20	30	40	50	60
AAD-12	MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH					
	
gi+AHw-439	MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVA					
	10	20	30	40		

	70	80
AAD-12	QRSARHSLVYSQSKLGHVQQ	
	...	
gi+AHw-439	QQTGCVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLP	
	50	100

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 93.7 bits: 22.6 E(): 3
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (9-37:23-50)

	10	20	30	40
AAD-12	MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA			

gi+AHw-444	MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEG DGGVGTIKKISF			
	10	20	30	50

	50	60	70	80
AAD-12	AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ			
gi+AHw-444	GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS			
	60	70	80	110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 92.1 bits: 22.3 E(): 3.8
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (13-37:27-50)

	10	20	30	40
AAD-12	MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA			

gi+AHw-165	MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF			
	10	20	30	50

	50	60	70	80
AAD-12	AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ			
gi+AHw-165	GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS			
	60	70	80	110

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 89.1 bits: 22.6 E(): 5.5
Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (10-59:23-71)

```

                        10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        .. :.. : : : : : : : : : : : : : :
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
                    . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                    60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.7 bits: 21.6 E(): 5.8
Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (9-37:23-50)

```

                        10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        .. :.. : : : : : : : : : : : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ
                    . . . . : :
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
                    60      70      80      90      100      110

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 88.0 bits: 21.4 E(): 6.3
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (15-63:5-52)

```

                    10      20      30      40      50      60
AAD-12 MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVH
                    :. :.. . : : : : : : : : : : : :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVA
                    10      20      30      40

```

```

                    70      80
AAD-12 QRSARHSLVYSQSKLGHVQQ
                    :..
gi+AHw-217 QQTGISISGSAVSTEPGNTPRDRCKKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLP
                    50      60      70      80      90      100

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 87.1 bits: 21.3 E(): 7.1
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (18-69:31-87)

```

                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                .: .:  .:  .:  .:  .:  .:  .:
gi+AHw-132  MGVFNJETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  DMRAAYDALDEATRVLHQR-SARHSLVYSQSKLGHVQQ
                :  .  .  .  .  .  .  :  ::::
gi+AHw-132  DEGSPFNLIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 85.9 bits: 21.0 E(): 8.3
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (48-71:29-52)

```

                20      30      40      50      60      70
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRSARHSLVYSQSKLGH
                :  :  :::  :  .  .:  .:  ::
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
                10      20      30      40      50

```

```

                80
AAD-12  VQQ
gi+AHw-144  DSKVDEKLDAGDKQKLTAIEDKTQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAG
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 36 initl: 36 opt: 51 Z-score: 85.5 bits: 20.8 E(): 8.7
 Smith-Waterman score: 51+ADs- 27.586+ACU- identity (63.793+ACU- similar)
 in 58 aa overlap (25-80:9-62)

```

                10      20      30      40      50
AAD-12  MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR
                :  :::  .:  .  .  .:  .:  .:  .:  .:  .:
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI
                10      20      30      40

```

```

                60      70      80
AAD-12  VHQRSARHSLVYSQSKLGHVQQ
                .....:  .:  ....
gi+AHw-111  ---EKGEHQLLYLQHQLDLENENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLN
                50      60      70      80      90      100

```

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .:  .:  ::  ::::.  .  ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```


+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                        10      20      30      40
AAD-12                MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                        10      20      30      40      50

                        50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                        10      20      30      40
AAD-12                MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                        10      20      30      40      50

                        50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                        10      20      30      40
AAD-12                MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ...  .:  .:  ::  ::::.  .  ::
gi+AHw-131  MGVFN YET EFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                        10      20      30      40      50

                        50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1.03B (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (13-37:27-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.4 bits: 21.0 E(): 8.8
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (9-37:23-50)

```

                                10      20      30      40
AAD-12      MMKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ..  ::.  .:  .:  .:  ::.  .  ::
gi+AHw-444  MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQ

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 36 initl: 36 opt: 50 Z-score: 85.0 bits: 20.5 E(): 9.3
 Smith-Waterman score: 50+ADs- 27.500+ACU- identity (72.500+ACU- similar)
 in 40 aa overlap (43-80:11-47)

```

                20      30      40      50      60      70
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                :.: : : .....: .....:
gi+AHw-160                GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                        10      20      30

                80
AAD-12 SQSKLGHVQQ
                :.: ....
gi+AHw-160 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQT
                40      50      60      70      80      90

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:55:55 2010 done: Fri Feb 5 12:55:55 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 99 - 178 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	0	0:	
26	0	0:	
28	1	0:+AD0-	
30	3	2:+ACo-	
32	5	8:+AD0AKg-	
34	13	21:+AD0APQA9AD0- +ACo-	
36	31	44:+AD0APQA9AD0APQA9AD0APQ- +ACo-	
38	48	72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-	

```

40      91
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
42      67      123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
44      131
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACo-
46      102
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q-      +ACo-
48      188
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
50      118
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACo-
52      89
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
54      76      91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      76      76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
58      51      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
60      48      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      46      40: +AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
64      64      32: +AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
66      35      25: +AD0APQA9AD0APQA9ACoAPQA9-
68      48      20: +AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
70      14      16: +AD0APQA9ACo-
72      30      12: +AD0APQAqAD0APQA9AD0APQ-
74      21      10: +AD0APQAqAD0APQA9-
76      25      7: +AD0AKgA9AD0APQA9AD0-
78      9      6: +AD0AKgA9-
80      9      4: +ACoAPQA9-
82      0      3: +ACo-
84      20      3: +ACoAPQA9AD0APQ-
86      2      2: +ACo-
88      3      2: +ACo-      inset +AD0- represents 1 library sequences
90      0      1: +ACo-
92      1      1: +ACo-      : +ACo-
94      2      1: +ACo-      : +ACoAPQ-
96      0      1: +ACo-      : +ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     1      0: +AD0-      +ACoAPQ-
104     1      0: +AD0-      +ACoAPQ-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-

```

```
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.01450.00323+ADs- mu+AD0- 0.2313
0.170
mean+AF8-var+AD0-36.389910.135, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.212610
Kolmogorov-Smirnov statistic: 0.1039 (N+AD0-28) at 46
```

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
```

```
join: 42, opt: 30, open/ext: -10/-2, width: 32
```

```
Scan time: 0.080
```

```
The best scores are: opt bits E(1471)
```

```
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 62 24.1 0.86
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.1 0.94
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.6 2.7
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.5 3.1
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.2 3.9
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.6 5.7
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.6 5.9
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.3 6.4
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.3 7.3
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.0 8.5
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 51 20.8 8.9
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
51 20.8 8.9
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.0 9
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.0 9
```

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.0 9
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.0 9
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 50 20.5 9.5
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 50 20.5 9.7

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)

initn: 36 initl: 36 opt: 62 Z-score: 103.6 bits: 24.1 E(): 0.86
 Smith-Waterman score: 62+ADs- 29.310+ACU- identity (65.517+ACU- similar)
 in 58 aa overlap (24-79:9-62)

	10	20	30	40	50
AAD-12	MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALV				
		:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI-				
	10	20	30	40	

	60	70	80
AAD-12	HQRSARHSLVYSQSKLGHVQQA		
: : : :		
gi+AHw-111	--EKGEHQLLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNI		
	50	60	70

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)

initn: 55 initl: 55 opt: 62 Z-score: 102.8 bits: 24.1 E(): 0.94
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (14-62:5-52)

	10	20	30	40	50	60
AAD-12	MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ					
	:	:	:	:	:	:
gi+AHw-189	MASKSSITPLLLAASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQ					
	10	20	30	40	50	

	70	80
AAD-12	RSARHSLVYSQSKLGHVQQA	
	..	
gi+AHw-189	QTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGC	
	60	70

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)

initn: 50 initl: 50 opt: 57 Z-score: 94.5 bits: 22.6 E(): 2.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (14-62:5-52)

10	20	30	40	50	60
----	----	----	----	----	----

AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
 : : : : : : : : : : : : : : : : : :
 gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQ
 10 20 30 40 50

70 80
 AAD-12 RSARHSLVYSQSKLGHVQQA
 ..
 gi+AHw-439 QTCGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLP
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 93.5 bits: 22.5 E(): 3.1
 Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (8-36:23-50)

10 20 30 40
 AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 : : : : : : : : : : : : : : : : : :
 gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 56 Z-score: 91.8 bits: 22.2 E(): 3.9
 Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

10 20 30 40
 AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. : : : : : : : : : : : : : : : : : :
 gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
 gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 49 initl: 49 opt: 58 Z-score: 88.9 bits: 22.6 E(): 5.7
 Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
 in 50 aa overlap (9-58:23-71)

10 20 30 40

AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .. :: : : : : : : : : : :
 gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
 10 20 30 40 50

50 60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
 : :
 gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 88.5 bits: 21.6 E(): 5.9
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (8-36:23-50)

10 20 30 40
 AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. :: : : : : : : : : : :
 gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 87.9 bits: 21.3 E(): 6.4
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (14-62:5-52)

10 20 30 40 50 60
 AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
 :. :. . : . . . : : : : : : : : :
 gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQ
 10 20 30 40 50

70 80
 AAD-12 RSARHSLVYSQSKLGHVQQA
 ..
 gi+AHw-217 QTCGISISGS AVSTEPGNTPRDRCCKEYLDASQHCRC EAVRYFIGRRSDPNSSVLKDLPG
 60 70 80 90 100 110

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 86.9 bits: 21.3 E(): 7.3
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (17-68:31-87)

10 20 30 40

AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
 : : : : : : : : : : : : : : : : : :
 gi+AHw-132 MGVFNJETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
 10 20 30 40 50

50 60 70 80
 AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQA
 : : : : : : : : : : : : : : : : : :
 gi+AHw-132 DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
 60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 init1: 52 opt: 52 Z-score: 85.7 bits: 21.0 E(): 8.5
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (47-70:29-52)

20 30 40 50 60 70
 AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
 : : : : : : : : : : : : : : : : : :
 gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
 10 20 30 40 50

80
 AAD-12 VQQA
 gi+AHw-144 DSKVDEKLDAGDKQKLTAIEDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
 60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 36 init1: 36 opt: 51 Z-score: 85.3 bits: 20.8 E(): 8.9
 Smith-Waterman score: 51+ADs- 27.586+ACU- identity (63.793+ACU- similar)
 in 58 aa overlap (24-79:9-62)

10 20 30 40 50
 AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALV
 : : : : : : : : : : : : : : : : : :
 gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI-
 10 20 30 40

60 70 80
 AAD-12 HQRSARHSLVYSQSKLGHVQQA
 : : : : : : : : : : : : : : : : : :
 gi+AHw-111 --EKGEHQLLYLQHQLDLNLNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNI
 50 60 70 80 90 100

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein Bl (134 aa)
 initn: 36 init1: 36 opt: 51 Z-score: 85.3 bits: 20.8 E(): 8.9
 Smith-Waterman score: 51+ADs- 27.586+ACU- identity (63.793+ACU- similar)
 in 58 aa overlap (24-79:9-62)

10 20 30 40 50

10 20 30 40

```

AAD-12                MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ... .. : : : : : :
gi+AHw-602 MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
                        10      20      30      40      50

```

```

                        50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                        10      20      30      40
AAD-12                MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ... .. : : : : : :
gi+AHw-602 MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
                        10      20      30      40      50

```

```

                        50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                        10      20      30      40
AAD-12                MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ... .. : : : : : :
gi+AHw-279 MGVFTYESEFTSVIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
                        10      20      30      40      50

```

```

                        50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (12-36:27-50)

```

                        10      20      30      40

```

AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (12-36:27-50)

10 20 30 40
AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (12-36:27-50)

10 20 30 40
AAD-12 MKVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-131 MGVFN YETEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQA
gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.3 bits: 21.0 E(): 9
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (12-36:27-50)

10 20 30 40

20 30 40 50 60

```

AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                                ::.  .:  :  .....  .....:
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLY
                                10      20      30

```

```

      70      80
AAD-12  SQSKLGHVQQA
      :  .:  ....
gi+AHw-160  LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQT
      40      50      60      70      80      90

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 50 initl: 50 opt: 50 Z-score: 84.7 bits: 20.5 E(): 9.7
Smith-Waterman score: 50+ADs- 26.829+ACU- identity (58.537+ACU- similar)
in 41 aa overlap (40-80:26-66)

```

      10      20      30      40      50      60
AAD-12  WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                                ::.  .:  .  :  ....  ...
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                                10      20      30      40      50

```

```

      70      80
AAD-12  SQSKLGHVQQA
      ..  .:  ....
gi+AHw-527  AKVNVVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQ
      60      70      80      90      100      110

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:55:55 2010 done: Fri Feb 5 12:55:55 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 100 - 179 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-

```

```

22      0      0: one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      1      0:+AD0-
30      3      2:+ACo-
32      6      8:+AD0APQAq-
34     12     21:+AD0APQA9AD0- +ACo-
36     26     44:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
38     49     72:+AD0APQA9AD0APQA9AD0-+AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
40     87
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQ- +ACo-
42     70
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
44    123
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
46    112
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
48    179
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
9AD0APQA9AD0APQA9-
50    130
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
52     98
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQA9AD0APQA9- +ACo-
54     59     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
56     78
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58     50     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60     51     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62     48     40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64     59     32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
66     43     25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
68     43     20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-+AD0APQ-
70     19     16:+AD0APQA9AD0APQAqAD0-
72     32     12:+AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
74     15     10:+AD0APQA9ACoAPQ-
76     24       7:+AD0APQAqAD0APQA9AD0APQ-
78     10       6:+AD0AKgA9AD0-
80     12       4:+AD0AKgA9AD0-
82      0       3:+ACo-
84     15       3:+ACoAPQA9AD0APQ-
86      7       2:+ACoAPQA9-
88      3       2:+ACo- inset +AD0- represents 1 library sequences
90      0       1:+ACo-

```

```

92      1      1:+ACo-      :+ACo-
94      2      1:+ACo-      :+ACoAPQ-
96      0      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     2      0:+AD0-      +ACoAPQA9-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.96160.0032+ADs- mu+AD0- 0.4624
0.168
mean+AF8-var+AD0-35.842310.035, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.214228
Kolmogorov-Smirnov statistic: 0.1060 (N+AD0-28) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 62 24.2 0.81
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.2 0.89
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.6 2.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.6 3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.3 3.7
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.7 5.4
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.7 5.6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.4 6.2
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.4 7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.1 8.1
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 51 20.8 8.5
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
51 20.8 8.5
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.1 8.6

```



```

gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.1      8.6
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.1      8.6
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.1      8.6
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.1      8.6
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.1      8.6
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.1      8.6
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.1      8.6
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.1      8.6
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.1      8.6
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.1      8.6
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
50 20.6      9.1
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  50 20.5      9.3
gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi ( 107)
49 20.3      9.8

```

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
  initn: 36 initl: 36 opt: 62 Z-score: 104.0 bits: 24.2 E(): 0.81
Smith-Waterman score: 62+ADs- 29.310+ACU- identity (65.517+ACU- similar)
in 58 aa overlap (23-78:9-62)

```

```

          10          20          30          40          50
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVH
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111          MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI--
          10          20          30          40

          60          70          80
AAD-12 QRSARHSLVYSQSKLGHVQQAG
          .....: : : : :
gi+AHw-111 -EKGEHQLLYLQHQQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNIL
          50          60          70          80          90          100

```

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+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
  initn: 55 initl: 55 opt: 62 Z-score: 103.3 bits: 24.2 E(): 0.89
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (13-61:5-52)

```

```

          10          20          30          40          50          60
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

AAD-12
KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 10 20 30 40
 ::: ::: ::: ::: ::: ::: ::: :::

AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQR

AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVH

AAD-12 10 20 30 40
KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPVAVGGRTCFADMRA
 :::: :: : :: :::: . ::

gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSIIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::

gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::

gi+AHw-131 MGVFNYETEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (11-35:27-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :::: . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAG

gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.5 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (7-35:23-50)

10 20 30 40
AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.. ::: : .: .: .: :::: . ::

AAD-12 KVIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQR

 10 20 30 40 50 60

 .:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:

[illegible]

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46 122 138:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9- +ACo-
48 174
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA
9AD0APQA9AD0-
50 121
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
52 100
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA
9AD0APQA9AD0APQA9AD0- +ACo-
54 57 91:+AD0APQA9AD0APQA9AD0APQA9AD0-+AD0APQA9AD0APQA9AD0APQA9-
+ACo-
56 82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58 51 62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60 55 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62 47 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64 48 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66 50 25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
68 46 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
70 14 16:+AD0APQA9AD0APQAq-
72 34 12:+AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
74 14 10:+AD0APQA9ACoAPQ-
76 23 7:+AD0APQAqAD0APQA9AD0APQ-
78 10 6:+AD0AKgA9AD0-
80 7 4:+AD0AKgA9-
82 8 3:+ACoAPQA9-
84 12 3:+ACoAPQA9AD0-
86 5 2:+ACoAPQ-
88 6 2:+ACoAPQ- inset +AD0- represents 1 library
sequences
90 0 1:+ACo-
92 1 1:+ACo- :+ACo-
94 2 1:+ACo- :+ACoAPQ-
96 0 1:+ACo- :+ACo-
98 0 0: +ACo-
100 0 0: +ACo-
102 0 0: +ACo-
104 1 0:+AD0- +ACoAPQ-
106 1 0:+AD0- +ACoAPQ-
108 0 0: +ACo-
110 0 0: +ACo-
112 0 0: +ACo-
114 0 0: +ACo-
116 0 0: +ACo-
118 0 0: +ACo-
+AD4-120 0 0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.80580.00317+ADs- mu+AD0- 1.2308
0.167

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mean+AF8-var+AD0-35.883610.156, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
 Lambda+AD0- 0.214105
 Kolmogorov-Smirnov statistic: 0.1003 (N+AD0-29) at 58

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.8 0.53

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 24.2 0.89

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.6 2.6

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 57 22.6 3

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.3 3.7

gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 58 22.7 5.2

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.4 5.6

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.4 5.6

gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 54 21.7 5.6

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 21.2 6

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.4 6.2

gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.4 7

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.1 8.1

gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6

gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6

gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6

gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159) 52 21.1 8.6

gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6

gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6

gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159) 52 21.1 8.6

gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6

gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159) 52 21.1 8.6

gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.6
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.1 8.6
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 50 20.5 9.4
 gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi (107)
 49 20.3 9.9
 gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA (301)
 55 21.8 10

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 107.3 bits: 24.8 E(): 0.53
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (22-80:9-65)

	10	20	30	40	50
AAD-12	VIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDAL--DEATRALVHQ				
		:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---				
	10	20	30	40	

	60	70	80
AAD-12	RSARHSLVYSQSKLGHVQQAGS		
: : : : : :		
gi+AHw-111	EKGEHQLLYLQHQQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILE		
	50	60	70

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 init1: 55 opt: 62 Z-score: 103.3 bits: 24.2 E(): 0.89
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (12-60:5-52)

	10	20	30	40	50	60
AAD-12	VIVGNMAWHADSTYMPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRS					
	:	:	:	:	:	:
gi+AHw-189	MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQT					
	10	20	30	40	50	

	70	80
AAD-12	ARHSLVYSQSKLGHVQQAGS	
gi+AHw-189	CGVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPK	
	60	70

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 init1: 50 opt: 57 Z-score: 94.9 bits: 22.6 E(): 2.6
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (12-60:5-52)

10	20	30	40	50	60
----	----	----	----	----	----

10 20 30 40

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .. :. :
 gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
 10 20 30 40 50

50 60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
 : : : :
 gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
 60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 89.0 bits: 21.4 E(): 5.6
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (22-80:9-65)

10 20 30 40 50
 AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQ
 :
 gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---
 10 20 30 40

60 70 80
 AAD-12 RSARHSLVYSQSKLGHVQQAGS
 :
 gi+AHw-111 EKGEHQLLYLQHQLDLNLNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILE
 50 60 70 80 90 100

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein Bl (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 89.0 bits: 21.4 E(): 5.6
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (22-80:9-65)

10 20 30 40 50
 AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQ
 :
 gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---
 10 20 30 40

60 70 80
 AAD-12 RSARHSLVYSQSKLGHVQQAGS
 :
 gi+AHw-420 EKGEHQLLYLQHQLDLNLNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILE
 50 60 70 80 90 100

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 88.9 bits: 21.7 E(): 5.6
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (6-34:23-50)

10 20 30 40

10 20 30

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
gi+AHw-132 MGVFN YETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
10 20 30 40 50

40 50 60 70 80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGS
: : : : :
gi+AHw-132 DEGSPFN YIKQKV EIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (45-68:29-52)

20 30 40 50 60 70
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
: : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
10 20 30 40 50

80
AAD-12 VQQAGS
gi+AHw-144 DSKVDEKLDAGDKQKLTA EIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

10 20 30 40
AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
: : : : : : : :
gi+AHw-602 MGVFTY ESEFTSVIPPARLFNAFVLADNL-IPK IAPQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

10 20 30 40

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

10 20 30 40
AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

10 20 30 40
AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

10 20 30 40

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50
50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110
+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50
50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
60 70 80 90 100 110
+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-131 MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50
50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110
+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

10 20 30 40

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

10 20 30 40
AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (10-34:27-50)

10 20 30 40
AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 50 initl: 50 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (6-34:23-50)

10 20 30 40

AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. .:: : .: .: .: .::: . : :
 gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 50 initl: 50 opt: 50 Z-score: 84.9 bits: 20.5 E(): 9.4
 Smith-Waterman score: 50+ADs- 26.829+ACU- identity (58.537+ACU- similar)
 in 41 aa overlap (38-78:26-66)

10 20 30 40 50 60
 AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
 .:: :. . : .::: :..
 gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
 10 20 30 40 50

70 80
 AAD-12 SQSKLGHVQQAGS
 .. .::: :
 gi+AHw-527 AKVNVDPVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQ
 60 70 80 90 100 110

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle
 parvalbumin +AFs-T (107 aa)
 initn: 42 initl: 42 opt: 49 Z-score: 84.5 bits: 20.3 E(): 9.9
 Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
 in 58 aa overlap (20-77:4-59)

10 20 30 40 50 60
 AAD-12 VIVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRS
 .::: .::: .: : : : : : : : : : : :
 gi+AHw-777 MAFKGVLDADVTAALDGCKSAFDHKAFFKACGLAAKSADDIKK
 10 20 30 40

70 80
 AAD-12 ARHSLVYSQSKLGHVQQAGS
 : . .::: : : :
 gi+AHw-777 AFA--IIDQDKSGFIEEDELKFLQNFCAARALSDAETKAFKAGDSGDGKIGVDEFA
 50 60 70 80 90 100

+AD4APg-gi+AHw-4416516+AHw-gb+AHw-AAD20386.1+AHw- pollen allergen Lol p VA
 pre (301 aa)
 initn: 53 initl: 53 opt: 55 Z-score: 84.4 bits: 21.8 E(): 10
 Smith-Waterman score: 55+ADs- 25.532+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (1-46:16-62)

10 20 30 40

```

AAD-12          VIVGNMA-WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
               ...:  .  :.  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-441 MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
               10      20      30      40      50      60

               50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGS
               :
gi+AHw-441 EDVNAGFKA AVAAAAANAPPADKFKIFEAAFSESSKGLLATSAAKAPGLIPKLD TAYDVAY
               70      80      90      100     110     120

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:55 2010 done: Fri Feb 5 12:55:55 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 102 - 181 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      3      0:+AD0-
      30      2      2:+ACo-
      32      4      8:+AD0APQAq-
      34      8      21:+AD0APQA9- +ACo-
      36      31     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      38      44     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      40      87
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-
      42      72
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      44      128
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-

```

46 119 138:+AD0-
 +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
 D0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 48 172
 132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA
 9AD0APQA9AD0-
 50 113
 121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
 52 101
 106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
 QA9AD0APQA9AD0APQA9AD0- +ACo-
 54 61
 91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
 +ACo-
 56 82
 76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
 A9AD0-
 58 52 62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
 60 67
 50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
 62 44 40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
 64 41 32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
 66 58 25:+AD0APQA9AD0APQA9AD0APQAqAD0-
 +AD0APQA9AD0APQA9AD0APQA9AD0-
 68 44 20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
 70 12 16:+AD0APQA9AD0- +ACo-
 72 29 12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
 74 16 10:+AD0APQA9ACoAPQA9-
 76 17 7:+AD0APQAqAD0APQA9-
 78 17 6:+AD0AKgA9AD0APQA9-
 80 10 4:+AD0AKgA9AD0-
 82 7 3:+ACoAPQA9-
 84 5 3:+ACoAPQ-
 86 12 2:+ACoAPQA9AD0-
 88 4 2:+ACoAPQ- inset +AD0- represents 1 library
 sequences
 90 2 1:+ACo-
 92 1 1:+ACo- :+ACo-
 94 2 1:+ACo- :+ACoAPQ-
 96 0 1:+ACo- :+ACo-
 98 0 0: +ACo-
 100 0 0: +ACo-
 102 0 0: +ACo-
 104 1 0:+AD0- +ACoAPQ-
 106 0 0: +ACo-
 108 1 0:+AD0- +ACoAPQ-
 110 0 0: +ACo-
 112 0 0: +ACo-
 114 0 0: +ACo-
 116 0 0: +ACo-
 118 0 0: +ACo-
 +AD4-120 0 0: +ACo-

331323 residues in 1471 sequences
 Expectation+AF8-n fit: rho(ln(x))+AD0- 5.81550.00313+ADs- mu+AD0- 1.1633
 0.165
 mean+AF8-var+AD0-35.0524 9.934, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
 Lambda+AD0- 0.216628
 Kolmogorov-Smirnov statistic: 0.1044 (N+AD0-29) at 58

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1
 join: 42, opt: 30, open/ext: -10/-2, width: 32
 Scan time: 0.090
 The best scores are: opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)	64 25.0 0.48
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)	62 24.3 0.82
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145)	
57 22.7	2.4
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160)	
57 22.7	2.8
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)	56 22.4 3.4
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301)	58 22.8 4.9
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)	53 21.5 5.2
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)	
53 21.5	5.2
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160)	
54 21.8	5.3
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)	
52 21.3	5.6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145)	53 21.5 5.8
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160)	
53 21.5	6.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-	
(152)	52 21.2 7.6
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. (159)	
52 21.1	8.1
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. (159)	
52 21.1	8.1
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. (159)	
52 21.1	8.1
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 (159)	
52 21.1	8.1
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. (159)	
52 21.1	8.1
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. (159)	
52 21.1	8.1
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 (159)	
52 21.1	8.1
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. (159)	
52 21.1	8.1

gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.1
 gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. (159)
 52 21.1 8.1
 gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P (160)
 52 21.1 8.1
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 50 20.6 8.8
 gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi (107)
 49 20.4 9.4

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 108.0 bits: 25.0 E(): 0.48
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (21-79:9-65)

	10	20	30	40	50
AAD-12	IVGNMAWHADSTYMPVMAQGA	VFSAEVVP	AVGGRTCFAD	MRAAYDAL--	DEATRALVHQR
		:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---				
	10	20	30	40	

	60	70	80
AAD-12	SARHSLVYSQSKLGHVQQAGSA		
:..: : ..: :		
gi+AHw-111	KGEHQLLYLQHQLDDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILER		
	50	60	70

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 103.9 bits: 24.3 E(): 0.82
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (11-59:5-52)

	10	20	30	40	50	60
AAD-12	IVGNMAWHADSTYMPVMAQGA	VFSAEVVP	AVGGRTCFAD	MRAAYDALDE	ATRALVHQ	RSARSA
	:	:	:	:	:	:
gi+AHw-189	MASKSSITPLLLAAVLASVF	AAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTC				
	10	20	30	40	50	

	70	80
AAD-12	RHSLVYSQSKLGHVQQAGSA	
gi+AHw-189	GVTIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKE	
	60	70

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 95.4 bits: 22.7 E(): 2.4
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (11-59:5-52)

10	20	30	40	50	60
----	----	----	----	----	----

10 20 30 40

10 20 30 40

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 .. .:: : .: .: .: .::: . :
 gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
 60 70 80 90 100 110

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.9 bits: 21.3 E(): 5.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (39-79:11-50)

10 20 30 40 50 60
 AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
 :.: .: : :
 gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
 10 20 30

70 80
 AAD-12 SQSKLGHVQQAGSA
 :.: :
 gi+AHw-160 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQT
 40 50 60 70 80 90

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 88.7 bits: 21.5 E(): 5.8
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (11-59:5-52)

10 20 30 40 50 60
 AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
 :. :.. .. :. :. : : : : : : : :
 gi+AHw-217 MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTC
 10 20 30 40 50

70 80
 AAD-12 RHSLVYSQSKLGHVQQAGSA
 gi+AHw-217 GISISGSAVSTEPGNTPRDRCCCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPR
 60 70 80 90 100 110

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 87.7 bits: 21.5 E(): 6.6
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (14-65:31-87)

10 20 30

40 50 60 70 80
 AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSA
 : : : : :
 gi+AHw-132 DEGSPFN~~Y~~IKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
 60 70 80 90 100 110

AAD-12 MPVMAQGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
gi+AHw-144 KTNKIVITNDKGRLSKEEIEMLAEEAKYKAEDAEAAARISAKNALESYAYSRLNTLS

80
AAD-12 VQQAGSA

gi+AHw-144 DSKVDEKLDAGDKQKLTAIEDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG

60 70 80 90 100 110

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (9-33;27-50)

10
20
30
40

AAD-12
 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA

::
::
::
::
::
::
::

gi+AHw-602
 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEGDDGGVGTIKKINF

10
20
30
40
50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (9-33;27-50)

10 20 30 40

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50
50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110
+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (9-33:27-50)

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50
50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110
+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (9-33:27-50)

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . ::
gi+AHw-279 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50
50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
gi+AHw-279 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110
+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (9-33:27-50)

10 20 30 40

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :... . ::
 gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

10 20 30 40
 AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :... . ::
 gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

10 20 30 40
 AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :... . ::
 gi+AHw-131 MGVFN YETEFTSVIPPARLFNAFVLADADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 gi+AHw-131 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

10 20 30 40

AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :... . ::
 gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
 1.03B (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

10 20 30 40
 AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :... . ::
 gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (9-33:27-50)

10 20 30 40
 AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
 ::. .: .: :: :... . ::
 gi+AHw-602 MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
 10 20 30 40 50

50 60 70 80
 AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
 gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
 60 70 80 90 100 110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 50 initl: 50 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.1
 Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (5-33:23-50)

10 20 30 40


```

AAD-12          IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                .. ::: : : : : : : : : : : : : : : : :
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSA

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 50 initl: 50 opt: 50 Z-score: 85.4 bits: 20.6 E(): 8.8
Smith-Waterman score: 50+ADs- 26.829+ACU- identity (58.537+ACU- similar)
in 41 aa overlap (37-77:26-66)

```

                10          20          30          40          50          60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                ::: : : : : : : : : : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                10          20          30          40          50

```

```

                70          80
AAD-12 SQSKLGHVQQAGSA
                .. .. : : : :
gi+AHw-527 AKVNVVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGGLAQ
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle
parvalbumin +AFs-T (107 aa)
initn: 42 initl: 42 opt: 49 Z-score: 84.9 bits: 20.4 E(): 9.4
Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
in 58 aa overlap (19-76:4-59)

```

                10          20          30          40          50          60
AAD-12 IVGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSA
                .... : : : : : : : : : : : : : : : :
gi+AHw-777 MAFKGVLDADVTAALDGCKSAFDHKAFFKACGLAAKSADDIKKA
                10          20          30          40

```

```

                70          80
AAD-12 RHSLVYSQSKLGHVQQAGSA
                . : : : : : : :
gi+AHw-777 FA--IIDQDKSGFIEEDELKLFQNFCAGARALSDAETKAFKAGDSGDGKIGVDEFEEA
                50          60          70          80          90          100

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:56 2010 done: Fri Feb 5 12:55:57 2010

Total Scan time: 0.090 Total Display time: 0.000

[illegible]

```

58      54      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
60      58      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
62      47      40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64      39      32: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66      60      25: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
68      45      20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9-
70      11      16: +AD0APQA9AD0- +ACo-
72      29      12: +AD0APQA9ACoAPQA9AD0APQA9AD0-
74      17      10: +AD0APQA9ACoAPQA9-
76      13      7: +AD0APQA9AD0APQ-
78      19      6: +AD0AKgA9AD0APQA9AD0-
80      9       4: +AD0AKgA9-
82      8       3: +ACoAPQA9-
84      4       3: +ACoAPQ-
86      12      2: +ACoAPQA9AD0-
88      5       2: +ACoAPQ-          inset +AD0- represents 1 library
sequences
90      2       1: +ACo-
92      1       1: +ACo-          : +ACo-
94      2       1: +ACo-          : +ACoAPQ-
96      1       1: +ACo-          : +ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     1       0: +AD0-          +ACoAPQ-
106     0       0:              +ACo-
108     1       0: +AD0-          +ACoAPQ-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.74680.00312+ADs- mu+AD0- 1.4535
0.165
mean+AF8-var+AD0-35.1416 9.966, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.216353
Kolmogorov-Smirnov statistic: 0.1012 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 25.0 0.48
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.3 0.82
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 57 22.8 1.9
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.7 2.4

```

```

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.7      2.7
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  56 22.4      3.4
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301)  58 22.8      4.8
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.5      5.2
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  53 21.5      5.2
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.8      5.2
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (
116)  52 21.3      5.4
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.3      5.6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145)  53 21.5      5.8
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.5      6.5
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.2      7.6
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.2      8
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.2      8
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.2      8
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.2      8
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.2      8
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.2      8
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.2      8
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.2      8
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.2      8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.2      8
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.2      8.1
gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi ( 107)
49 20.4      9.4

```

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
  initn: 38 initl: 38 opt: 64 Z-score: 108.0 bits: 25.0 E(): 0.48
Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (20-78:9-65)

```

10

20

30

40

50

10 20 30 40 50 60

10 20 30 40

AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .. :. : : : : : : : : : : : : : : :
 gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
 10 20 30 40 50

50 60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
 : :
 gi+AHw-663 LEDVNAGFKAABAADANAPPADKFKIFEAFSECKGLLATSDAKAPGLILKLDTDYDVA
 60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein Bl (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 89.5 bits: 21.5 E(): 5.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (20-78:9-65)

10 20 30 40 50
 AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRS
 : : : : : : : : : : : : : : : :
 gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EK
 10 20 30 40

60 70 80
 AAD-12 ARHSLVYSQSKLGHVQQAGSAY
 : : : : : :
 gi+AHw-420 GEHQLLYLQHQLDDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERF
 50 60 70 80 90 100

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 89.5 bits: 21.5 E(): 5.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (20-78:9-65)

10 20 30 40 50
 AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRS
 : : : : : : : : : : : : : : : :
 gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EK
 10 20 30 40

60 70 80
 AAD-12 ARHSLVYSQSKLGHVQQAGSAY
 : : : : : :
 gi+AHw-111 GEHQLLYLQHQLDDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERF
 50 60 70 80 90 100

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 initl: 52 opt: 54 Z-score: 89.4 bits: 21.8 E(): 5.2
 Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
 in 29 aa overlap (4-32:23-50)

10 20 30 40

```

AAD-12                VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        .. .:: : .: .: .: .::: . : :
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                        10         20         30         40         50

                        50         60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
                        60         70         80         90         100        110

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytozystatin +AFs-
Actinidia de (116 aa)
  initn: 34 initl: 34 opt: 52 Z-score: 89.2 bits: 21.3 E(): 5.4
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (12-80:11-80)

                        10         20         30         40         50
AAD-12  VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSA
                        .. . .::: ... . :::: . . .: . : : : .: .:::
gi+AHw-408  MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQA
                        10         20         30         40         50

                        60         70         80
AAD-12  RHSLVYSQSKLGHVQQ-AGSAY
                        : :. . :::: :. :
gi+AHw-408  NDELQYQSVMRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMHFRNLTSFRKV
                        60         70         80         90         100        110

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
  initn: 38 initl: 38 opt: 52 Z-score: 88.9 bits: 21.3 E(): 5.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (38-78:11-50)

                        10         20         30         40         50         60
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                        :. : .: : .:::.. . :.:::..:
gi+AHw-160                GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                        10         20         30

                        70         80
AAD-12  SQSKLGHVQQAGSAY
                        : :. .... :
gi+AHw-160  LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                        40         50         60         70         80         90

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
  initn: 46 initl: 46 opt: 53 Z-score: 88.7 bits: 21.5 E(): 5.8
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (10-58:5-52)

                        10         20         30         40         50         60

```



```

AAD-12  VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
      ..  ...  ..  ..  ..  ..  :  ::  :  .  :  :  :  :  ...
gi+AHw-217  MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTCG
      10      20      30      40      50

```

```

      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAY

gi+AHw-217  ISISGSAVSTEPGNTPRDRCCKEYLDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPRE
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 87.8 bits: 21.5 E(): 6.5
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (13-64:31-87)

```

      10      20      30
AAD-12  VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
      ..  ..  ..  :  ...  :  .  :
gi+AHw-132  MGVFNJETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
      10      20      30      40      50

```

```

      40      50      60      70      80
AAD-12  DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAY
      :  .  .  .  .  .  .  :  ::::
gi+AHw-132  DEGSPFNIIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (43-66:29-52)

```

      20      30      40      50      60      70
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
      :  :  ::  :  .  ...  :  :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
      10      20      30      40      50

```

```

      80
AAD-12  VQQAGSAY

gi+AHw-144  DSKVDEKLDAGDKQKLTAIEDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (8-32:27-50)

10 20 30 40

```

AAD-12                      VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                               ... .. : : : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
              10          20          30          40          50

```

```

              50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

              10          20          30          40
AAD-12                      VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                               ... .. : : : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
              10          20          30          40          50

```

```

              50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

              10          20          30          40
AAD-12                      VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                               ... .. : : : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
              10          20          30          40          50

```

```

              50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

              10          20          30          40

```

```

AAD-12                      VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ... .. : : : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (8-32:27-50)

```

                        10          20          30          40
AAD-12                      VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ... .. : : : : : : : :
gi+AHw-131 MGVFNYTEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-131 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (8-32:27-50)

```

                        10          20          30          40
AAD-12                      VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ... .. : : : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (8-32:27-50)

```

                        10          20          30          40

```

```

AAD-12                VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                        10      20      30      40      50

```

```

                        50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

                        10      20      30      40
AAD-12                VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                        10      20      30      40      50

```

```

                        50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

                        10      20      30      40
AAD-12                VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        ::.  .: .:  :: :...  .  ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                        10      20      30      40      50

```

```

                        50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                        60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)
 initn: 51 initl: 51 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (8-32:27-50)

```

                        10      20      30      40

```

AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
::: .: .: :: :... . :
gi+AHw-602 MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEGDGGVGTIKKINF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
60 70 80 90 100 110

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 50 initl: 50 opt: 52 Z-score: 86.1 bits: 21.2 E(): 8.1
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (4-32:23-50)

10 20 30 40
AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
.. ::: : .: .: .: :... . :
gi+AHw-444 MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGAEIVEGDGGVGTIKKISF
10 20 30 40 50

50 60 70 80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
60 70 80 90 100 110

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle
parvalbumin +AFs-T (107 aa)
initn: 42 initl: 42 opt: 49 Z-score: 84.9 bits: 20.4 E(): 9.4
Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
in 58 aa overlap (18-75:4-59)

10 20 30 40 50 60
AAD-12 VGNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
:... :... :. : : :. : : :... :..
gi+AHw-777 MAFKGVLDADVTAALDGCKSAFDHKAFFKACGLAAKSADDIKKAF
10 20 30 40

70 80
AAD-12 HSLVYSQSKLGHVQQAGSAY
. :... : ...
gi+AHw-777 A--IIDQDKSGFIEEDELKLFQNFCAGARALSDAETKAFLKAGDSGDGKIGVDEFAAM
50 60 70 80 90 100

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:55:57 2010 done: Fri Feb 5 12:55:57 2010

Total Scan time: 0.090 Total Display time: 0.010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

56      83
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58      50      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
60      61
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      42      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      40      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      62      25:+AD0APQA9AD0APQA9AD0-
+AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
68      43      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
70      11      16:+AD0APQA9AD0- +ACo-
72      30      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      17      10:+AD0APQA9ACoAPQA9-
76      15      7:+AD0APQA9AD0APQ-
78      18      6:+AD0AKgA9AD0APQA9-
80      8       4:+AD0AKgA9-
82      8       3:+ACoAPQA9-
84      4       3:+ACoAPQ-
86      12      2:+ACoAPQA9AD0-
88      5       2:+ACoAPQ-      inset +AD0- represents 1 library
sequences
90      2       1:+ACo-
92      1       1:+ACo-      :+ACo-
94      2       1:+ACo-      :+ACoAPQ-
96      1       1:+ACo-      :+ACo-
98      0       0:      +ACo-
100     0       0:      +ACo-
102     0       0:      +ACo-
104     1       0:+AD0-      +ACoAPQ-
106     0       0:      +ACo-
108     1       0:+AD0-      +ACoAPQ-
110     0       0:      +ACo-
112     0       0:      +ACo-
114     0       0:      +ACo-
116     0       0:      +ACo-
118     0       0:      +ACo-
+AD4-120     0       0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.80120.00311+ADs- mu+AD0- 1.1680
0.164
mean+AF8-var+AD0-35.492010.042, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.215283
Kolmogorov-Smirnov statistic: 0.1067 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 24.9 0.5
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.3 0.84

```

```

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   57 22.8       2
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.7       2.5
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.7       2.8
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)   56 22.4       3.5
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301)   58 22.8       5
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.5       5.3
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   53 21.5       5.3
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.7       5.4
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (
116)   52 21.2       5.5
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2       5.7
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145)   53 21.5       5.9
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.4       6.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.1       7.7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.1       8.2
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.1       8.2
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.1       8.2
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.1       8.2
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.1       8.2
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.1       8.2
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.1       8.2
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.1       8.2
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.1       8.2
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.1       8.2
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.1       8.3
gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi ( 107)
49 20.3       9.5

```

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

```

```

initn: 38 initl: 38 opt: 64 Z-score: 107.8 bits: 24.9 E(): 0.5

```


Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (19-77:9-65)

```

          10          20          30          40          50
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKG
          10          20          30          40

```

```

          60          70          80
AAD-12  RHSLVYSQSKLGHVQQAGSAYI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111  EHQLLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFN
          50          60          70          80          90          100

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)

initn: 55 init1: 55 opt: 62 Z-score: 103.7 bits: 24.3 E(): 0.84
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (9-57:5-52)

```

          10          20          30          40          50          60
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-189      MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGV
          10          20          30          40          50

```

```

          70          80
AAD-12  SLVYSQSKLGHVQQAGSAYI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-189  TIAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQ
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 57 init1: 57 opt: 57 Z-score: 97.0 bits: 22.8 E(): 2
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (35-79:26-70)

```

          10          20          30          40          50          60
AAD-12  WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFFADWCPCKAIAPVYEQNSTKHSVPDVLAF
          10          20          30          40          50

```

```

          70          80
AAD-12  SQSKLGHVQQAGSAYI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527  AKVNVDPVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQ
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of
tetrameric (145 aa)

initn: 50 init1: 50 opt: 57 Z-score: 95.3 bits: 22.7 E(): 2.5

Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (9-57:5-52)

```

                10         20         30         40         50         60
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH
                ..   ...   ...   ..   ..   ..   ..   ..   ..   ..   ..   ..
gi+AHw-439  MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGV
                10         20         30         40         50

```

```

                70         80
AAD-12  SLVYSQSKLGHVQQAGSAYI

gi+AHw-439  TIAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEP
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 94.3 bits: 22.7 E(): 2.8
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (3-31:23-50)

```

                10         20         30         40
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..   ...   ..   ..   ..   ..   ..   ..   ..   ..
gi+AHw-444  MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 92.6 bits: 22.4 E(): 3.5
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                10         20         30         40
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ...   ..   ..   ..   ..   ..   ..   ..   ..
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90         100        110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 89.8 bits: 22.8 E(): 5

Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (4-53:23-71)

```

                        10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                .. ::: : : : . : ..... : :
gi+AHw-663 MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
                . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAFSECKGLLATSDAKAPGLILKLDTDYDVA
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 89.3 bits: 21.5 E(): 5.3
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (19-77:9-65)

```

                10      20      30      40      50
AAD-12 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSA
                : ::: : : . : : : : ..... : :
gi+AHw-420      MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKG
                10      20      30      40

```

```

                60      70      80
AAD-12 RHSLVYSQSKLGHVQQAGSAYI
                ..... : : ..... :
gi+AHw-420 EHQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFN
                50      60      70      80      90      100

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 89.3 bits: 21.5 E(): 5.3
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (19-77:9-65)

```

                10      20      30      40      50
AAD-12 GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSA
                : ::: : : . : : : : ..... : :
gi+AHw-111      MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKG
                10      20      30      40

```

```

                60      70      80
AAD-12 RHSLVYSQSKLGHVQQAGSAYI
                ..... : : ..... :
gi+AHw-111 EHQLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFN
                50      60      70      80      90      100

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 89.3 bits: 21.7 E(): 5.4

Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (3-31:23-50)

```

                        10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                ..  :::  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
                10      20      30      40      50

                        50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 init1: 34 opt: 52 Z-score: 89.0 bits: 21.2 E(): 5.5
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (11-79:11-80)

```

                        10      20      30      40      50
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                . . .  :::  . . .  :  :  :  . . .  :  :  :  :  :  :  :
gi+AHw-408  MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10      20      30      40      50

                        60      70      80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYI
                :  : .  :  :  :  :  :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 init1: 38 opt: 52 Z-score: 88.8 bits: 21.2 E(): 5.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (37-77:11-50)

```

                        10      20      30      40      50      60
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
                10      20      30

                        70      80
AAD-12  SQSKLGHVQQAGSAYI
                :  :  :  :  :
gi+AHw-160  LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
                40      50      60      70      80      90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 init1: 46 opt: 53 Z-score: 88.5 bits: 21.5 E(): 5.9

```
initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
```

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::.  .  ::
gi+AHw-131  MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-131  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.2

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (7-31:27-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
              10      20      30      40      50

              50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
              60      70      80      90      100     110
```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.9 bits: 21.1 E(): 8.3
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (3-31:23-50)

```

                                10      20      30      40
AAD-12      GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ..  ::  :  .:  .:  .:  ::::.  .  ::
gi+AHw-444  MGVFTYADESTSVITPPRLF KALVLEAD-TLIPKIA PQSVKGAEIVEG DGGVGTIKKISF
              10      20      30      40      50

              50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
              60      70      80      90      100     110
```

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle
parvalbumin +AFs-T (107 aa)

initn: 42 initl: 42 opt: 49 Z-score: 84.8 bits: 20.3 E(): 9.5
Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
in 58 aa overlap (17-74:4-59)

```

              10      20      30      40      50      60
AAD-12  GNMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARH
              ....  ::::.  .:  :  :  .:  .:  :  ....  ...
gi+AHw-777      MAFKGVLDADVTAALDGCKSAFDHKAFFKACGLAAKSADDIKKAFA
              10      20      30      40

              70      80
AAD-12  SLVYSQSKLGHVQQAGSAYI
              .  ::::.  :  ...
gi+AHw-777  --IIDQDKSGFIEEDELKLF LQNFCAGARALSDAETKAFLKAGDSGDGKIGVDEFAAMV
              50      60      70      80      90      100
```

80 residues in 1 query sequences

[illegible]

```

56      78
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58      52      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
60      61
50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      47      40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64      50      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
66      53      25: +AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
68      41      20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
70      13      16: +AD0APQA9AD0APQAq-
72      30      12: +AD0APQA9ACoAPQA9AD0APQA9AD0-
74      16      10: +AD0APQA9ACoAPQA9-
76      21      7: +AD0APQAqAD0APQA9AD0-
78      10      6: +AD0AKgA9AD0-
80      9       4: +AD0AKgA9-
82      9       3: +ACoAPQA9-
84      9       3: +ACoAPQA9-
86      5       2: +ACoAPQ-
88      7       2: +ACoAPQA9-          inset +AD0- represents 1 library
sequences
90      0       1: +ACo-
92      1       1: +ACo-          : +ACo-
94      2       1: +ACo-          : +ACoAPQ-
96      1       1: +ACo-          : +ACo-
98      0       0:          +ACo-
100     0       0:          +ACo-
102     1       0: +AD0-          +ACo-+AD0-
104     0       0:          +ACo-
106     1       0: +AD0-          +ACoAPQ-
108     0       0:          +ACo-
110     0       0:          +ACo-
112     0       0:          +ACo-
114     0       0:          +ACo-
116     0       0:          +ACo-
118     0       0:          +ACo-
+AD4-120 0       0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.79830.00318+ADs- mu+AD0- 1.1997
0.167
mean+AF8-var+AD0-36.168910.134, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.213259
Kolmogorov-Smirnov statistic: 0.1046 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 24.8 0.54
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.2 0.9

```

```

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   57 22.7   2.1
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.6   2.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.6   3
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)   56 22.3   3.7
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301)   58 22.7   5.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.4   5.6
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   53 21.4   5.6
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.7   5.7
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (
116)   52 21.2   5.8
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2   6
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145)   53 21.4   6.2
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.4   7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.1   8.1
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.1   8.6
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.1   8.6
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.1   8.6
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.1   8.6
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.1   8.6
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.1   8.6
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.1   8.6
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.1   8.6
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.1   8.6
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.1   8.6
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.1   8.7
gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle parvalbumi ( 107)
49 20.3   10

```

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

```

```

initn: 38 initl: 38 opt: 64 Z-score: 107.2 bits: 24.8 E(): 0.54

```

Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (18-76:9-65)

```

                10         20         30         40         50
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSAR
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGE
                10         20         30         40

```

```

                60         70         80
AAD-12 HSLVYSQSKLGHVQQAGSAYIG
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 HQLLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNY
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)

initn: 55 init1: 55 opt: 62 Z-score: 103.2 bits: 24.2 E(): 0.9
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (8-56:5-52)

```

                10         20         30         40         50         60
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-189      MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVT
                10         20         30         40         50

```

```

                70         80
AAD-12 LVYSQSKLGHVQQAGSAYIG
gi+AHw-189      IAGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQR
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 57 init1: 57 opt: 57 Z-score: 96.5 bits: 22.7 E(): 2.1
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (34-78:26-70)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIG
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      AKVNVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQ
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of
tetrameric (145 aa)
initn: 50 init1: 50 opt: 57 Z-score: 94.8 bits: 22.6 E(): 2.6

Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (8-56:5-52)

```

                10         20         30         40         50         60
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
      .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVT
                10         20         30         40         50

```

```

                70         80
AAD-12 LVYSQSKLGHVQQAGSAYIG

```

```

gi+AHw-439 IAGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQ
        60         70         80         90        100        110

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 93.9 bits: 22.6 E(): 3
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (2-30:23-50)

```

                10         20         30
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

        40         50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
        60         70         80         90        100        110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)

initn: 55 initl: 55 opt: 56 Z-score: 92.2 bits: 22.3 E(): 3.7
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                10         20         30
AAD-12 NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

        40         50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

```

```

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
        60         70         80         90        100        110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 89.4 bits: 22.7 E(): 5.3

Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (3-52:23-71)

```

                                10      20      30      40
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
              .. ::: : : : . : ..... : :
gi+AHw-663  MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
              10      20      30      40      50

              50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG
              . . . . :
gi+AHw-663  LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 88.9 bits: 21.4 E(): 5.6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (18-76:9-65)

```

              10      20      30      40      50
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSAR
              : ::: : : . : : : : ..... : :
gi+AHw-420      MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGE
              10      20      30      40

              60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIG
              : : : : : : : : :
gi+AHw-420  HQLLYLQHQLDLNLNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNY
              50      60      70      80      90      100

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 88.9 bits: 21.4 E(): 5.6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (18-76:9-65)

```

              10      20      30      40      50
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSAR
              : ::: : : . : : : : ..... : :
gi+AHw-111      MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGE
              10      20      30      40

              60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIG
              : : : : : : : : :
gi+AHw-111  HQLLYLQHQLDLNLNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNY
              50      60      70      80      90      100

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 initl: 52 opt: 54 Z-score: 88.9 bits: 21.7 E(): 5.7

Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (2-30:23-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ..  :::  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
              10      20      30      40      50

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 init1: 34 opt: 52 Z-score: 88.6 bits: 21.2 E(): 5.8
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (10-78:11-80)

```

              10      20      30      40      50
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
              ..  .  ::::  ...  .  ::::  .  .  :  .  :  :  :  :  :  :
gi+AHw-408  MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
              10      20      30      40      50

              60      70      80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYIG
              :  :..  ::::  :..  :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 init1: 38 opt: 52 Z-score: 88.4 bits: 21.2 E(): 6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (36-76:11-50)

```

              10      20      30      40      50      60
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
              10      20      30

              70      80
AAD-12  SQSKLGHVQQAGSAYIG
              :  :  :  :  :
gi+AHw-160  LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
              40      50      60      70      80      90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 init1: 46 opt: 53 Z-score: 88.2 bits: 21.4 E(): 6.2

Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (8-56:5-52)

```

                10         20         30         40         50         60
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
                ..   ...   ..   ..   ..   :   :   :   :   :   :   :   :   :   :   :   :
gi+AHw-217  MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTCGIS
                10         20         30         40         50
```

```

                70         80
AAD-12  LVYSQSKLGHVQQAGSAYIG

gi+AHw-217  ISGSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRRSDPNSSVLKDLPGCPREPQ
                60         70         80         90        100        110
```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)

initn: 47 init1: 47 opt: 53 Z-score: 87.2 bits: 21.4 E(): 7
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (11-62:31-87)

```

                10         20         30
AAD-12                      NMAWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
                ..   ..   :   :   :   :   :   :   :   :   :   :
gi+AHw-132  MGVFNYETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10         20         30         40         50
```

```

                40         50         60         70         80
AAD-12  DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIG
                :   .   .   .   .   .   :   :   :   :
gi+AHw-132  DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60         70         80         90        100        110
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)

initn: 52 init1: 52 opt: 52 Z-score: 86.0 bits: 21.1 E(): 8.1
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (41-64:29-52)

```

                20         30         40         50         60         70
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
                :   :   :   :   :   :   :   :   :   :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAEARISAKNALESYAYSLRNTLS
                10         20         30         40         50
```

```

                80
AAD-12  VQQAGSAYIG

gi+AHw-144  DSKVDEKLDAGDKQKLTA EIDKTVQWLDDNQ TATKDEYESQQKELEGVANPIMMKFYGAG
                60         70         80         90        100        110
```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1.03A (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  :: :...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-131  MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::...  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::...  .  ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.6 bits: 21.1 E(): 8.6

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (6-30:27-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  ::...  .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.5 bits: 21.1 E(): 8.7
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (2-30:23-50)

```

                                10      20      30
AAD-12      NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ..  ::  :  .:  .:  .:  ::...  .  ::
gi+AHw-444  MGVFTYADESTSVITPPRLF KALVLEAD-TLIPKIA PQSVKGA EIVEG DGGVGTIKKISF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-77799800+AHw-dbj+AHw-BAE46763.1+AHw- dark muscle
parvalbumin +AFs-T (107 aa)

initn: 42 initl: 42 opt: 49 Z-score: 84.4 bits: 20.3 E(): 10
Smith-Waterman score: 49+ADs- 22.414+ACU- identity (56.897+ACU- similar)
in 58 aa overlap (16-73:4-59)

```

                                10      20      30      40      50      60
AAD-12  NMAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHS
                                ....  ::...  .:  :  :  .:  .:  :  ::...  ...
gi+AHw-777      MAFKGV LNDADVTAALDGCKSAFDHKAFFKACGLAAKSADDIKKAFA-
                                10      20      30      40

                                70      80
AAD-12  LVYSQSKLGHVQQAGSAYIG
                                .  ::...  :  ...
gi+AHw-777  -IIDQDKSGFIEEDELKLF LQNF CAGARALSDAETKAFLKAGDSGDGDKIGVDEFAAMVK
                                50      60      70      80      90      100

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

```
start: Fri Feb 5 12:55:59 2010 done: Fri Feb 5 12:55:59 2010
```

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
```

```
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
```

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

```
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

1+AD4APqA+-AAD-12: 106 - 185 80 aa - 80 aa

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

54      73
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58      53      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
60      55      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      47      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64      69
32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
66      36      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
68      43      20:+AD0APQA9AD0APQA9ACoAPQA9AD0-+AD0APQA9AD0APQ-
70      16      16:+AD0APQA9AD0APQA9-
72      30      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      19      10:+AD0APQA9ACoAPQA9AD0-
76      23      7:+AD0APQA9AD0APQA9AD0APQ-
78      6      6:+AD0AKg-
80      11      4:+AD0AKgA9AD0-
82      6      3:+ACoAPQ-
84      13      3:+ACoAPQA9AD0APQ-
86      1      2:+ACo-
88      7      2:+ACoAPQA9-          inset +AD0- represents 1 library
sequences
90      0      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:          +ACo-
106     1      0:+AD0-      +ACoAPQ-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120     0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.81910.00326+ADs- mu+AD0- 1.1377
0.172
mean+AF8-var+AD0-37.029210.120, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.210767
Kolmogorov-Smirnov statistic: 0.1121 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)    64 24.7    0.59

```

```

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 24.0 0.98
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 57 22.6 2.3
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram ( 145)
57 22.5 2.8
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
57 22.5 3.2
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.2 4
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.6 5.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.3 6
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 53 21.3 6
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
54 21.6 6
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (
116) 52 21.1 6.2
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.1 6.4
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.3 6.6
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.3 7.5
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.0 8.7
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.1
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.1
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.1
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.1
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 21.0 9.1
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.1
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.1
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.1
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 21.0 9.1
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 21.0 9.1
gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen P ( 160)
52 21.0 9.2

```

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

```

```

initn: 38 init1: 38 opt: 64 Z-score: 106.5 bits: 24.7 E(): 0.59

```


Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (17-75:9-65)

```

                10         20         30         40         50
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARH
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEH
                10         20         30         40

```

```

                60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGY
                . : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 QLLYLQHQLDLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYE
                50         60         70         80         90         100

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)

initn: 55 initl: 55 opt: 62 Z-score: 102.5 bits: 24.0 E(): 0.98
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (7-55:5-52)

```

                10         20         30         40         50         60
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-189      MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTI
                10         20         30         40         50

```

```

                70         80
AAD-12 VYSQSKLGHVQQAGSAYIGY
gi+AHw-189      AGSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRD
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 57 initl: 57 opt: 57 Z-score: 95.9 bits: 22.6 E(): 2.3
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (33-77:26-70)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527      MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGY
                . . . : : : : : : : : : : : : : : : : : :
gi+AHw-527      AKVNVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQ
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of
tetrameric (145 aa)

initn: 50 initl: 50 opt: 57 Z-score: 94.2 bits: 22.5 E(): 2.8

Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (7-55:5-52)

```

                10         20         30         40         50         60
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
      .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTI
                10         20         30         40         50

```

```

                70         80
AAD-12 VYSQSKLGHVQQAGSAYIGY

gi+AHw-439 AGSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQR
                60         70         80         90        100        110

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 55 initl: 55 opt: 57 Z-score: 93.3 bits: 22.5 E(): 3.2
Smith-Waterman score: 57+ADs- 41.379+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (1-29:23-50)

```

                10         20         30
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                60         70         80         90        100        110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 91.6 bits: 22.2 E(): 4
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                10         20         30
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90        100        110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)

initn: 49 initl: 49 opt: 58 Z-score: 88.9 bits: 22.6 E(): 5.6

Smith-Waterman score: 58+ADs- 26.000+ACU- identity (56.000+ACU- similar)
in 50 aa overlap (2-51:23-71)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
              .. ::: : : : . : ..... : :
gi+AHw-663  MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
              10      20      30      40      50

```

```

        40      50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
          . . . . : :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
          60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 init1: 38 opt: 53 Z-score: 88.4 bits: 21.3 E(): 6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (17-75:9-65)

```

                10      20      30      40      50
AAD-12  MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARH
              : ::: : : . : : : : ..... : : :
gi+AHw-420      MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEH
              10      20      30      40

```

```

        60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGY
          . . . : : : : :
gi+AHw-420 QLLYLQHQLDLNLNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYE
          50      60      70      80      90      100

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 init1: 38 opt: 53 Z-score: 88.4 bits: 21.3 E(): 6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (17-75:9-65)

```

                10      20      30      40      50
AAD-12  MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARH
              : ::: : : . : : : : ..... : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEH
              10      20      30      40

```

```

        60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGY
          . . . : : : : :
gi+AHw-111 QLLYLQHQLDLNLNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYE
          50      60      70      80      90      100

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 52 init1: 52 opt: 54 Z-score: 88.3 bits: 21.6 E(): 6

Smith-Waterman score: 54+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (1-29:23-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ..  :::  :  :  :  :  :  :  :  :  :  :
gi+AHw-444  MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTA EIVEGDGGVGTIKKISF
              10      20      30      40      50

```

```

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 init1: 34 opt: 52 Z-score: 88.1 bits: 21.1 E(): 6.2
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (9-77:11-80)

```

              10      20      30      40      50
AAD-12  MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
              ..  .  .:::  .  .  ::::  .  .  :  :  :  :  :  :  :  :  :  :
gi+AHw-408  MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
              10      20      30      40      50

```

```

              60      70      80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYIGY
              :  :..  ::::  :..  :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.9 bits: 21.1 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (35-75:11-50)

```

              10      20      30      40      50      60
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
              :::  :  :  :  :  :  :  :  :  :  :
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
              10      20      30

```

```

              70      80
AAD-12  SQSKLGHVQQAGSAYIGY
              :  :  :  :  :
gi+AHw-160  LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
              40      50      60      70      80      90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 init1: 46 opt: 53 Z-score: 87.6 bits: 21.3 E(): 6.6

Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (7-55:5-52)

```

                10         20         30         40         50         60
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSL
      .. ... .. .. : ... : . : . : . : . : . : . : . : . : . : . : . :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTCGISI
                10         20         30         40         50

```

```

                70         80
AAD-12 VYSQSKLGHVQQAGSAYIGY

gi+AHw-217 SGSAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQR
                60         70         80         90        100        110

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)

initn: 47 init1: 47 opt: 53 Z-score: 86.7 bits: 21.3 E(): 7.5
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (10-61:31-87)

```

                10         20         30
AAD-12 MAWHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi+AHw-132 MGVFNYETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGY
      : . . . . . : : : : . : . : . : . : . : . : . : . : . : . :
gi+AHw-132 DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                60         70         80         90        100        110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)

initn: 52 init1: 52 opt: 52 Z-score: 85.5 bits: 21.0 E(): 8.7
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (40-63:29-52)

```

                10         20         30         40         50         60
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
      : : : : : : . . : : . : . : . : . : . : . : . : . : . : . :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAEARISAKNALESYAYSLRNTLS
                10         20         30         40         50

```

```

                70         80
AAD-12 VQQAGSAYIGY

gi+AHw-144 DSKVDEKLDAGDKQKLTAIEDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAG
                60         70         80         90        100        110

```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAASSGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-131  MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASSNGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)

initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1.03D (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 +AFs-Mal (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .: .:  :: :... . ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1.03E (159 aa)
initn: 51 init1: 51 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.1

Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (5-29:27-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  ::  :::.  .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-44409496+AHw-gb+AHw-AAS47037.1+AHw- major cherry allergen
Pru a (160 aa)

initn: 50 initl: 50 opt: 52 Z-score: 85.1 bits: 21.0 E(): 9.2
Smith-Waterman score: 52+ADs- 37.931+ACU- identity (68.966+ACU- similar)
in 29 aa overlap (1-29:23-50)

```

                                10      20      30
AAD-12      MAWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ..  ::  :  .:  .:  .:  :::.  .  ::
gi+AHw-444  MGVFTYADESTSVITPPRLFKALVLEAD-TLIPKIA PQSVKGA EIVEG DGGVGTIKKISF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                                60      70      80      90      100     110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:00 2010 done: Fri Feb 5 12:56:00 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 107 - 186 80 aa - 80 aa

[illegible]

```

82      4      3:+ACoAPQ-
84     12     3:+ACoAPQA9AD0-
86      3     2:+ACo-
88      7     2:+ACoAPQA9-      inset +AD0- represents 1 library
sequences
90      1     1:+ACo-
92      2     1:+ACo-      :+ACoAPQ-
94      1     1:+ACo-      :+ACo-
96      0     1:+ACo-      :+ACo-
98      0     0:      +ACo-
100     0     0:      +ACo-
102     1     0:+AD0-      +ACoAPQ-
104     0     0:      +ACo-
106     1     0:+AD0-      +ACoAPQ-
108     0     0:      +ACo-
110     0     0:      +ACo-
112     0     0:      +ACo-
114     0     0:      +ACo-
116     0     0:      +ACo-
118     0     0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.00980.00333+ADs- mu+AD0- -
0.1006 0.176
mean+AF8-var+AD0-39.083210.559, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.205154
Kolmogorov-Smirnov statistic: 0.1216 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 24.5 0.67
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144) 62 23.9 1.1
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 57 22.4 2.5
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.4 3.1
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160) 56 22.1 4.3
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
56 22.1 4.3
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
56 22.0 5.7
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204) 56 22.0 5.8
gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (
301) 58 22.4 6.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.2 6.4

```

```

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 53 21.2 6.4
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (
116) 52 21.0 6.6
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.0 6.8
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (
145) 53 21.2 7.1
gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P ( 160)
53 21.2 8
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
53 21.2 8
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 20.9 9.2
gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.8
gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.8
gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.8
gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.8
gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.8
gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1 ( 159)
52 20.9 9.8
gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.8
gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1 ( 159)
52 20.9 9.8
gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.8
gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d 1. ( 159)
52 20.9 9.8

```

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
  initn: 38 initl: 38 opt: 64 Z-score: 105.5 bits: 24.5 E(): 0.67
Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (16-74:9-65)

```

```

                10      20      30      40      50
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHS
          : : : : . : : . : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQ
                10      20      30      40

        60      70      80
AAD-12 LVYSQSKLGHVQQAGSAYIGY
          : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 LLYLQHQLDLENENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEE
        50      60      70      80      90      100

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 55 initl: 55 opt: 62 Z-score: 101.6 bits: 23.9 E(): 1.1
Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (6-54:5-52)

```

      10      20      30      40      50      60
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
      .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIA
      10      20      30      40      50
```

```

      70      80
AAD-12 YSQSKLGHVQQAGSAYIGYG
```

```

gi+AHw-189 GSPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDF
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 57 initl: 57 opt: 57 Z-score: 95.2 bits: 22.4 E(): 2.5
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (32-76:26-70)

```

      10      20      30      40      50      60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
      ::: .. . . : .... :..
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
      10      20      30      40      50
```

```

      70      80
AAD-12 SQSKLGHVQQAGSAYIGYG
      .. .. ::::: :
gi+AHw-527 AKVNVVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQ
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
initn: 50 initl: 50 opt: 57 Z-score: 93.5 bits: 22.4 E(): 3.1
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (6-54:5-52)

```

      10      20      30      40      50      60
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
      .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIA
      10      20      30      40      50
```

```

      70      80
AAD-12 YSQSKLGHVQQAGSAYIGYG
```

```

gi+AHw-439 GSPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRD
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)

initn: 55 initl: 55 opt: 56 Z-score: 90.9 bits: 22.1 E(): 4.3
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::.  .:  .:  .:  ::::.  .  ::
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 initl: 55 opt: 56 Z-score: 90.9 bits: 22.1 E(): 4.3
Smith-Waterman score: 56+ADs- 48.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ::  :  .:  .:  .:  ::::.  .  ::
gi+AHw-444  MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)

initn: 40 initl: 40 opt: 56 Z-score: 88.8 bits: 22.0 E(): 5.7
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (33-80:93-144)

```

                                10      20      30      40      50
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....:  ::  ::  .  ..
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100     110     120

                                60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGY
                                ..  :  .:  .:  .....:
gi+AHw-144  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

```

      60      70      80
AAD-12 LVYSQSKLGHVQQAGSAYIGYG
      :: : .: ... :
gi+AHw-420 LLYLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEE
      50      60      70      80      90     100

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.9 bits: 21.2 E(): 6.4
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (16-74:9-65)

```

      10      20      30      40      50
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQ
      10      20      30      40

```

```

      60      70      80
AAD-12 LVYSQSKLGHVQQAGSAYIGYG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 LLYLQHQLDLENENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEE
      50      60      70      80      90      100

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 52 Z-score: 87.6 bits: 21.0 E(): 6.6
 Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
 in 71 aa overlap (8-76:11-80)

```

      10      20      30      40      50
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
      . . . . : : : : . : : : . . . : : : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLLALSAAVVGGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
      10      20      30      40      50

```

```

      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYG
      : : . : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.4 bits: 21.0 E(): 6.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (34-74:11-50)

```

      10      20      30      40      50      60
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLY
      10      20      30

```

```

      70      80
AAD-12 SQSKLGHVQQAGSAYIGYG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160 LQHQLDLENENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQT
      40      50      60      70      80      90

```


+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 87.1 bits: 21.2 E(): 7.1
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (6-54:5-52)

```

      10      20      30      40      50      60
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLV
      .. ... .. .. : : : : : : : : : :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTCGISIS
      10      20      30      40      50
```

```

      70      80
AAD-12 YSQSKLGHVQQAGSAYIGYG
```

```

gi+AHw-217 GSAVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRRSDPNSSVLKDLPGCPREPQRD
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 initl: 52 opt: 53 Z-score: 86.2 bits: 21.2 E(): 8
Smith-Waterman score: 53+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

      10      20      30
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      :: : : : : : : : : : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
      10      20      30      40      50
```

```

      40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
```

```

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 86.2 bits: 21.2 E(): 8
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (9-60:31-87)

```

      10      20      30
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
      .. : : : : : : : : : :
gi+AHw-132 MGVFN YETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
      10      20      30      40      50
```

```

      40      50      60      70      80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYG
      : . . . . . : : : . . .
```

```

gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.2
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (39-62:29-52)

```
      10      20      30      40      50      60
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
      : : : : : : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
      10      20      30      40      50
```

```
      70      80
AAD-12 VQQAGSAYIGYG
```

```
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAG
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-60280841+AHw-gb+AHw-AAX18313.1+AHw- major allergen Mal d
1.03A (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```
      10      20      30
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      : : : : : : : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10      20      30      40      50
```

```
      40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
```

```
gi+AHw-602 GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-60280853+AHw-gb+AHw-AAX18319.1+AHw- major allergen Mal d
1.03E (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```
      10      20      30
AAD-12 AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
      : : : : : : : : : : : :
gi+AHw-602 MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
      10      20      30      40      50
```

```
      40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
```

```
gi+AHw-602 GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-60280849+AHw-gb+AHw-AAX18317.1+AHw- major allergen Mal d
1.03D (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAASSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280861+AHw-gb+AHw-AAX18323.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVAASSNGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280859+AHw-gb+AHw-AAX18322.1+AHw- major allergen Mal d
1.03F (159 aa)

initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-1313966+AHw-emb+AHw-CAA96534.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .: .:  :: ::... .  ::
gi+AHw-131  MGVFNYETEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-131  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280843+AHw-gb+AHw-AAX18314.1+AHw- major allergen Mal d
1.03B (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .: .:  :: ::... .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-602  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-27922941+AHw-gb+AHw-AAO25113.1+AHw- major allergen Mal d 1
+AFs-Mal (159 aa)
initn: 51 initl: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                ...  .: .:  :: ::... .  ::
gi+AHw-279  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIA PQAVKSAEILEG DGGVGTIKKINF
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY

gi+AHw-279  GEGSTYSYVKHRIDGVDKENFVKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
                                60      70      80      90      100     110
```

+AD4APg-gi+AHw-60280851+AHw-gb+AHw-AAX18318.1+AHw- major allergen Mal d
 1.03D (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSVIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
              10      20      30      40      50

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSH
              60      70      80      90      100     110

```

+AD4APg-gi+AHw-60280855+AHw-gb+AHw-AAX18320.1+AHw- major allergen Mal d
 1.03E (159 aa)
 initn: 51 init1: 51 opt: 52 Z-score: 84.6 bits: 20.9 E(): 9.8
 Smith-Waterman score: 52+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (4-28:27-50)

```

                                10      20      30
AAD-12      AWHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::.  .:  .:  ::  ::::.  .  ::
gi+AHw-602  MGVFTYESEFTSIIPPARLFNAFVLDADNL-IPKIAPQAVKSAEILEGDDGGVGTIKKINF
              10      20      30      40      50

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG

gi+AHw-602  GEGSTYSYVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSH
              60      70      80      90      100     110

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:00 2010 done: Fri Feb 5 12:56:00 2010
 Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

78      8      6:+AD0AKgA9-
80      8      4:+AD0AKgA9-
82      6      3:+ACoAPQ-
84     12      3:+ACoAPQA9AD0-
86      5      2:+ACoAPQ-
88      3      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      1      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120    0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.04060.00337+ADs- mu+AD0- -
0.2234 0.177
mean+AF8-var+AD0-40.063710.748, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.202628
Kolmogorov-Smirnov statistic: 0.1271 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   64 24.3      0.74
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)   62 23.7      1.2
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   57 22.3      2.7
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.3      3.4
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)   56 22.0      4.6
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
56 22.0      4.6
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
56 21.9      6.1
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   56 21.9      6.3
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   53 21.1      6.9
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.1      6.9

```

gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.9 7
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.9 7.3
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.6
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 57 22.0 8.2
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 53 21.1 8.5
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.5
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 104.7 bits: 24.3 E(): 0.74
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (15-73:9-65)

	10	20	30	40	50
AAD-12	WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSL				
		:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQL				
	10	20	30	40	50

	60	70	80
AAD-12	VYSQSKLGHVQQAGSAYIGYGM		
	:	:	:
gi+AHw-111	LYLQHQLDLLENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEA		
	60	70	80

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 100.9 bits: 23.7 E(): 1.2
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (5-53:5-52)

	10	20	30	40	50	60
AAD-12	WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY					
	:	:	:	:	:	:
gi+AHw-189	MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG					
	10	20	30	40	50	

	70	80
AAD-12	SQSKLGHVQQAGSAYIGYGM	
gi+AHw-189	SPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFA	
	60	70

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 57 initl: 57 opt: 57 Z-score: 94.6 bits: 22.3 E(): 2.7

Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (31-75:26-70)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                :::         :. . . : . . . : . . . : . . . : . . . :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAF
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGYGM
                .. .. : . . . . . :
gi+AHw-527 AKVNVDPVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAEKLGGLAQ
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
tetrameric (145 aa)
initn: 50 initl: 50 opt: 57 Z-score: 92.9 bits: 22.3 E(): 3.4
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
in 49 aa overlap (5-53:5-52)

```

                10         20         30         40         50         60
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                :. . . . . : . . . . : . . . . : . . . . : . . . . :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTGCVTIAG
                10         20         30         40         50

```

```

                70         80
AAD-12 SQSKLGHVQQAGSAYIGYGM
gi+AHw-439 SPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDF
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 90.4 bits: 22.0 E(): 4.6
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (3-27:27-50)

```

                10         20         30
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : . . : . : : . : : : . : : : . : : :
gi+AHw-165 MGVFTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
                10         20         30         40         50

```

```

                40         50         60         70         80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 90.4 bits: 22.0 E(): 4.6

Smith-Waterman score: 56+ADs- 48.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (3-27:27-50)

```

                                10      20      30
AAD-12                      WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                :: : .: .: .: : ::::: . ::
gi+AHw-444 MGVFYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 40 init1: 40 opt: 56 Z-score: 88.3 bits: 21.9 E(): 6.1
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (32-79:93-144)

```

                                10      20      30      40      50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .: ::::: ::::: .: .: .: .: .:
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100     110     120

```

```

                                60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGM
                                .. : .: .: : ::::: .:
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 40 init1: 40 opt: 56 Z-score: 88.1 bits: 21.9 E(): 6.3
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (32-79:97-148)

```

                                10      20      30      40      50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .: ::::: ::::: .: .: .: .: .:
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100     110     120

```

```

                                60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGM
                                .. : .: .: : ::::: .:
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 53 Z-score: 87.3 bits: 21.1 E(): 6.9

Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (15-73:9-65)

```

                10         20         30         40         50
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSL
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111      MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQL
                10         20         30         40         50

```

```

                60         70         80
AAD-12 VYSQSKLGHVQQAGSAYIGYGM
                . : : . : . : . : :
gi+AHw-111 LYLQHQLDLLENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEA
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 87.3 bits: 21.1 E(): 6.9
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (15-73:9-65)

```

                10         20         30         40         50
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSL
                : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420      MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQL
                10         20         30         40         50

```

```

                60         70         80
AAD-12 VYSQSKLGHVQQAGSAYIGYGM
                . : : . : . : . : :
gi+AHw-420 LYLQHQLDLLENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEA
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)

initn: 34 initl: 34 opt: 52 Z-score: 87.1 bits: 20.9 E(): 7
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (7-75:11-80)

```

                10         20         30         40         50
AAD-12 WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                . . . . : : : . . . : : : . . . : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10         20         30         40         50

```

```

                60         70         80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGM
                : : . . : : : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 86.9 bits: 20.9 E(): 7.3

```
+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a  (160 aa)
  initn:  52 init1:  52 opt:   53 Z-score: 85.7 bits: 21.1 E():  8.5
```

Smith-Waterman score: 53+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (3-27:27-50)

```

                        10      20      30
AAD-12                WHADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        :: : .: .: .: .: .: .: .: .: .: .:
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
                        10      20      30      40      50
```

```

                        40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
                        60      70      80      90      100     110
```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)

initn: 47 initl: 47 opt: 53 Z-score: 85.7 bits: 21.1 E(): 8.5
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (8-59:31-87)

```

                        10      20      30
AAD-12                WHADSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
                        .: .: .: .: .: .: .: .: .: .:
gi+AHw-132 MGVFN YETETTSVIPPARL FKRFLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
                        10      20      30      40      50
```

```

                        40      50      60      70      80
AAD-12 DMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                        : . . . . . . . . : : : :
gi+AHw-132 DEGSPFN YIKQKV E EIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                        60      70      80      90      100     110
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)

initn: 52 initl: 52 opt: 52 Z-score: 84.6 bits: 20.8 E(): 9.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (38-61:29-52)

```

                        10      20      30      40      50      60
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
                        : : : : : : . . .: .: .:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAEARISAKNALESYAYSLRNTLS
                        10      20      30      40      50
```

```

                        70      80
AAD-12 VQQAGSAYIGYGM

gi+AHw-144 DSKVDEKLDAGDKQKLTA EIDKT VQWLDDNQ TATKDEYESQQKELEGVANPIMMKFYGAG
                        60      70      80      90      100     110
```

80 residues in 1 query sequences

[illegible]

```

54      85
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQ- +ACo-
56      80
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9-
58      69
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
60      55      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      52      40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
64      61
32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
66      43      25: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
68      43      20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9-
70      19      16: +AD0APQA9AD0APQA9AD0-
72      28      12: +AD0APQA9ACoAPQA9AD0APQA9AD0-
74      16      10: +AD0APQA9ACoAPQA9-
76      27      7: +AD0APQA9AD0APQA9AD0APQA9-
78      7      6: +AD0AKgA9-
80      8      4: +AD0AKgA9-
82      5      3: +ACoAPQ-
84      12      3: +ACoAPQA9AD0-
86      6      2: +ACoAPQ-
88      3      2: +ACo-          inset +AD0- represents 1 library sequences
90      2      1: +ACo-
92      2      1: +ACo-          : +ACoAPQ-
94      1      1: +ACo-          : +ACo-
96      0      1: +ACo-          : +ACo-
98      0      0:          +ACo-
100     1      0: +AD0-          +ACoAPQ-
102     0      0:          +ACo-
104     1      0: +AD0-          +ACoAPQ-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.64750.00351+ADs- mu+AD0- 1.6202
0.184
mean+AF8-var+AD0-40.238310.863, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.202188
Kolmogorov-Smirnov statistic: 0.1259 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 24.3 0.74

```

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 23.8 1.2
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 57 22.3 2.7
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.3 3.3
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po (396) 62 23.5 3.8
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 56 22.0 4.6
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 56 22.0 4.6
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 56 21.9 5.9
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl (204) 56 21.9 6
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.1 6.8
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.1 6.8
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.9 7.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.9 7.3
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.5
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 57 22.1 7.7
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 53 21.1 8.4
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.4
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.6

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)

initn: 38 init1: 38 opt: 64 Z-score: 104.7 bits: 24.3 E(): 0.74
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (14-72:9-65)

	10	20	30	40	50
AAD-12	HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLV				
	:	::	::	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLL				
	10	20	30	40	50
	60	70	80		
AAD-12	YSQSKLGHVQQAGSAYIGYGMD				
	:	:	:	
gi+AHw-111	YLQHQLDLLENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQ				
	60	70	80	90	100 110

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 55 initl: 55 opt: 62 Z-score: 100.9 bits: 23.8 E(): 1.2
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (4-52:5-52)

```

                10      20      30      40      50
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
        .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTGCVTIAG
                10      20      30      40      50

```

```

        60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMD

```

```

gi+AHw-189 SPVSSEPGDTPKDRCCQELDEAPQHCRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFA
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 57 initl: 57 opt: 57 Z-score: 94.6 bits: 22.3 E(): 2.7
 Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (30-74:26-70)

```

                10      20      30      40      50      60
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYS
                        :::      .. . . : .... ....
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQNSTKHSVPDVLFAFA
                10      20      30      40      50

```

```

                70      80
AAD-12  QSKLGHVQQAGSAYIGYGMD
        . . ::::: . :
gi+AHw-527 KVNVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAEKLGGLAQK
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 93.0 bits: 22.3 E(): 3.3
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (4-52:5-52)

```

                10      20      30      40      50
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
        .. ... .. .. .. .. .. .. .. .. .. .. .. .. .. ..
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTGCVTIAG
                10      20      30      40      50

```

```

        60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMD

```

```

gi+AHw-439 SPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDF
        60      70      80      90      100      110

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:

Full+AD0-Pollen (396 aa)

initn: 45 init1: 45 opt: 62 Z-score: 91.9 bits: 23.5 E(): 3.8

Smith-Waterman score: 62+ADs- 23.214+ACU- identity (53.571+ACU- similar)

in 56 aa overlap (25-80:309-358)

```

                10      20      30      40      50
AAD-12      HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                : : : : : : : : : : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
            280      290      300      310      320      330

```

```

                60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMD
                : : : : : : : : : :
gi+AHw-113 ESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
            340      350      360      370      380      390

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen Pru a (160 aa)

initn: 55 init1: 55 opt: 56 Z-score: 90.5 bits: 22.0 E(): 4.6

Smith-Waterman score: 56+ADs- 48.000+ACU- identity (68.000+ACU- similar)

in 25 aa overlap (2-26:27-50)

```

                10      20      30
AAD-12      HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : : : : : : : : :
gi+AHw-444 MGVTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDGGVGTIKKISF
            10      20      30      40      50

```

```

                40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
            60      70      80      90      100      110

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)

initn: 55 init1: 55 opt: 56 Z-score: 90.5 bits: 22.0 E(): 4.6

Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)

in 25 aa overlap (2-26:27-50)

```

                10      20      30
AAD-12      HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                : : : : : : : : : :
gi+AHw-165 MGVTTHENEITSAIPPGRLFKAFVLDADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
            10      20      30      40      50

```

```

                40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD
gi+AHw-165 GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
            60      70      80      90      100      110

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 40 initl: 40 opt: 56 Z-score: 88.6 bits: 21.9 E(): 5.9
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (31-78:93-144)

```

      10      20      30      40      50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
      . . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
      70      80      90     100     110     120
```

```

      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGM
      . . : . . . : . . . . . :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
      130     140     150     160     170     180
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 40 initl: 40 opt: 56 Z-score: 88.4 bits: 21.9 E(): 6
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (31-78:97-148)

```

      10      20      30      40      50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
      . . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
      70      80      90     100     110     120
```

```

      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGM
      . . : . . . : . . . . . :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
      130     140     150     160     170     180
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 87.4 bits: 21.1 E(): 6.8
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (14-72:9-65)

```

      10      20      30      40      50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLV
      : : : : : . : : : . . . . .
gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLL
      10      20      30      40      50
```

```

      60      70      80
AAD-12 YSQSKLGHVQQAGSAYIGYGM
      : : . . . :
gi+AHw-111 YLQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQ
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein B1 (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 87.4 bits: 21.1 E(): 6.8
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (14-72:9-65)

```

      10      20      30      40      50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLL
      10      20      30      40      50

```

```

      60      70      80
AAD-12 YSQSKLGHVQQAGSAYIGYGM
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420 YLQHQDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQ
      60      70      80      90     100     110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 52 Z-score: 87.1 bits: 20.9 E(): 7.1
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (6-74:11-80)

```

      10      20      30      40      50
AAD-12 HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
      10      20      30      40      50

```

```

      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGM
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
      60      70      80      90     100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 86.9 bits: 20.9 E(): 7.3
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (32-72:11-50)

```

      10      20      30      40      50
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
      10      20      30

```

```

      60      70      80
AAD-12 SQSKLGHVQQAGSAYIGYGM
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160 LQHQDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
      40      50      60      70      80      90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 86.7 bits: 21.1 E(): 7.5
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (4-52:5-52)

```

      10      20      30      40      50
AAD-12  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
      .. ... .. .. : ... : . : . : : ...
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTGCGISISG
      10      20      30      40      50
```

```

      60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMD
```

```

gi+AHw-217 SAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDF
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
Lolium per (301 aa)
initn: 48 initl: 48 opt: 57 Z-score: 86.5 bits: 22.1 E(): 7.7
Smith-Waterman score: 57+ADs- 27.660+ACU- identity (55.319+ACU- similar)
in 47 aa overlap (2-48:26-71)

```

                        10      20      30
AAD-12                  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        .. : .. : . : ..... : .
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
      10      20      30      40      50
```

```

      40      50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD
      . . . . :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 52 initl: 52 opt: 53 Z-score: 85.8 bits: 21.1 E(): 8.4
Smith-Waterman score: 53+ADs- 44.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (2-26:27-50)

```

                        10      20      30
AAD-12                  HADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                        :: : .. : . : ..... : ::
gi+AHw-444 MGVTYSDESTSVIPPPRLFKALVLEAD-TLIPKIAPQSVKTAEIVEGDGGVGTIKKISF
      10      20      30      40      50
```

```

      40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMD

gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTS
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 85.8 bits: 21.1 E(): 8.4
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (7-58:31-87)

```

                                10      20      30
AAD-12                      HADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
                                .: .: .: .: .: .: .: .:
gi+AHw-132  MGVFN YETETTSVIPPARLFKRFLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
                   10      20      30      40      50

                   40      50      60      70      80
AAD-12  DMRAAYDALDEATRALVHQ-R-SARHSLVYSQSKLGHVQQAGSAYIGYGMD
                   : . . . . . : : : :
gi+AHw-132  DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                   60      70      80      90     100     110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 84.7 bits: 20.8 E(): 9.6
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (37-60:29-52)

```

                   10      20      30      40      50      60
AAD-12  MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQ-R-SARHSLVYSQSKLGH
                                : : : : : : . . . : : :
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
                   10      20      30      40      50

                   70      80
AAD-12  VQQAGSAYIGYGMD

gi+AHw-144  DSKVDEKLDAGDKQKLTA EIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
                   60      70      80      90     100     110

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:01 2010 done: Fri Feb 5 12:56:01 2010
 Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

opt      E()
+ADw- 20      2      0: +AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      0      0:
30      2      2: +ACo-
32      4      8: +AD0APQAq-
34      7      21: +AD0APQA9- +ACo-
36      31     44: +AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
38      37     72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
40      67
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
42      87
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-
44      107
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ- +AD0APQA9AD0- +ACo-
46      126
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
48      128
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
50      140
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
52      120
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
54      75
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      72
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
58      69
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      51     50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62      60     40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      63     32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
+AD0APQA9AD0APQA9AD0-
66      43     25: +AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
68      43     20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
70      26     16: +AD0APQA9AD0APQAqAD0APQA9-
72      22     12: +AD0APQA9ACoAPQA9AD0APQ-
74      14     10: +AD0APQA9ACoAPQ-

```

```

76      27      7:+AD0APQAqAD0APQA9AD0APQA9-
78      8      6:+AD0AKgA9-
80      8      4:+AD0AKgA9-
82      5      3:+ACoAPQ-
84      12     3:+ACoAPQA9AD0-
86      6      2:+ACoAPQ-
88      2      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      1      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120  0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.56990.00353+ADs- mu+AD0- 2.0442
0.185
mean+AF8-var+AD0-40.979410.974, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.200351
Kolmogorov-Smirnov statistic: 0.1232 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  64 24.2      0.79
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  62 23.7      1.3
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.5      2.4
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram ( 145)
57 22.2      3.5
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  62 23.5      4
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P ( 160)
56 21.9      4.8
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  56 21.9      4.8
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
56 21.9      6.2
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  56 21.9      6.3

```


gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.1 7.2
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.1 7.2
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.8 7.5
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.8 7.7
 gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.9
 gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-Lolium (301) 57 22.1 8
 gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen P (160) 53 21.0 8.8
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.0 8.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)

initn: 38 initl: 38 opt: 64 Z-score: 104.2 bits: 24.2 E(): 0.79
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (13-71:9-65)

	10	20	30	40	50
AAD-12	ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY				
	:	::	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLY				
	10	20	30	40	50

	60	70	80
AAD-12	SQSKLGHVQQAGSAYIGYGMT		
	:	::	:
gi+AHw-111	LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT		
	60	70	80

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)

initn: 55 initl: 55 opt: 62 Z-score: 100.4 bits: 23.7 E(): 1.3
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (3-51:5-52)

	10	20	30	40	50
AAD-12	ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY				
	::	::	::	::	::
gi+AHw-189	MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG				
	10	20	30	40	50

	60	70	80
AAD-12	SQSKLGHVQQAGSAYIGYGMT		
	:	::	:
gi+AHw-189	SPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFA		
	60	70	80

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:

Full+AD0-Thior (121 aa)

initn: 58 initl: 58 opt: 58 Z-score: 95.7 bits: 22.5 E(): 2.4
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (29-80:26-77)

```

                10         20         30         40         50         60
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQ
                :::         :. . . : .....
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPCKAIAPVYEQSLSTKHSVPDVLAFK
                10         20         30         40         50

```

```

                70         80
AAD-12 SKLGHVQQAGSAYIGYGMT
        .. ::::... :   .: :
gi+AHw-527 VNVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGKLGGLAQKR
        60         70         80         90        100        110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetrameric (145 aa)

initn: 50 initl: 50 opt: 57 Z-score: 92.5 bits: 22.2 E(): 3.5
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (3-51:5-52)

```

                10         20         30         40         50
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                :. :.. ... :. . . :. :: : . : : : : : :
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG
                10         20         30         40         50

```

```

        60         70         80
AAD-12 SQSKLGHVQQAGSAYIGYGMT
gi+AHw-439 SPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDF
        60         70         80         90        100        110

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:

Full+AD0-Pollen (396 aa)

initn: 45 initl: 45 opt: 62 Z-score: 91.6 bits: 23.5 E(): 4
 Smith-Waterman score: 62+ADs- 23.214+ACU- identity (53.571+ACU- similar)
 in 56 aa overlap (24-79:309-358)

```

                10         20         30         40         50
AAD-12 ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                :: : : : :. :. : : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
        280        290        300        310        320        330

```

```

        60         70         80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMT
        :. . . : . :. :. :. :
gi+AHw-113 ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
        340        350        360        370        380        390

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
Smith-Waterman score: 56+ADs- 48.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (1-25:27-50)

```

                                10      20      30
AAD-12      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              :: : .: .: .: ::::: . ::
gi+AHw-444  MGVFTYADESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKSAEIVEGDDGGVGTIKKISF
              10      20      30      40      50
```

```

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
gi+AHw-444  GEGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTS
              60      70      80      90      100     110
```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 initl: 55 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
Smith-Waterman score: 56+ADs- 40.000+ACU- identity (68.000+ACU- similar)
in 25 aa overlap (1-25:27-50)

```

                                10      20      30
AAD-12      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
              ::. .: .: .: ::::. . ::
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLADNL-IPKLAPHAIKSAEIIIEGNGGPGTIKKITF
              10      20      30      40      50
```

```

              40      50      60      70      80
AAD-12  AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
gi+AHw-165  GEGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTS
              60      70      80      90      100     110
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 40 initl: 40 opt: 56 Z-score: 88.2 bits: 21.9 E(): 6.2
Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
in 53 aa overlap (30-77:93-144)

```

              10      20      30      40      50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              ..... ::: ::. . . .
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
              70      80      90      100     110     120
```

```

              60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMT
              .. : .:. .: ..... :
gi+AHw-144  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130     140     150     160     170     180
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:

Full+AD0-Glutat (204 aa)

initn: 40 initl: 40 opt: 56 Z-score: 88.0 bits: 21.9 E(): 6.3

Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)

in 53 aa overlap (30-77:97-148)

```

      10      20      30      40      50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              .....      ::  ..  .  ..
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
      70      80      90      100      110      120

```

```

      60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMT
      .. :  ... .. :  ..... :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
      130     140     150     160     170     180

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 87.0 bits: 21.1 E(): 7.2

Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)

in 61 aa overlap (13-71:9-65)

```

      10      20      30      40      50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
              :  ::  .. :  .  :  ::  .. :  ..... :  ..... :
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
              10      20      30      40      50

```

```

      60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMT
      :  ::  .... :
gi+AHw-111 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 87.0 bits: 21.1 E(): 7.2

Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)

in 61 aa overlap (13-71:9-65)

```

      10      20      30      40      50
AAD-12  ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
              :  ::  .. :  .  :  ::  .. :  ..... :  ..... :
gi+AHw-420  MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLY
              10      20      30      40      50

```

```

      60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMT
      :  ::  .... :
gi+AHw-420 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 52 Z-score: 86.7 bits: 20.8 E(): 7.5
 Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
 in 71 aa overlap (5-73:11-80)

```

                10         20         30         40         50
AAD-12      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                . . . . . : : : : : . . . . . : : : : : . . . . .
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                10         20         30         40         50

```

```

                60         70         80
AAD-12      HSLVYSQSKLGHVQQ-AGSAYIGYGMDT
                : : . . . : : . . : : . :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNIEAVVWDKPWMHFRNLTSFRKV
                60         70         80         90        100        110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 86.5 bits: 20.8 E(): 7.7
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (31-71:11-50)

```

                10         20         30         40         50
AAD-12      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVY
                : : . . : : : : : : : : : : : : : : : : : : : :
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLY
                10         20         30

```

```

                60         70         80
AAD-12      SQSKLGHVQQAGSAYIGYGMDT
                : : . . . : : . . : : . :
gi+AHw-160 LQHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNIEEAQT
                40         50         60         70         80         90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)
 initn: 46 initl: 46 opt: 53 Z-score: 86.3 bits: 21.1 E(): 7.9
 Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
 in 49 aa overlap (3-51:5-52)

```

                10         20         30         40         50
AAD-12      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                : . . . . . : : : : : . : : : : : : : : :
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTCGISISG
                10         20         30         40         50

```

```

                60         70         80
AAD-12      SQSKLGHVQQAGSAYIGYGMDT
                : : . . . : : . . : : . :
gi+AHw-217 SAVSTEPGNTPRDRCKKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDF
                60         70         80         90        100        110

```

+AD4APg-gi+AHw-6634467+AHw-emb+AHw-CAB64344.1+AHw- pollen allergen +AFs-
 Lolium per (301 aa)
 initn: 48 initl: 48 opt: 57 Z-score: 86.2 bits: 22.1 E(): 8
 Smith-Waterman score: 57+ADs- 27.660+ACU- identity (55.319+ACU- similar)
 in 47 aa overlap (1-47:26-71)

```

                                10      20      30
AAD-12                      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                                :: : : : . : ..... : :
gi+AHw-663 MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPA-ATPAAGGGKATTDEQKL
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
                                . . . . :
gi+AHw-663 LEDVNAGFKAAVAADANAPPADKFKIFEAAFSECKGLLATSDAKAPGLILKLDTDYDVA
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-44409451+AHw-gb+AHw-AAS47035.1+AHw- major cherry allergen
 Pru a (160 aa)
 initn: 52 initl: 52 opt: 53 Z-score: 85.4 bits: 21.0 E(): 8.8
 Smith-Waterman score: 53+ADs- 44.000+ACU- identity (68.000+ACU- similar)
 in 25 aa overlap (1-25:27-50)

```

                                10      20      30
AAD-12                      ADSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRA
                                :: : : : . : ..... : :
gi+AHw-444 MGVFTYSDESTSVIPPPRLFKALVLEAD-TLIPKIA PQSVKTAEIVEGDGGVGTIKKISF
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 AYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMT
gi+AHw-444 GEGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIIKSTS
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 53 Z-score: 85.4 bits: 21.0 E(): 8.8
 Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
 in 58 aa overlap (6-57:31-87)

```

                                10      20      30
AAD-12                      ADSTYMPVMAQGAVFSAEVVPAVGG----RTCFA
                                . : : : : . : ..... : :
gi+AHw-132 MGVFN YETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
                                10      20      30      40      50

```

```

                                40      50      60      70      80
AAD-12 DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYGMT
                                : . . . . : : : :
gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
                                60      70      80      90      100      110

```

[illegible]

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
  join: 42, opt: 30, open/ext: -10/-2, width: 32
  Scan time: 0.090
```


opt bits E(1471)

gi	Accession	Species	Protein	Length	Score	E-value	Ident	Positives	Negatives
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw-	Blo t 5 allergen	+AFs-Blom	(134)	64	24.3	0.76			
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw-	alpha-amylase inhibitor	+AFs-	(144)	62	23.7	1.2			
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU	RecName: Full+AD0-T	(121)	58	22.6	2.3				
gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw-	CMA, component of tetram	(145)	57	22.3	3.4				
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR	RecName: Full+AD0-Po	(396)	62	23.5	3.8				
gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw-	major cherry allergen P	(160)	55	21.7	5.7				
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw-	ypr10 +AFs-Castanea sativa	(160)	55	21.7	5.7				
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw-	Bla g 5 variant allerg	(200)	56	21.9	6				
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE	RecName: Full+AD0-Gl	(204)	56	21.9	6.1				
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw-	Blo t 5 allergen +AFs-Blom	(134)	53	21.1	7				
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw-	major IgE-binding protei	(134)	53	21.1	7				
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw-	phytocystatin +AFs-Actinidi	(116)	52	20.8	7.3				
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru	(119)	52	20.8	7.5					
gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw-	unnamed protein product +AFs-	(145)	53	21.1	7.6				
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw-	major allergen Cor a 1	(160)	53	21.1	8.5				
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL	RecName: Full+AD0-	(152)	52	20.8	9.8				

```

      initn: 38 initl: 38 opt: 64 Z-score: 104.5 bits: 24.3 E(): 0.76
Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (12-70:9-65)

```

```

      10      20      30      40      50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYS
      :  ::  ::  :  :  .      ::  ::  :  .....  .....::
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYL
      10      20      30      40      50

      60      70      80
AAD-12  QSKLGHVQQAGSAYIGYGMDTT
      :  .:  ....  :
gi+AHw-111  QHQDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)

initn: 55 initl: 55 opt: 62 Z-score: 100.7 bits: 23.7 E(): 1.2
 Smith-Waterman score: 62+ADs- 26.531+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (2-50:5-52)

```

          10          20          30          40          50
AAD-12   DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
          ..   ...   ...   ..   ..   ..   ..   ..   ..   ..   ..   ..
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTTCGVTIAG
          10          20          30          40          50

```

```

          60          70          80
AAD-12   SQSKLGHVQQAGSAYIGYGMDTT

```

```

gi+AHw-189 SPVSSEPGDTPKDRCCQELDEAPQHCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFA
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)

initn: 58 initl: 58 opt: 58 Z-score: 95.9 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (28-79:26-77)

```

          10          20          30          40          50          60
AAD-12   DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQS
          ::          ..   ..   :   ....   .....
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAIPVYQLSTKHSVPDVLAFAKV
          10          20          30          40          50

```

```

          70          80
AAD-12   KLGHVQQAGSAYIGYGMDTT

```

```

          .. ::::... :   .. :
gi+AHw-527 NVDHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRV
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of
 tetrameric (145 aa)

initn: 50 initl: 50 opt: 57 Z-score: 92.8 bits: 22.3 E(): 3.4
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (59.184+ACU- similar)
 in 49 aa overlap (2-50:5-52)

```

          10          20          30          40          50
AAD-12   DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
          ..   ...   ...   ..   ..   ..   ..   ..   ..   ..   ..   ..
gi+AHw-439 MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPL-EGCREYVAQQTTCGVTIAG
          10          20          30          40          50

```

```

          60          70          80
AAD-12   SQSKLGHVQQAGSAYIGYGMDTT

```

```

gi+AHw-439 SPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDF
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)

initn: 45 initl: 45 opt: 62 Z-score: 92.0 bits: 23.5 E(): 3.8
 Smith-Waterman score: 62+ADs- 23.214+ACU- identity (53.571+ACU- similar)
 in 56 aa overlap (23-78:309-358)

```

                10      20      30      40      50
AAD-12          DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                        :.:. : :.:. :.:. :.:. :.:.
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
                280      290      300      310      320      330

```

```

                60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDT
                :.:. :.:. :.:. :.:. :.:.
gi+AHw-113 ESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
                340      350      360      370      380      390

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
 Pru a (160 aa)

initn: 55 initl: 55 opt: 55 Z-score: 88.8 bits: 21.7 E(): 5.7
 Smith-Waterman score: 55+ADs- 45.455+ACU- identity (68.182+ACU- similar)
 in 22 aa overlap (3-24:29-50)

```

                10      20      30
AAD-12          DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        :.:. :.:. :.:. :.:. :.:.
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEADTLIPKIA PQSVKSAEIVEGDGGVGTIKKISFG
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
gi+AHw-444 EGSYHSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTSN
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)

initn: 55 initl: 55 opt: 55 Z-score: 88.8 bits: 21.7 E(): 5.7
 Smith-Waterman score: 55+ADs- 40.000+ACU- identity (70.000+ACU- similar)
 in 20 aa overlap (5-24:31-50)

```

                10      20      30
AAD-12          DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        :.:. :.:. :.:. :.:. :.:.
gi+AHw-165 MGVFTHENEITS AIPPGRLFKAFVLDADNLIPKLAPHAIKSAEIIIEGNGGPGTIKKITFG
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
gi+AHw-165 EGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTSK
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)

initn: 40 initl: 40 opt: 56 Z-score: 88.4 bits: 21.9 E(): 6
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (29-76:93-144)

```

      10      20      30      40      50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              .....      :: :: ..      .  ..
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
              70      80      90      100      110      120

      60      70      80
AAD-12  SLVYSQSKLGHVQAGSAYIGYGMDDT
      .. :  ... :  ..... :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 88.3 bits: 21.9 E(): 6.1
 Smith-Waterman score: 56+ADs- 28.302+ACU- identity (62.264+ACU- similar)
 in 53 aa overlap (29-76:97-148)

```

      10      20      30      40      50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              .....      :: :: ..      .  ..
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
              70      80      90      100      110      120

      60      70      80
AAD-12  SLVYSQSKLGHVQAGSAYIGYGMDDT
      .. :  ... :  ..... :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130      140      150      160      170      180

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.2 bits: 21.1 E(): 7
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (12-70:9-65)

```

      10      20      30      40      50
AAD-12  DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYS
              : :: : . :  :: : :  .....  .....
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYL
              10      20      30      40      50

      60      70      80
AAD-12  QSKLGHVQAGSAYIGYGMDDT
      : :: .... :
gi+AHw-111 QHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein B1 (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 87.2 bits: 21.1 E(): 7
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (12-70:9-65)

```

      10      20      30      40      50
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYL
      10      20      30      40      50

      60      70      80
AAD-12 QSKLGHVQQAGSAYIGYGMDDT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-420 QHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
      60      70      80      90     100     110

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 52 Z-score: 86.9 bits: 20.8 E(): 7.3
 Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
 in 71 aa overlap (4-72:11-80)

```

      10      20      30      40      50
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
      . . . . : : : : . : : : . . . : : : : : : : : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
      10      20      30      40      50

      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDDT
      : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
      60      70      80      90     100     110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 86.7 bits: 20.8 E(): 7.5
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (30-70:11-50)

```

      10      20      30      40      50
AAD-12 DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYL
      10      20      30

      60      70      80
AAD-12 QSKLGHVQQAGSAYIGYGMDDT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-160 QHQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQT
      40      50      60      70      80      90

```

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
 +AFs-Trit (145 aa)

initn: 46 initl: 46 opt: 53 Z-score: 86.5 bits: 21.1 E(): 7.6
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (2-50:5-52)

```
          10          20          30          40          50
AAD-12    DSTYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
          ..   ...   ..   .   .   .   .   .   .   .   .   .   .   .   .   .
gi+AHw-217 MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTTCGISISG
          10          20          30          40          50
```

```
          60          70          80
AAD-12    SQSKLGHVQQAGSAYIGYGMDTT

gi+AHw-217 SAVSTEPGNTPRDRCKKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDF
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)

initn: 47 initl: 47 opt: 53 Z-score: 85.7 bits: 21.1 E(): 8.5
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (5-56:31-87)

```
          10          20
AAD-12                                DSTYMPVMAQGAVFSAEVVPAVGG-----RTCFA
          .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-132 MGVFNJETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-
          10          20          30          40          50
```

```
          30          40          50          60          70          80
AAD-12    DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYGMDTT
          :   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
gi+AHw-132 DEGSPFNLIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 84.5 bits: 20.8 E(): 9.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (35-58:29-52)

```
          10          20          30          40          50          60
AAD-12    MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
          :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAEARISAKNALESYAYSLRNTLS
          10          20          30          40          50
```

```
          70          80
AAD-12    VQQAGSAYIGYGMDTT

gi+AHw-144 DSKVDEKLDAGDKQKLTAIEDKTQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAG
          60          70          80          90          100          110
```

```
80 residues in 1 query sequences
331323 residues in 1471 library sequences
```

Scomplib +AFs-34t26+AF0-

```
start: Fri Feb 5 12:56:02 2010 done: Fri Feb 5 12:56:03 2010
```

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
```

```
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
```

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

```
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

1+AD4APcA+-AAD-12: 112 - 191 80 aa - 80 aa

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 62 23.7 1.2

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 58 22.6 2.3

gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetram (145) 57 22.3 3.4

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po (396) 62 23.5 3.8

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 57 22.2 4.9

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl (204) 57 22.2 5

gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 55 21.7 5.7

gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 55 21.7 5.7

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.1 6.9

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.1 6.9

gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281) 57 22.1 7.1

gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.9 7.2

gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P (284) 57 22.1 7.2

gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287) 57 22.1 7.3

gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290) 57 22.1 7.4

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.8 7.4

gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295) 57 22.1 7.5

gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product +AFs- (145) 53 21.1 7.6

gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.5

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.8

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)

initn: 38 initl: 38 opt: 64 Z-score: 104.5 bits: 24.3 E(): 0.76

Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)

in 61 aa overlap (11-69:9-65)

	10	20	30	40	50
AAD-12	STYMPVMAQGAVFSAEVPFVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQ				
	:	::	::	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLYLQ				
	10	20	30	40	50
	60	70	80		

60 70 80

60 70 80

```

      10      20      30      40      50
AAD-12 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQ
      :  ::  :  :      .      ::  ::  :  .....  .....:  :
gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQ
      10      20      30      40      50

      60      70      80

```

AAD-12 SKLGHVQQAGSAYIGYMDTTA

```

      .: .... :
gi+AHw-111 HQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLS
           60          70          80          90         100         110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 87.3 bits: 21.1 E(): 6.9
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (11-69:9-65)

```

           10          20          30          40          50
AAD-12 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQ
           : :. :. : . :. : :. : :. :. :. :. :. :. :. :. :. :. :
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLYLQ
           10          20          30          40          50

```

```

           60          70          80
AAD-12 SKLGHVQQAGSAYIGYMDTTA
           .: .... :
gi+AHw-420 HQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLS
           60          70          80          90         100         110

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 +AFs-Phl (281 aa)

initn: 34 initl: 34 opt: 57 Z-score: 87.0 bits: 22.1 E(): 7.1
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (11-80:183-264)

```

           10          20          30
AAD-12 STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
           :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :
gi+AHw-168 QIIDKIDAFAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
           160         170         180         190         200         210

```

```

           40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYMDTTA
           :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
           220         230         240         250         260         270

```

gi+AHw-168 TVAAGGYKV
 280

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidia de (116 aa)

initn: 34 initl: 34 opt: 52 Z-score: 87.0 bits: 20.9 E(): 7.2
 Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
 in 71 aa overlap (3-71:11-80)

```

           10          20          30          40          50
AAD-12 STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
           . . . :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN

```

```

                10          20          30          40          50
                60          70          80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTA
          : ... :... :... :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 initl: 34 opt: 57 Z-score: 86.9 bits: 22.1 E(): 7.2
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (11-80:186-267)

```

                10          20          30
AAD-12          STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
          :... . ...: .. ...:
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160          170          180          190          200          210

```

```

                40          50          60          70          80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTA
          :: : . : ..: . . .... :... :... : .. : ...
gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220          230          240          250          260          270

```

gi+AHw-285 TVAAGGYKV
280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)
initn: 34 initl: 34 opt: 57 Z-score: 86.9 bits: 22.1 E(): 7.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (11-80:189-270)

```

                10          20          30
AAD-12          STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
          :... . ...: .. ...:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160          170          180          190          200          210

```

```

                40          50          60          70          80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTA
          :: : . : ..: . . .... :... :... : .. : ...
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220          230          240          250          260          270

```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)
initn: 34 initl: 34 opt: 57 Z-score: 86.8 bits: 22.1 E(): 7.4

Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (11-80:192-273)

```

                                10      20      30
AAD-12      STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :...  .  ....  :. ....:
gi+AHw-330  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                   170      180      190      200      210      220

                   40      50      60      70      80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTA
                   :: : . :      ..: . . .... :... :. : :::
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                   230      240      250      260      270      280

gi+AHw-330  TVAAGGYKV
                   290
```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 86.7 bits: 20.8 E(): 7.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (29-69:11-50)

```

                   10      20      30      40      50
AAD-12  STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRVLHQRSARHSLVYSQ
                   :.. :. :  .....  .....::
gi+AHw-160      GSQEHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLYLQ
                   10      20      30

                   60      70      80
AAD-12  SKLGHVQQAGSAYIGYGMDTTA
                   :: .... :
gi+AHw-160  HQLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLS
                   40      50      60      70      80      90
```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.6 bits: 22.1 E(): 7.5
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (11-80:197-278)

```

                                10      20      30
AAD-12      STYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :...  .  ....  :. ....:
gi+AHw-330  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                   170      180      190      200      210      220

                   40      50      60      70      80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTA
                   :: : . :      ..: . . .... :... :. : :::
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                   230      240      250      260      270      280
```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-21701+AHw-emb+AHw-CAA35598.1+AHw- unnamed protein product
+AFs-Trit (145 aa)
initn: 46 initl: 46 opt: 53 Z-score: 86.6 bits: 21.1 E(): 7.6
Smith-Waterman score: 53+ADs- 24.490+ACU- identity (55.102+ACU- similar)
in 49 aa overlap (1-49:5-52)

	10	20	30	40	50
AAD-12	STYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY				
	:: : :: : . : : : ::				
gi+AHw-217	MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPL-EGCREYVAQQTGCGISISG				
	10	20	30	40	50

	60	70	80
AAD-12	SQSKLGHVQQAGSAYIGYGMDDTA		

gi+AHw-217	SAVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDF					
	60	70	80	90	100	110

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)
initn: 47 initl: 47 opt: 53 Z-score: 85.7 bits: 21.1 E(): 8.5
Smith-Waterman score: 53+ADs- 22.414+ACU- identity (55.172+ACU- similar)
in 58 aa overlap (4-55:31-87)

		10	20		
AAD-12		STYMPVMAQGAVFSAEVVPAVGG----	RTCF	A	
		:: :: : : : : : : : : ::			
gi+AHw-132	MGVFNYETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-				
	10	20	30	40	50

	30	40	50	60	70	80
AAD-12	DMRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA					
	:	:	:	:	:	:
gi+AHw-132	DEGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS					
	60	70	80	90	100	110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 84.6 bits: 20.8 E(): 9.8
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (34-57:29-52)

	10	20	30	40	50	60
AAD-12	MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH					
	:	:	:	:	:	:
gi+AHw-144	KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAEARISAKNALESYAYSLRNTLS					
	10	20	30	40	50	

	70	80
AAD-12	VQQAGSAYIGYGMDDTA	


```
gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAG
          60          70          80          90         100         110
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:03 2010 done: Fri Feb 5 12:56:03 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 113 - 192 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      2      2:+ACo-
      32      4      8:+AD0APQAq-
      34      7     21:+AD0APQA9-   +ACo-
      36     33     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
      38     35     72:+AD0APQA9AD0APQA9AD0APQA9-+AD0APQA9-   +ACo-
      40     65
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      42     92
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0-   +ACo-
      44    107
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9-   +ACo-
      46    123
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
      48    129
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
```

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
  join: 42, opt: 30, open/ext: -10/-2, width: 32
```

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 64 24.4 0.73
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T (121) 58 22.6 2.2
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po (396) 64 24.2 2.5
 gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281) 62 23.7 2.5
 gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290) 62 23.6 2.6
 gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 57 22.3 3.3
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 57 22.3 4.7
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl (204) 57 22.3 4.8
 gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen P (160) 55 21.7 5.5
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 55 21.7 5.5
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.2 6.7
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 21.2 6.7
 gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P (284) 57 22.2 7
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.9 7
 gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287) 57 22.2 7.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.9 7.2
 gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295) 57 22.2 7.3
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 53 21.1 8.2
 gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMA, component of tetram (145) 52 20.9 9
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 20.8 9.5

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)

initn: 38 initl: 38 opt: 64 Z-score: 104.8 bits: 24.4 E(): 0.73
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (10-68:9-65)

	10	20	30	40	50
AAD-12	TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQS				
	:	::	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQH				
	10	20	30	40	50

```

        60          70          80
AAD-12  KLGHVQQAGSAYIGYGMDDTTAT
        .: . . . . :
gi+AHw-111 QLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSK
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 96.3 bits: 22.6 E(): 2.2
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (26-77:26-77)

```

        10          20          30          40          50          60
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
        .: . . . . : . . . . : . . . . : . . . . :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYQLSTKHSVPDVLAFKVN
        10          20          30          40          50          60

```

```

        70          80
AAD-12  GHVQQAGSAYIGYGMDDTTAT
        .: . . . . : . . . . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGIAQKRVAG
        70          80          90          100          110          120

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 47 initl: 47 opt: 64 Z-score: 95.4 bits: 24.2 E(): 2.5
Smith-Waterman score: 64+ADs- 23.333+ACU- identity (53.333+ACU- similar)
in 60 aa overlap (21-80:309-362)

```

        10          20          30          40          50
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
        .: . . . . : . . . . : . . . . : . . . . :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
        280          290          300          310          320          330

```

```

        60          70          80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT
        .: . . . . : . . . . : . . . . : . . . . :
gi+AHw-113 ESMKWNWRTNKNVDLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
        340          350          360          370          380          390

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)
initn: 39 initl: 39 opt: 62 Z-score: 95.2 bits: 23.7 E(): 2.5
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (10-80:183-265)

```

        10          20          30
AAD-12  TYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
        .: . . . . : . . . . : . . . . :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
        160          170          180          190          200          210

```

```

      40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYMDTTAT
      :: : . :      .:: . . . . . .:: .::: . . : ::::
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
      220          230          240          250          260          270

```

```

gi+AHw-168 TVAAGGYKV
      280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5.020 (290 aa)

initn: 39 initl: 39 opt: 62 Z-score: 94.9 bits: 23.6 E(): 2.6
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (10-80:192-274)

```

                        10          20          30
AAD-12                  TYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                        :... . .::: . . .:::
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
      170          180          190          200          210          220

```

```

      40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYMDTTAT
      :: : . :      .:: . . . . . .:: .::: . . : ::::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
      230          240          250          260          270          280

```

```

gi+AHw-330 TVAAGGYKV
      290

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs-Hord (144 aa)

initn: 50 initl: 50 opt: 57 Z-score: 93.2 bits: 22.3 E(): 3.3
 Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (4-48:9-52)

```

                        10          20          30          40          50
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
                        :.. ... :. . . :. :.::: . . : : : : : : : : : :
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG
      10          20          30          40          50

```

```

      60          70          80
AAD-12 SQSKLGHVQQAGSAYIGYMDTTAT

```

```

gi+AHw-189 SPVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFA
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)

initn: 41 initl: 41 opt: 57 Z-score: 90.3 bits: 22.3 E(): 4.7
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (27-79:93-149)

```

                10         20         30         40         50
AAD-12      TYPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                .....      ::: :: ..      .      ..
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

```

```

                60         70         80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTAT
                .. :   ... .. : ..... :   :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 90.1 bits: 22.3 E(): 4.8
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (27-79:97-153)

```

                10         20         30         40         50
AAD-12      TYPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                .....      ::: :: ..      .      ..
gi+AHw-622  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100        110        120

```

```

                60         70         80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTAT
                .. :   ... .. : ..... :   :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-44409474+AHw-gb+AHw-AAS47036.1+AHw- major cherry allergen
Pru a (160 aa)
initn: 55 init1: 55 opt: 55 Z-score: 89.1 bits: 21.7 E(): 5.5
Smith-Waterman score: 55+ADs- 45.455+ACU- identity (68.182+ACU- similar)
in 22 aa overlap (1-22:29-50)

```

                                10         20         30
AAD-12                                TYPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                                : .. :   .. : ..... :   :
gi+AHw-444 MGVFTYADESTSVIPPPRLFKALVLEADTLIPKIA PQSVKSAEIVEGDGGVGTIKKISFG
                                10         20         30         40         50         60

```

```

                40         50         60         70         80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT
                .....
gi+AHw-444 EGSYHSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIIKSTSN
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
sativa+AF0- (160 aa)
initn: 55 init1: 55 opt: 55 Z-score: 89.1 bits: 21.7 E(): 5.5
Smith-Waterman score: 55+ADs- 40.000+ACU- identity (70.000+ACU- similar)
in 20 aa overlap (3-22:31-50)

```

                                10      20      30
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                                .: .: .: :... . :
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLDADNLI PKLAPHAIKSAEIIIEGNGGPGTIKKITFG
                                10      20      30      40      50      60

```

```

                                40      50      60      70      80
AAD-12  YDALDEATR LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTAT

gi+AHw-165  EGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTSK
                                70      80      90      100     110     120

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.5 bits: 21.2 E(): 6.7
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (10-68:9-65)

```

                                10      20      30      40      50
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR LVHQRSARHSLVYSQS
                                : :... : . :... : : :... : :... : :
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQH
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12  KLGHVQQAGSAYIGYGMDDTTAT
                                .: .... :
gi+AHw-111  QLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTL SK
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein Bl (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.5 bits: 21.2 E(): 6.7
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (10-68:9-65)

```

                                10      20      30      40      50
AAD-12  TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATR LVHQRSARHSLVYSQS
                                : :... : . :... : : :... : :... : :
gi+AHw-420  MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQH
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12  KLGHVQQAGSAYIGYGMDDTTAT
                                .: .... :
gi+AHw-420  QLDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTL SK
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
 Full+AD0-Polle (284 aa)
 initn: 34 initl: 34 opt: 57 Z-score: 87.2 bits: 22.2 E(): 7
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (10-79:186-267)

```

                                10      20      30
AAD-12      TYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-285  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                                160      170      180      190      200      210

```

```

                                40      50      60      70      80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTAT
                                :: : . : ... . . .... :... : . : ...
gi+AHw-285  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                                220      230      240      250      260      270

```

```

gi+AHw-285  TVAAGGYKV
                280

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 52 Z-score: 87.2 bits: 20.9 E(): 7
 Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
 in 71 aa overlap (2-70:11-80)

```

                                10      20      30      40      50
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVL-HQRSAR
                                .. . ...: ... . :... . . . : : .. :...:
gi+AHw-408  MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12  HSLVYSQSKLGHVQQ--AGSAYIGYGMDTTAT
                                : ... :... :... :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
 5.020 (287 aa)
 initn: 34 initl: 34 opt: 57 Z-score: 87.1 bits: 22.2 E(): 7.1
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (10-79:189-270)

```

                                10      20      30
AAD-12      TYMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330  GELQIIDKIDAAFKVAATAAATAPADTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                                160      170      180      190      200      210

```

```

                                40      50      60      70      80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTAT
                                :: : . : ... . . .... :... : . : ...
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                                220      230      240      250      260      270

```

```

gi+AHw-330  TVAAGGYKV
                280

```


30 40 50 60 70 80
AAD-12 DMRAAYDALDEATRALVHOR-SARHSLVYSOSKLGHVQOAGSAYIGYGMDDTTAT

```

      : . . . . . : : : :
gi+AHw-132 DEGSPFN YIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSIS
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-439275+AHw-emb+AHw-CAA49555.1+AHw- CMa, component of tetrameric (145 aa)

initn: 37 initl: 37 opt: 52 Z-score: 85.2 bits: 20.9 E(): 9
 Smith-Waterman score: 52+ADs- 24.444+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (4-48:9-52)

```

      10          20          30          40          50
AAD-12      TYMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVY
      : . . . . . : : : :
gi+AHw-439 MASKSSITPLLLAAVLASVF AAATATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG
      10          20          30          40          50

```

```

      60          70          80
AAD-12      SQSKLGHVQQAGSAYIGYGMDDTTAT

```

```

gi+AHw-439 SPVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDF
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)

initn: 52 initl: 52 opt: 52 Z-score: 84.8 bits: 20.8 E(): 9.5
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (33-56:29-52)

```

      10          20          30          40          50          60
AAD-12      MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGH
      : : : : : : . . . : : :
gi+AHw-144      KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLS
      10          20          30          40          50

```

```

      70          80
AAD-12      VQQAGSAYIGYGMDDTTAT

```

```

gi+AHw-144 DSKVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAG
      60          70          80          90          100          110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:03 2010 done: Fri Feb 5 12:56:04 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

```
1+AD4APgA+-AAD-l2: 114 - 193 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

64      63
32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9-
66      55      25: +AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0-
68      35      20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      20      16: +AD0APQA9AD0APQAqAD0-
72      13      12: +AD0APQA9ACoAPQ-
74      18      10: +AD0APQA9ACoAPQA9-
76      8        7: +AD0APQAq-
78      5        6: +AD0AKg-
80      18      4: +AD0AKgA9AD0APQA9-
82      2        3: +ACo-
84      1        3: +ACo-
86      7        2: +ACoAPQA9-
88      5        2: +ACoAPQ-          inset +AD0- represents 1 library
sequences
90      1        1: +ACo-
92      1        1: +ACo-          : +ACo-
94      3        1: +ACo-          : +ACoAPQA9-
96      0        1: +ACo-          : +ACo-
98      0        0:              +ACo-
100     0        0:              +ACo-
102     1        0: +AD0-        +ACoAPQ-
104     0        0:              +ACo-
106     0        0:              +ACo-
108     0        0:              +ACo-
110     1        0: +AD0-        +ACoAPQ-
112     0        0:              +ACo-
114     0        0:              +ACo-
116     0        0:              +ACo-
118     0        0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.10670.00357+ADs- mu+AD0- 5.1625
0.186
mean+AF8-var+AD0-40.349010.483, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.201910
Kolmogorov-Smirnov statistic: 0.1147 (N+AD0-29) at 54

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 74 26.9 0.36
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 64 24.1 0.89
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 58 22.3 2.7
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.5 2.9
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.5 3

```

gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (144) 57 22.0 4
 gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 (160) 57 22.0 4.4
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200) 57 22.0 5.5
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1 (204) 57 22.0 5.7
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160) 55 21.4 6.6
 gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d 1. (160) 55 21.4 6.6
 gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d 1. (160) 55 21.4 6.6
 gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P (284) 57 22.0 8
 gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287) 57 22.0 8
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 20.9 8.2
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 53 20.9 8.2
 gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295) 57 22.0 8.3
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 52 20.6 8.7
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.6 8.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 init1: 57 opt: 74 Z-score: 110.3 bits: 26.9 E(): 0.36
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (20-80:309-363)

	10	20	30	40
AAD-12	YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR			
		:: :	: ::	... :
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA			
	280	290	300	310
				320
				330
	50	60	70	80
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATP			
	... :	: . :	... :	... :
gi+AHw-113	ESMKWNWRTNKKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP			
	340	350	360	370
				380
				390

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 init1: 38 opt: 64 Z-score: 103.3 bits: 24.1 E(): 0.89

Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (9-67:9-65)

```

                10         20         30         40         50
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
          : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
          10         20         30         40         50

```

```

                60         70         80
AAD-12  LGHVQQAGSAYIGYGMDTTATP
          : : : : :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKI
          60         70         80         90        100        110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 94.6 bits: 22.3 E(): 2.7
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (25-76:26-77)

```

                10         20         30         40         50
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
          : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFKVN
          10         20         30         40         50         60

```

```

                60         70         80
AAD-12  GHVQQAGSAYIGYGMDTTATP
          : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAG
          70         80         90        100        110        120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)
initn: 39 initl: 39 opt: 62 Z-score: 94.1 bits: 23.5 E(): 2.9
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (9-79:183-265)

```

                10         20         30
AAD-12  YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
          : : : . : : : : : : : : : : : : : : :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160        170        180        190        200        210

```

```

                40         50         60         70         80
AAD-12  LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATP
          : : : . : : : . . : : : : : : : : : : : : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
          220        230        240        250        260        270

```

```

gi+AHw-168 TVAAGGYKV
          280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
 5.020 (290 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 93.9 bits: 23.5 E(): 3
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (9-79:192-274)

```

                                10      20      30
AAD-12      YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330  QIIDKIDAAFKVAATAAATAPADDKFTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                                170      180      190      200      210      220

                                40      50      60      70      80
AAD-12  LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATP
                                :: : . : ... . . .... :... :... : : :...
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                                230      240      250      260      270      280

gi+AHw-330  TVAAGGYKV
                                290

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
 +AFs-Hord (144 aa)
 initn: 50 initl: 50 opt: 57 Z-score: 91.7 bits: 22.0 E(): 4
 Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (3-47:9-52)

```

                                10      20      30      40      50
AAD-12      YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRSARHSLVY
                                :.. ... :. . :. :... : . : : : : :...
gi+AHw-189  MASKSSITPLLLAASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTCGVTIAG
                                10      20      30      40      50

                                60      70      80
AAD-12  SQSKLGHVQQAGSAYIGYGMDTTATP

gi+AHw-189  SPVSSEPGDTPKDRCCQELDEAPQHCRVRVYFIGRRSHPDWRVLKDLPGCPKEPQRDFA
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
 +AFs-Cor (160 aa)
 initn: 47 initl: 47 opt: 57 Z-score: 90.8 bits: 22.0 E(): 4.4
 Smith-Waterman score: 57+ADs- 20.000+ACU- identity (55.294+ACU- similar)
 in 85 aa overlap (2-80:31-109)

```

                                10      20
AAD-12      YMPVMAQGAVFSAEVVPAVGG----RTCF
                                :. : :. : ... . : : . : :
gi+AHw-132  MGVFNYETETTSVIPPARLFKRFLVLDSDNLIPKVAPKAIKSIEIIIEGNGGPGTIKKICF-
                                10      20      30      40      50

                                30      40      50      60      70      80
AAD-12  DMRAAYDALDEATRVLHQ--SARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATP
                                : . . . . . . . : : : : . . . . . : : . . . :

```

gi+AHw-132 DEGSPFNFIKQKVEEIDQANFSYRYSVIEGDALSDKLEK-----INYEIKIVASPHGGSI
 60 70 80 90 100 110

gi+AHw-132 LKSISKYHTIGDHELIKDEQIKAGKEKASGLFKAVEGYLLAHSDAYN
 120 130 140 150 160

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 89.0 bits: 22.0 E(): 5.5
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (26-78:93-149)

10 20 30 40 50
 AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
 : : : : :
 gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
 70 80 90 100 110 120

60 70 80
 AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATP
 . . : . . : : : : : : : :
 gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
 130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 88.9 bits: 22.0 E(): 5.7
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (26-78:97-153)

10 20 30 40 50
 AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
 : : : : :
 gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
 70 80 90 100 110 120

60 70 80
 AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATP
 . . : . . : : : : : : : :
 gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
 130 140 150 160 170 180

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)
 initn: 55 initl: 55 opt: 55 Z-score: 87.7 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 40.000+ACU- identity (70.000+ACU- similar)
 in 20 aa overlap (2-21:31-50)

10 20 30
 AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 . : : : : : : : : :
 gi+AHw-165 MGVFTHENEITS AIPPGR LFKAFVLDADNLIPKLAPHAIKSAEIIIEGNGGPGTIKKITFG
 10 20 30 40 50 60

40 50 60 70 80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATP

gi+AHw-165 EGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTSK
70 80 90 100 110 120

+AD4APg-gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d
1.0502 (160 aa)

initn: 49 initl: 49 opt: 55 Z-score: 87.7 bits: 21.4 E(): 6.6
Smith-Waterman score: 55+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (2-80:31-109)

10 20 30
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRRA
.: .: .: .: .: .: .: .: .: .:
gi+AHw-602 MGVFTYETEFSSAIPAPGLFKAFILDGDNLIPKIA PQAIKSTEIVEGDGGVGTIKKITFG
10 20 30 40 50 60

40 50 60 70 80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYMDTTATP
. . : . .: .: .: .: .: .: .: .: .:
gi+AHw-602 EGSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIA YETKLTASPDGGSIIKTTS
70 80 90 100 110

gi+AHw-602 HCHTKGGVEIKEEHVKAGKEKASSLFLKLETYLVANPNAYN
120 130 140 150 160

+AD4APg-gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d
1.0501 (160 aa)

initn: 49 initl: 49 opt: 55 Z-score: 87.7 bits: 21.4 E(): 6.6
Smith-Waterman score: 55+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (2-80:31-109)

10 20 30
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRRA
.: .: .: .: .: .: .: .: .: .:
gi+AHw-602 MGVFTYETEFSSAIPAPRLFKAFILDGDNLIPKIA PQAIKSTEIVEGDGGVGTIKKITFG
10 20 30 40 50 60

40 50 60 70 80
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYMDTTATP
. . : . .: .: .: .: .: .: .: .: .:
gi+AHw-602 EGSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIA YETKLTASPDGGSIIKTTS
70 80 90 100 110

gi+AHw-602 HCHTKGGVEIKEEHVKAGKEKASGLFLKLETYLVANPNAYN
120 130 140 150 160

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.2 bits: 22.0 E(): 8
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (9-78:186-267)

```

                                10      20      30
AAD-12      YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-285  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
                                160      170      180      190      200      210

```

```

                                40      50      60      70      80
AAD-12  LDEATRALLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATP
                                :: : . : ..: . . .... :...: .. : ...:
gi+AHw-285  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                                220      230      240      250      260      270

```

```

gi+AHw-285  TVAAGGYKV
                280

```

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5.020 (287 aa)
 initn: 34 initl: 34 opt: 57 Z-score: 86.1 bits: 22.0 E(): 8
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (9-78:189-270)

```

                                10      20      30
AAD-12      YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330  GELQIIDKIDAAFKVAATAAATAPADTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
                                160      170      180      190      200      210

```

```

                                40      50      60      70      80
AAD-12  LDEATRALLVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATP
                                :: : . : ..: . . .... :...: .. : ...:
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                                220      230      240      250      260      270

```

```

gi+AHw-330  TVAAGGYKV
                280

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 85.9 bits: 20.9 E(): 8.2
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (9-67:9-65)

```

                                10      20      30      40      50
AAD-12  YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALLVHQRSARHSLVYSQSK
                                : :: : . : ..: . : : ..... : .....:
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                                10      20      30      40      50

```

```

                                60      70      80
AAD-12  LGHVQQAAGSAYIGYGMDTTATP
                                : .... :
gi+AHw-111  LDELNENKSKELQEKIIRELDVVCAMIEGAQAGALERELKRTDLNILERFNYYEEAQTLSKI
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 85.9 bits: 20.9 E(): 8.2
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (9-67:9-65)

```

      10      20      30      40      50
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
      : : : : : . : : : : : : : : : : : : : : : : : :
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
      10      20      30      40      50

```

```

      60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTTATP
      : : : : :
gi+AHw-420 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 85.9 bits: 22.0 E(): 8.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (9-78:197-278)

```

      10      20      30
AAD-12 YMPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
      : : : . : : : : : : : : : : : : : : :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
      170      180      190      200      210      220

```

```

      40      50      60      70      80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATP
      : : : . : : : : : : : : : : : : : : : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
      230      240      250      260      270      280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs- Actinidia de (116 aa)

initn: 34 initl: 34 opt: 52 Z-score: 85.5 bits: 20.6 E(): 8.7
Smith-Waterman score: 52+ADs- 25.352+ACU- identity (60.563+ACU- similar)
in 71 aa overlap (1-69:11-80)

```

      10      20      30      40
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
      . . . : : : . . . : : : . . . : : : . . . : : :
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDDTTATP
      : : . : : : : : : :

```

```
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
          60          70          80          90         100         110
```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 85.3 bits: 20.6 E(): 8.9
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (27-67:11-50)

```

          10          20          30          40          50
AAD-12 YMPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
          ::  ::  :  .....  .....  :  .
gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                   10          20          30          40

          60          70          80
AAD-12 LGHVQQAGSAYIGYGMTTATP
          :  ....  :
gi+AHw-160 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
                   50          60          70          80          90         100
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:05 2010 done: Fri Feb 5 12:56:05 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 115 - 194 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      2      0:+AD0-
      30      2      2:+ACo-
      32      4      8:+AD0APQAq-
      34     19     21:+AD0APQA9AD0APQA9ACo-
      36     36     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
```

```

38      45      72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
40      61
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42      103
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
44      117
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
46      123
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
48      121
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
50      128
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
52      95
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ-      +ACo-
54      75
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
56      97
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
58      65
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60      58      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
62      62
40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
64      67
32: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
66      52      25: +AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
68      35      20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      18      16: +AD0APQA9AD0APQAq-
72      15      12: +AD0APQA9ACoAPQ-
74      16      10: +AD0APQA9ACoAPQA9-
76      8       7: +AD0APQAq-
78      5       6: +AD0AKg-
80      19      4: +AD0AKgA9AD0APQA9AD0-
82      1       3: +ACo-
84      2       3: +ACo-
86      6       2: +ACoAPQ-
88      5       2: +ACoAPQ-      inset +AD0- represents 1 library
sequences
90      1       1: +ACo-
92      1       1: +ACo-      : +ACo-
94      3       1: +ACo-      : +ACoAPQA9-
96      0       1: +ACo-      : +ACo-
98      0       0:      +ACo-
100     0       0:      +ACo-

```

```

102      1      0:+AD0-      +ACoAPQ-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      1      0:+AD0-      +ACoAPQ-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.08810.00359+ADs- mu+AD0- 5.3253
0.187
mean+AF8-var+AD0-40.169610.344, 0's: 2 Z-trim: 2 B-trim: 213 in 1/42
Lambda+AD0- 0.202360
Kolmogorov-Smirnov statistic: 0.1113 (N+AD0-29) at 54

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  74 26.9      0.36
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  64 24.1      0.89
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.3      2.7
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.5      2.9
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.5      3
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)  57 22.0      4
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
57 22.0      4.4
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.0      5.6
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.0      5.7
gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (
160)  55 21.4      6.6
gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d 1. ( 160)
55 21.4      6.6
gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d 1. ( 160)
55 21.4      6.6
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)  57 22.0      8
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.0      8.1
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  53 20.9      8.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 20.9      8.3

```

gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295)
 57 22.0 8.3
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 20.6 9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 110.3 bits: 26.9 E(): 0.36
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (19-79:309-363)

```

                10      20      30      40
AAD-12      MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                : : : : : : : : : : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
            280      290      300      310      320      330

            50      60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL
            : : : : : : : : : : : :
gi+AHw-113 ESMKWNWRTNKNVDLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
            340      350      360      370      380      390

```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 103.3 bits: 24.1 E(): 0.89
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (8-66:9-65)

```

                10      20      30      40      50
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                : : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10      20      30      40      50

            60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPL
            : : : : :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
            60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 94.6 bits: 22.3 E(): 2.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (24-75:26-77)

```

                10      20      30      40      50
AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                : : : : : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQSLSTKHSVPDVLAFKVN

```

```

                10          20          30          40          50          60
AAD-12  60      70      80
        GHVQQAGSAYIGYGMDDTTATPL
        ::::: :  :: :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGGLAQKRVAG
                70          80          90          100          110          120
```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)
initn: 39 initl: 39 opt: 62 Z-score: 94.2 bits: 23.5 E(): 2.9
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (8-78:183-265)

```

                        10          20          30
AAD-12                MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                        :::. .  ::::  :: .....
gi+AHw-168 QIIDKIDA AFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                160          170          180          190          200          210
```

```

                40          50          60          70          80
AAD-12  LDEATR LVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPL
                :: : . :  :: : . .  ::::  ::::  :: :  ::::
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                220          230          240          250          260          270
```

gi+AHw-168 TVAAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)
initn: 39 initl: 39 opt: 62 Z-score: 93.9 bits: 23.5 E(): 3
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (8-78:192-274)

```

                        10          20          30
AAD-12                MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                        :::. .  ::::  :: .....
gi+AHw-330 QIIDKIDA AFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                170          180          190          200          210          220
```

```

                40          50          60          70          80
AAD-12  LDEATR LVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPL
                :: : . :  :: : . .  ::::  ::::  :: :  ::::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230          240          250          260          270          280
```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 50 initl: 50 opt: 57 Z-score: 91.6 bits: 22.0 E(): 4

50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPL
.. : .. : : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:

Full+AD0-Glutat (204 aa)

initn: 41 initl: 41 opt: 57 Z-score: 88.8 bits: 22.0 E(): 5.7
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (25-77:97-153)

```

                10      20      30      40
AAD-12      MPVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                .....  :::  ::  ..  .  ..
gi+AHw-622  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120

                50      60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL
                .. :  ...  :  .....  :  :  :
gi+AHw-622  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130      140      150      160      170      180

```

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa+AF0- (160 aa)

initn: 55 initl: 55 opt: 55 Z-score: 87.6 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 40.000+ACU- identity (70.000+ACU- similar)
 in 20 aa overlap (1-20:31-50)

```

                        10      20      30
AAD-12                        MPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        ..  ..  ..  .....  ..  :
gi+AHw-165  MGVFTHENEITSAIPPGRLFKAFVLADNLIPKLAPHAIKSAEIIIEGNGGPGTIKKITFG
                        10      20      30      40      50      60

                        40      50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPL

gi+AHw-165  EGSQFKYVKHRIDEIDQANFTYCYSVIEGDDVVNELLEKISYEIKIVASPDGGSILKNTSK
                        70      80      90      100      110      120

```

+AD4APg-gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d 1.0502 (160 aa)

initn: 49 initl: 49 opt: 55 Z-score: 87.6 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (1-79:31-109)

```

                        10      20      30
AAD-12                        MPVMAQGAVFSAEVVPAVGGRTCFADMRAA
                        ..  ..  ..  .....  ..  .  .  .
gi+AHw-602  MGVFTYETEFSSAIPAPGLFKAFILDGDNLPKIAPQAIKSTEIVEGDDGGVGTIKKITFG
                        10      20      30      40      50      60

                        40      50      60      70      80
AAD-12  YDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYGMDDTTATPL
                .  ..  :  .  .....  :  .  :  .  .  :  :  :
gi+AHw-602  EGSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIAYETKLTASPDGGSIIKTTS
                70      80      90      100      110

```

gi+AHw-602 HCHTKGGVEIKEEHVKAGKEKASSLFLKLETYLVANPNAYN
 120 130 140 150 160

+AD4APg-gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d
 1.0501 (160 aa)

initn: 49 initl: 49 opt: 55 Z-score: 87.6 bits: 21.4 E(): 6.6
 Smith-Waterman score: 55+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (1-79:31-109)

AAD-12 MPVMAQGAVFSAEVVPAVGGRTCFADMRAA
 .: .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 MGVFTYETEFSSAIPAPRLFKAFILDGDNLIPKIAQAIKSTEIVEGDGGVGTIKKITFG
 10 20 30 40 50 60
 40 50 60 70 80
 AAD-12 YDALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYMDTTATPL
 . . .: .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 EGSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIAYETKLTASPDGGSIIKTTS
 70 80 90 100 110

gi+AHw-602 HCHTKGGVEIKEEHVKAGKEKASGLFLKLETYLVANPNAYN
 120 130 140 150 160

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
 Full+AD0-Polle (284 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.2 bits: 22.0 E(): 8
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (8-77:186-267)

AAD-12 MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
 :... .: .: .: .: .: .: .: .: .: .:
 gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPSLEAAVKQ
 160 170 180 190 200 210
 40 50 60 70 80
 AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYMDTTATPL
 :: : .: .: .: .: .: .: .: .: .: .:
 gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
 220 230 240 250 260 270

gi+AHw-285 TVAAGGYKV
 280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
 5.020 (287 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.1 bits: 22.0 E(): 8.1
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (8-77:189-270)

AAD-12 MPVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
 :... .: .: .: .: .: .: .: .: .: .:

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)
initn: 34 initl: 34 opt: 57 Z-score: 85.9 bits: 22.0 E(): 8.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (8-77:197-278)

1+AD4APqA+-AAD-12: 116 - 195 80 aa - 80 aa

[illegible]

```

76      9      7:+AD0APQAq-
78     15      6:+AD0AKgA9AD0APQ-
80      3      4:+AD0AKg-
82      4      3:+ACoAPQ-
84      5      3:+ACoAPQ-
86      8      2:+ACoAPQA9-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      3      1:+ACo-          :+ACoAPQA9-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     1      0:+AD0-          +ACoAPQ-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120    0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.02070.00354+ADs- mu+AD0- 5.6837
0.185
mean+AF8-var+AD0-38.799010.102, 0's: 2 Z-trim: 3 B-trim: 213 in 1/42
Lambda+AD0- 0.205904
Kolmogorov-Smirnov statistic: 0.1092 (N+AD0-29) at 54

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  74 27.2      0.31
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   64 24.2      0.8
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.5      2.5
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.6      2.6
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.6      2.7
gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor +AFs- (
144)   57 22.2      3.6
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.1      5.1
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.1      5.2
gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1 ( 160)
55 21.6      6.1

```

gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
 (284) 57 22.1 7.3
 gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 (287)
 57 22.1 7.4
 gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295)
 57 22.1 7.6
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 53 21.0 7.7
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 53 21.0 7.7
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.7 8.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 20.7 8.3
 gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea sativa (160)
 53 21.0 9.2
 gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d 1. (160)
 53 21.0 9.2
 gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d 1. (160)
 53 21.0 9.2
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116)
 51 20.4 10

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 111.5 bits: 27.2 E(): 0.31
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (18-78:309-363)

	10	20	30	40
AAD-12	PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR			
		:: :	: :
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA			
	280	290	300	310
				320
				330

	50	60	70	80
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR			
	. . .	:
gi+AHw-113	ESMKWNWRTNKKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP			
	340	350	360	370
				380
				390

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 104.1 bits: 24.2 E(): 0.8
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (7-65:9-65)

	10	20	30	40	50
AAD-12	PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK				
	:	:: :	: :
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ				


```

                10          20          30          40          50
        60          70          80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLR
      : . . . . :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKI
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 95.3 bits: 22.5 E(): 2.5
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (23-74:26-77)

```

                10          20          30          40          50
AAD-12 PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
      : . . . . :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQLSKHSVPDVLAFKVN
        10          20          30          40          50          60

```

```

        60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLR
      : . . . . :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAG
        70          80          90          100          110          120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)
initn: 39 initl: 39 opt: 62 Z-score: 95.0 bits: 23.6 E(): 2.6
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (7-77:183-265)

```

                10          20          30
AAD-12 PVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
      : . . . . :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
        160          170          180          190          200          210

```

```

        40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLR
      : . . . . :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
        220          230          240          250          260          270

```

```

gi+AHw-168 TVAAGGYKV
        280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)
initn: 39 initl: 39 opt: 62 Z-score: 94.7 bits: 23.6 E(): 2.7
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (7-77:192-274)

```

AAD-12                PVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                        :... . ...: .. ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                170      180      190      200      210      220

```

```

                40      50      60      70      80
AAD-12 LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLR
                :: : . : ..: . . .... :...: .. : ....
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230      240      250      260      270      280

```

```

gi+AHw-330 TVAAGGYKV
                290

```

+AD4APg-gi+AHw-18955+AHw-emb+AHw-CAA41956.1+AHw- alpha-amylase inhibitor
+AFs-Hord (144 aa)
initn: 50 initl: 50 opt: 57 Z-score: 92.3 bits: 22.2 E(): 3.6
Smith-Waterman score: 57+ADs- 26.667+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (1-45:9-52)

```

                10      20      30      40      50
AAD-12          PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRVLHQRSARHSLVY
                ... .. : . : : : : : : : : : : : : : : :
gi+AHw-189 MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPL-EGCREYVAQQTTCGVTIAG
                10      20      30      40      50

```

```

                60      70      80
AAD-12 SQSKLGHVQQAGSAYIGYGMDDTTATPLR

```

```

gi+AHw-189 SPVSSEPGDTPKDRCCQELDEAPQHCRVRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFA
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 89.7 bits: 22.1 E(): 5.1
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (24-76:93-149)

```

                10      20      30      40
AAD-12          PVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRVLHQRSARH
                        ..... :...: :. . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120

```

```

                50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
                .. : ... : ..... : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 89.5 bits: 22.1 E(): 5.2

Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (24-76:97-153)

```

                10      20      30      40
AAD-12      PVMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                .....   :::  ::  ..  .  ..
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120

```

```

                50      60      70      80
AAD-12      SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
                .. :  ...  .:  .....  :  :  :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130      140      150      160      170      180

```

+AD4APg-gi+AHw-1321733+AHw-emb+AHw-CAA96549.1+AHw- major allergen Cor a 1
+AFs-Cor (160 aa)

initn: 45 initl: 45 opt: 55 Z-score: 88.3 bits: 21.6 E(): 6.1
Smith-Waterman score: 55+ADs- 20.238+ACU- identity (54.762+ACU- similar)
in 84 aa overlap (1-78:32-109)

```

                        10      20
AAD-12      PVMAQGAVFSAEVVPAVGG-----RTCFAD
                        :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-132 GVFNYETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIIEGNGGPGTIKKICF-D
                        10      20      30      40      50      60

```

```

                30      40      50      60      70      80
AAD-12      MRAAYDALDEATRALVHQR-SARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR
                .  .  .  .  .  .  :  :  :  .  .  .  .  :  :  .  :  :
gi+AHw-132 EGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEK-----INYEIKIVASPHGGSIL
                70      80      90      100      110

```

```

gi+AHw-132 KSISKYHTIGDHELKDEQIKAGKEKASGLFKAVEGYLLAHSDAYN
                120      130      140      150      160

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.9 bits: 22.1 E(): 7.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (7-76:186-267)

```

                        10      20      30
AAD-12      PVMAQGAVFSAEVVPAVGG-----RTCFADMRAAYDA
                        :  :  .  :  :  :  :  :  :  :  :
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ
                160      170      180      190      200      210

```

```

                40      50      60      70      80
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLR
                ::  :  .  :  :  :  .  .  :  :  :  :  :  :  :  :  :
gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                220      230      240      250      260      270

```

gi+AHw-285 TVAAGGYKV
280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.8 bits: 22.1 E(): 7.4
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (7-76:189-270)

```

                                10          20          30
AAD-12          PVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                        :... . ...: .. ...:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160      170      180      190      200      210
```

```

                40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYMDTTATPLR
          :: : . :      ..: . . .... ..: :...: .. : :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220      230      240      250      260      270
```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.5 bits: 22.1 E(): 7.6
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (7-76:197-278)

```

                                10          20          30
AAD-12          PVMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                        :... . ...: .. ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          170      180      190      200      210      220
```

```

                40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYMDTTATPLR
          :: : . :      ..: . . .... ..: :...: .. : :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          230      240      250      260      270      280
```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 86.5 bits: 21.0 E(): 7.7
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (7-65:9-65)

```

                10          20          30          40          50
AAD-12  PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
          : ...: . :      :...: . : : .....: .....: : .
```

gi+AHw-111 MKFAIVLIACFAASVL-AQEHEKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
 10 20 30 40 50

60 70 80
 AAD-12 LGHVQQAGSAYIGYGMDDTTATPLR
 : :

gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
 60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein B1 (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 86.5 bits: 21.0 E(): 7.7
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (7-65:9-65)

 10 20 30 40 50
 AAD-12 PVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
 : :: : . :: : : : :
 gi+AHw-420 MKFAIVLIACFAASVL-AQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
 10 20 30 40 50

60 70 80
 AAD-12 LGHVQQAGSAYIGYGMDDTTATPLR
 : :
 gi+AHw-420 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
 60 70 80 90 100 110

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 86.1 bits: 22.7 E(): 8.1
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (43-80:198-242)

 20 30 40 50 60
 AAD-12 VVPAVGGRCTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
 :: ::: :: : : :: :
 gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
 170 180 190 200 210 220

70 80
 AAD-12 YIGYGMDDTTATPLR
 : :
 gi+AHw-303 VLGFGMDTETARKVREGDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
 230 240 250 260 270 280

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 85.8 bits: 20.7 E(): 8.3
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (25-65:11-50)

 10 20 30 40 50
 AAD-12 PVMAQGAVFSAEVVPAVGGRCTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLG
 :: : : : : :

gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLD
 10 20 30 40

60 70 80
 AAD-12 HVQQAGSAYIGYGMDDTTATPLR
 :

gi+AHw-160 ELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKILL
 50 60 70 80 90 100

+AD4APg-gi+AHw-16555781+AHw-emb+AHw-CAD10374.1+AHw- ypr10 +AFs-Castanea
 sativa+AF0- (160 aa)
 initn: 53 init1: 53 opt: 53 Z-score: 85.1 bits: 21.0 E(): 9.2
 Smith-Waterman score: 53+ADs- 42.105+ACU- identity (68.421+ACU- similar)
 in 19 aa overlap (1-19:32-50)

10 20 30
 AAD-12 PVMAQGAVFSAEVVPAVGGRTCFADMRAAY
 : .: .: .: .: .: .: .:
 gi+AHw-165 GVFTHENEITSAIPPGRLFKAFVLADNLIPKLAPHAIKSAEIIIEGNGGPGTIKKITFGE
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 DALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLR

gi+AHw-165 GSQFKYVKHRIDEIDQANFTYCYSVIEGDVVNELLEKISYEIKIVASPDGGSILKNTSKY
 70 80 90 100 110 120

+AD4APg-gi+AHw-60280809+AHw-gb+AHw-AAX18297.1+AHw- major allergen Mal d
 1.0502 (160 aa)
 initn: 47 init1: 47 opt: 53 Z-score: 85.1 bits: 21.0 E(): 9.2
 Smith-Waterman score: 53+ADs- 24.051+ACU- identity (50.633+ACU- similar)
 in 79 aa overlap (1-78:32-109)

10 20 30
 AAD-12 PVMAQGAVFSAEVVPAVGGRTCFADMRAAY
 : .: .: .: .: .: .: .:
 gi+AHw-602 GVFTYETEFSSAIPAPGLFKAFILDGDNLIPKIAQAIKSTEIVEGDGGVGTIKKITFGE
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 DALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYGMDDTTATPLR

. .: .: .: .: .: .: .: .: .: .:
 gi+AHw-602 GSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIAYETKLTASPDGGSIIKTTS
 70 80 90 100 110 120

gi+AHw-602 CHTKGGVEIKEEHVKAGKEKASSLFLKLETYLVANPNAYN
 130 140 150 160

+AD4APg-gi+AHw-60280807+AHw-gb+AHw-AAX18296.1+AHw- major allergen Mal d
 1.0501 (160 aa)
 initn: 47 init1: 47 opt: 53 Z-score: 85.1 bits: 21.0 E(): 9.2
 Smith-Waterman score: 53+ADs- 24.051+ACU- identity (50.633+ACU- similar)
 in 79 aa overlap (1-78:32-109)

```

                                10      20      30
AAD-12      PVMAQGAVFSAEVVPAVGGRTCFADMRAAY
              :  :  :  :  :  :  :  :  :  :  :
gi+AHw-602  GVFTYETEFSSAIPAPRLFKAFILDGDNLIPKIA PQAIKSTEIVEGDGGVGTIKKITFGE
              10      20      30      40      50      60

              40      50      60      70      80
AAD-12  DALDEATRALVHQRSARHSLVYSQSKL-GHVQQAGSAYIGYGMDDTTATPLR
              .  .  :  .  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-602  GSQYGYVKHKVDGID-KHNFTYSYSMIEGDALSDKIEKIAYETKLTASPDGGSIIKTTSH
              70      80      90      100     110     120

gi+AHw-602  CHTKGGVEIKEEHVKAGKEKASGLFKLLETYLVANPNAYN
              130     140     150     160

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 51 Z-score: 84.4 bits: 20.4 E(): 10
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
 in 63 aa overlap (7-67:19-80)

```

                                10      20      30      40
AAD-12      PVMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
              :  :  .  .  :  :  :  .  .  :  :  :  :  :  :  :  :
gi+AHw-408  MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
              10      20      30      40      50

              50      60      70      80
AAD-12  HSLVYSQSKLGHVQQ-AGSAYIGYGMDDTTATPLR
              :  :  .  :  :  :  :  :  :  :
gi+AHw-408  DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
              60      70      80      90      100     110

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:06 2010 done: Fri Feb 5 12:56:06 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 117 - 196 80 aa - 80 aa

[illegible]


```

82      2      3:+ACo-
84      2      3:+ACo-
86      7      2:+ACoAPQA9-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      3      1:+ACo-          :+ACoAPQA9-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0:+AD0-          +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120    0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.03520.0034+ADs- mu+AD0- 6.7115
0.176
mean+AF8-var+AD0-34.7883 8.923, 0's: 2 Z-trim: 4 B-trim: 30 in 1/42
Lambda+AD0- 0.217449
Kolmogorov-Smirnov statistic: 0.0250 (N+AD0-28) at 32

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   74 27.4      0.26
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)    64 24.5      0.69
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 22.6      2.3
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.7      2.4
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.7      2.5
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.2      4.9
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.2      5
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)   57 22.2      7.1
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.2      7.2
gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 ( 295)
57 22.2      7.4
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.0      7.5

```

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 53 21.0 7.5
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.7 7.9
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 20.7 8.2
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 51 20.4 9.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 113.0 bits: 27.4 E(): 0.26
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (17-77:309-363)

	10	20	30	40
AAD-12	VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR			
		:	:	:
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA			
	280	290	300	310
	50	60	70	80
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP			
	:	:	:	:
gi+AHw-113	ESMKWNWRTNKNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP			
	340	350	360	370

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 105.3 bits: 24.5 E(): 0.69
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (6-64:9-65)

	10	20	30	40	50
AAD-12	VMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK				
	:	:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ				
	10	20	30	40	50
	60	70	80		
AAD-12	LGHVQQAGSAYIGYGMDDTTATPLRP				
	:	:	:	:	:
gi+AHw-111	LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI				
	60	70	80	90	100

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (22-73:26-77)

```

          10          20          30          40          50
AAD-12      VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
              :::          :. . . : . . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVN
          10          20          30          40          50          60

```

```

          60          70          80
AAD-12      GHVQQAGSAYIGYGMDDTTATPLRP
              : . . . . : . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGGLAQKRVAG
          70          80          90          100          110          120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
 +AFs-Phl (281 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 95.6 bits: 23.7 E(): 2.4
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (6-76:183-265)

```

                                10          20          30
AAD-12      VMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                : . . . : . . . :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160          170          180          190          200          210

```

```

          40          50          60          70          80
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRP
              : : . . : . . . . . : . . . : . : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
          220          230          240          250          260          270

```

gi+AHw-168 TVAAGGYKV
 280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
 5.020 (290 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 95.3 bits: 23.7 E(): 2.5
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (6-76:192-274)

```

                                10          20          30
AAD-12      VMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                : . . . : . . . :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          170          180          190          200          210          220

```

```

          40          50          60          70          80
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRP
              : : . . : . . . . . : . . . : . : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
          230          240          250          260          270          280

```

gi+AHw-330 TVAAGGYKV
 290

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 90.0 bits: 22.2 E(): 4.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (23-75:93-149)

```

                10         20         30         40
AAD-12          VMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                .....::: :: .. .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70         80         90        100        110        120

```

```

                50         60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP
                .. : ... : ..... : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 89.9 bits: 22.2 E(): 5
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (23-75:97-153)

```

                10         20         30         40
AAD-12          VMAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                .....::: :: .. .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70         80         90        100        110        120

```

```

                50         60         70         80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRP
                .. : ... : ..... : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
 Full+AD0-Polle (284 aa)
 initn: 34 initl: 34 opt: 57 Z-score: 87.0 bits: 22.2 E(): 7.1
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (6-75:186-267)

```

                10         20         30
AAD-12          VMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                .... : .. .....
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDXYKCIPSLEAAVKQ
                160        170        180        190        200        210

```

```

                40         50         60         70         80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRP
                :: : . : ... . . ..... : : : : : : :
gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                220        230        240        250        260        270

```

gi+AHw-285 TVAAGGYKV
280

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.9 bits: 22.2 E(): 7.2
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (6-75:189-270)

```

                                10          20          30
AAD-12                        VMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160          170          180          190          200          210
```

```

                40                50                60                70                80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRP
                :: : . : ..: . . .... :...: ...: .. : :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220          230          240          250          260          270
```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.7 bits: 22.2 E(): 7.4
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (6-75:197-278)

```

                                10          20          30
AAD-12                        VMAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          170          180          190          200          210          220
```

```

                40                50                60                70                80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRP
                :: : . : ..: . . .... :...: ...: .. : :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          230          240          250          260          270          280
```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 86.7 bits: 21.0 E(): 7.5
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (6-64:9-65)

```

                10                20                30                40                50
AAD-12      VMAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                : ...: . : ..: . : : .....: .....: : .
```



```
gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDE
                  10          20          30          40
```

```

        60          70          80
AAD-12 VQQAGSAYIGYGMDDTTATPLRP
      ... :
gi+AHw-160 LNEKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLISKILLK
          50          60          70          80          90          100
```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 51 Z-score: 84.5 bits: 20.4 E(): 9.9
Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
in 63 aa overlap (6-66:19-80)

```

                  10          20          30          40
AAD-12          VMAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
                  :: ... . :::: . . .: . . : : . : :...:
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
          10          20          30          40          50
```

```

        50          60          70          80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDDTTATPLRP
      : ... :...: ...:
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
        60          70          80          90          100          110
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:06 2010 done: Fri Feb 5 12:56:06 2010
Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 118 - 197 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
```

```

26      6      0:+AD0APQ-
28      6      0:+AD0APQ-
30     16     2:+ACoAPQA9AD0APQA9-
32     19     8:+AD0APQAqAD0APQA9AD0-
34     18    21:+AD0APQA9AD0APQA9ACo-
36     39    44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
38     74
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
40    100
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
42    123
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
44    128
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
46     98
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-+AD0APQ-
48    127
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
50    152
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
52     97
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
54     99
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
56     61
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
58     75
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
60     64
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
62     38    40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64     29    32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
66     27    25:+AD0APQA9AD0APQA9AD0APQAq-
68     18    20:+AD0APQA9AD0APQA9ACo-
70      6    16:+AD0APQ- +ACo-
72      6    12:+AD0APQ- +ACo-
74     10    10:+AD0APQA9ACo-
76      5     7:+AD0APQAq-
78      4     6:+AD0AKg-
80      6     4:+AD0AKg-
82      2     3:+ACo-
84      2     3:+ACo-
86      7     2:+ACoAPQA9-
88      0     2:+ACo- inset +AD0- represents 1 library sequences
90      2     1:+ACo-
92      0     1:+ACo- :+ACo-

```



```

94      1      1:+ACo-      :+ACo-
96      2      1:+ACo-      :+ACoAPQ-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     1      0:+AD0-      +ACoAPQ-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     1      0:+AD0-      +ACoAPQ-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.14520.00342+ADs- mu+AD0- 6.0269
0.177
mean+AF8-var+AD0-35.2009 9.134, 0's: 2 Z-trim: 4 B-trim: 30 in 1/42
Lambda+AD0- 0.216171
Kolmogorov-Smirnov statistic: 0.0250 (N+AD0-28) at 32

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   74 27.4    0.27
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)    64 24.4    0.69
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 22.6    2.3
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.7    2.4
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.7    2.5
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.2    4.9
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.2    5
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)   57 22.1    7.2
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.1    7.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.0    7.5
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)    53 21.0    7.5
gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 ( 295)
57 22.1    7.6
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 20.7    8.1
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)    59 22.7    8.1

```

gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116) 51 20.4 9.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 112.7 bits: 27.4 E(): 0.27
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (16-76:309-363)

```

                                10      20      30      40
AAD-12      MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                : : : : : : : : : : : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
          280      290      300      310      320      330

```

```

          50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL
          : : : : : : : : : : : :
gi+AHw-113  ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
          340      350      360      370      380      390

```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 105.2 bits: 24.4 E(): 0.69
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (5-63:9-65)

```

                                10      20      30      40      50
AAD-12      MAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                                : : : : : : : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
          10      20      30      40      50

```

```

          60      70      80
AAD-12  LGHVQQAGSAYIGYGMDDTTATPLRPL
          : : : : :
gi+AHw-111  LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKI
          60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 96.0 bits: 22.6 E(): 2.3
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (21-72:26-77)

```

                                10      20      30      40      50
AAD-12      MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                : : : : : : : : : : : :
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQSTKHSVPDVLAFKVVN
          10      20      30      40      50      60

```

```

        60          70          80
AAD-12  GHVQQAGSAYIGYGMDTTATPLRPL
        : : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGLGLAQLKRVAG
        70          80          90          100          110          120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
 +AFs-Phl (281 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 95.4 bits: 23.7 E(): 2.4
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (5-75:183-265)

```

                                10          20          30
AAD-12                          MAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                : : : . : : : : : : : : : : :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
        160          170          180          190          200          210

```

```

        40          50          60          70          80
AAD-12  LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPL
        : : : . : : : . : : : : : : : : : : : : : : : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
        220          230          240          250          260          270

```

```

gi+AHw-168 TVAAGGYKV
        280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
 5.020 (290 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 95.2 bits: 23.7 E(): 2.5
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (5-75:192-274)

```

                                10          20          30
AAD-12                          MAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                : : : . : : : : : : : : : : :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
        170          180          190          200          210          220

```

```

        40          50          60          70          80
AAD-12  LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPL
        : : : . : : : . : : : : : : : : : : : : : : : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
        230          240          250          260          270          280

```

```

gi+AHw-330 TVAAGGYKV
        290

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 90.0 bits: 22.2 E(): 4.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (22-74:93-149)

```

                10         20         30         40
AAD-12      MAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                .....      ::: :: .. .
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100         110         120

```

```

                50         60         70         80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL
                .. :   ... .. : ..... :   :
gi+AHw-144  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 89.8 bits: 22.2 E(): 5
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (22-74:97-153)

```

                10         20         30         40
AAD-12      MAQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                .....      ::: :: .. .
gi+AHw-622  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70         80         90         100         110         120

```

```

                50         60         70         80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPL
                .. :   ... .. : ..... :   :
gi+AHw-622  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130        140        150        160        170        180

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 init1: 34 opt: 57 Z-score: 86.9 bits: 22.1 E(): 7.2
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (5-74:186-267)

```

                10         20         30
AAD-12      MAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                :... . .... : .. .....
gi+AHw-285  QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                160        170        180        190        200        210

```

```

                40         50         60         70         80
AAD-12  LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPL
                :: : . :   ... . . .... :... :... : ...
gi+AHw-285  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
                220        230        240        250        260        270

```

```

gi+AHw-285  TVAAGGYKV
                280

```

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)
initn: 34 init1: 34 opt: 57 Z-score: 86.8 bits: 22.1 E(): 7.3

60 70 80
 AAD-12 LGHVQQAGSAYIGYGMDDTATPLRL
 : . . . :
 gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKI
 60 70 80 90 100 110

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 86.6 bits: 22.1 E(): 7.6
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (5-74:197-278)

```

                                10          20          30
AAD-12                      MAQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .  ...:  ..  ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          170          180          190          200          210          220

```

```

          40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPL
          :: : . :  ...: . .  ...:  ...:  .. :  ...:
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          230          240          250          260          270          280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 86.0 bits: 20.7 E(): 8.1
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (23-63:11-50)

```

          10          20          30          40          50
AAD-12 MAQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHV
                                :: :  :  .....  .....: :  ..
gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDEL
                                10          20          30          40

```

```

          60          70          80
AAD-12 QQAGSAYIGYGMDTTATPLRPL
          .. :
gi+AHw-160 NENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKD
          50          60          70          80          90          100

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 86.0 bits: 22.7 E(): 8.1
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (41-78:198-242)

```

          20          30          40          50          60
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ... :... :  :  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
          170          180          190          200          210          220

```

```

          70          80
AAD-12 YIGYGMDT-TATPLRPL
          .....: :  ..

```

gi+AHw-303 VLGFGMTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
 230 240 250 260 270 280

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 51 Z-score: 84.6 bits: 20.4 E(): 9.8
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
 in 63 aa overlap (5-65:19-80)

10 20 30 40
 AAD-12 MAQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
 :: :::: . . .: . . : : .: :....
 gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
 10 20 30 40 50
 50 60 70 80
 AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTATPLRPL
 : ... :::: :.. :
 gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
 60 70 80 90 100 110

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:06 2010 done: Fri Feb 5 12:56:07 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 119 - 198 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	4	0:+AD0APQ-	
28	5	0:+AD0APQ-	
30	16	2:+ACoAPQA9AD0APQA9-	
32	10	8:+AD0APQAqAD0-	
34	22	21:+AD0APQA9AD0APQA9ACoAPQ-	
36	33	44:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-	+ACo-

sequences


```

102      0      0:      +ACo-
104      0      0:      +ACo-
106      1      0:+AD0-      +ACoAPQ-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      1      0:+AD0-      +ACoAPQ-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.19370.00341+ADs- mu+AD0- 5.3399
0.177
mean+AF8-var+AD0-34.2961 8.821, 0's: 2 Z-trim: 4 B-trim: 30 in 1/42
Lambda+AD0- 0.219004
Kolmogorov-Smirnov statistic: 0.0333 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  74 27.7      0.22
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  64 24.7      0.57
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.8      1.9
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.9      2.1
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.9      2.1
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.4      4.2
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.4      4.3
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)  57 22.4      6.2
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.4      6.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.2      6.4
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  53 21.2      6.4
gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 ( 295)
57 22.3      6.5
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 20.9      6.9
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 22.9      7
gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (
116)  51 20.6      8.4
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 20.9      9.1

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 57 initl: 57 opt: 74 Z-score: 114.2 bits: 27.7 E(): 0.22
Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
in 61 aa overlap (15-75:309-363)

```

                        10      20      30      40
AAD-12      AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                        : : : : : : : : : : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
      280      290      300      310      320      330
```

```

                        50      60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLV
      : : : : : : : : : : : :
gi+AHw-113 ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
      340      350      360      370      380      390
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 64 Z-score: 106.7 bits: 24.7 E(): 0.57
Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
in 61 aa overlap (4-62:9-65)

```

                        10      20      30      40      50
AAD-12      AQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                        : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
      10      20      30      40      50
```

```

                        60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLV
      : : : : :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
      60      70      80      90      100      110
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 97.4 bits: 22.8 E(): 1.9
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (20-71:26-77)

```

                        10      20      30      40      50
AAD-12      AQGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                        : : : : : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQSLTKHSVPDVLAFKVN
      10      20      30      40      50      60
```

```

                        60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLV
```

```

      ..... :   :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGGLAQKRVAQ
              70              80              90              100              110              120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)

initn: 39 initl: 39 opt: 62 Z-score: 96.7 bits: 23.9 E(): 2.1
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (4-74:183-265)

```

                                10              20
AAD-12                        AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .   :... :.. :... :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
              160              170              180              190              200              210

```

```

      30      40      50      60      70      80
AAD-12 LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLV
      :: : . :   :.. : . . . . . :... :... :.. : :... :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
              220              230              240              250              260              270

```

gi+AHw-168 TVAAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)

initn: 39 initl: 39 opt: 62 Z-score: 96.5 bits: 23.9 E(): 2.1
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (4-74:192-274)

```

                                10              20
AAD-12                        AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .   :... :.. :... :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
              170              180              190              200              210              220

```

```

      30      40      50      60      70      80
AAD-12 LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLV
      :: : . :   :.. : . . . . . :... :... :.. : :... :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
              230              240              250              260              270              280

```

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)

initn: 41 initl: 41 opt: 57 Z-score: 91.2 bits: 22.4 E(): 4.2
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (21-73:93-149)

```

                                10              20              30              40
AAD-12                        AQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRVLHQRSARH

```

```

          . . . . .      . . . . .      . . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
          70          80          90          100          110          120

```

```

          50          60          70          80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLV
          . . . . .      . . . . .      . . . . .

```

```

gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
          130          140          150          160          170          180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 91.0 bits: 22.4 E(): 4.3
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (21-73:97-153)

```

          10          20          30          40
AAD-12  AQGAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
          . . . . .      . . . . .      . . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
          70          80          90          100          110          120

```

```

          50          60          70          80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLV
          . . . . .      . . . . .      . . . . .
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
          130          140          150          160          170          180

```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 init1: 34 opt: 57 Z-score: 88.1 bits: 22.4 E(): 6.2
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (4-73:186-267)

```

          10          20
AAD-12  AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
          . . . . .      . . . . .
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160          170          180          190          200          210

```

```

          30          40          50          60          70          80
AAD-12  LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLV
          . . . . .      . . . . .      . . . . .
gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220          230          240          250          260          270

```

```

gi+AHw-285 TVAAGGYKV
          280

```

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)
initn: 34 init1: 34 opt: 57 Z-score: 88.0 bits: 22.4 E(): 6.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (4-73:189-270)

```

                                10          20
AAD-12          AQQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                        :... . ...: . . . .:
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          160      170      180      190      200      210

```

```

          30      40      50      60      70      80
AAD-12 LDEATRVLHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLV
          :: : . :      ..: . . . . . . . .: . . . : . . : . . :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          220      230      240      250      260      270

```

```

gi+AHw-330 TVAAGGYKV
          280

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.9 bits: 21.2 E(): 6.4
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (4-62:9-65)

```

                                10      20      30      40      50
AAD-12          AQQGAVFSAEVVPAVGGRTCTCFADMRAAYDAL--DEATRVLHQRSARHSLVYSQSK
                        : : : : . .      : : : . . . . . . . . . . . . : .
gi+AHw-420 MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
          10      20      30      40      50

```

```

          60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLRPLV
          : . . . . :
gi+AHw-420 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEAAQTLSKI
          60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 53 Z-score: 87.9 bits: 21.2 E(): 6.4
 Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
 in 61 aa overlap (4-62:9-65)

```

                                10      20      30      40      50
AAD-12          AQQGAVFSAEVVPAVGGRTCTCFADMRAAYDAL--DEATRVLHQRSARHSLVYSQSK
                        : : : : . .      : : : . . . . . . . . . . . . : .
gi+AHw-111 MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
          10      20      30      40      50

```

```

          60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLRPLV
          : . . . . :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEAAQTLSKI
          60      70      80      90      100      110

```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 87.8 bits: 22.3 E(): 6.5
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (4-73:197-278)

```

                                10          20
AAD-12          AQGAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... .  ...:  ..  ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
          170          180          190          200          210          220

          30          40          50          60          70          80
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQ--AGSAYIGYGMDTTATPLRPLV
          :: : . :          ...: . .  ....  ...:  ...: .. :  :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
          230          240          250          260          270          280

gi+AHw-330 TVAAGGYKV
          290

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.3 bits: 20.9 E(): 6.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (22-62:11-50)

```

          10          20          30          40          50
AAD-12 AQGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQ
          :: : :  .....  .....: : :  ...
gi+AHw-160          GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLDELN
          10          20          30          40

          60          70          80
AAD-12 QAGSAYIGYGMDTTATPLRPLV
          .  :
gi+AHw-160 ENKSKELQEKKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKILLKDL
          50          60          70          80          90          100

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)

initn: 47 initl: 47 opt: 59 Z-score: 87.2 bits: 22.9 E(): 7
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (40-77:198-242)

```

          10          20          30          40          50          60
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
          ...  ...:  ... :          :  ... :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
          170          180          190          200          210          220

          70          80
AAD-12 YIGYGMDT-TATPLRPLV
          .....: :  ..
gi+AHw-303 VLGFGMDTETARKVREGDDQQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
          230          240          250          260          270          280

```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
 Actinidia de (116 aa)
 initn: 34 initl: 34 opt: 51 Z-score: 85.8 bits: 20.6 E(): 8.4
 Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
 in 63 aa overlap (4-64:19-80)

```

                                10      20      30      40
AAD-12      A Q G A V F S A E V V P A V G G R T C F A D M R A A Y D A L D E A T R A L V - H Q R S A R
              :: ... . :::: . . .: . . : : :: :....:
gi+AHw-408  M V P K P L S L L L F L L L A L S A A V V G G R K L V A A G G W R P I E S L N S A - E V Q D V A Q F A V S E H N K Q A N
              10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  H S L V Y S Q S K L G H V Q Q - A G S A Y I G Y G M D T T A T P L R P L V
          : ... :... :... :
gi+AHw-408 D E L Q Y Q S V V R G Y T Q V V A G T N Y R L V I A A K D G A V V G N Y E A V V W D K P W M H F R N L T S F R K V
          60      70      80      90      100     110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 85.1 bits: 20.9 E(): 9.1
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (27-50:29-52)

```

                    10      20      30      40      50
AAD-12  A Q G A V F S A E V V P A V G G R T C F A D M R A A Y D A L D E A T R A L V H Q R S A R H S L V Y S Q S K L G H V Q
              : : :::: : . ...: .: ...:
gi+AHw-144  K T N K I V I T N D K G R L S K E E I E R M L A E A E K Y K A E D E A E A A R I S A K N A L E S Y A Y S L R N T L S D S
              10      20      30      40      50      60

```

```

                    60      70      80
AAD-12  Q A G S A Y I G Y G M D T T A T P L R P L V
gi+AHw-144  K V D E K L D A G D K Q K L T A E I D K T V Q W L D D N Q T A T K D E Y E S Q Q K E L E G V A N P I M M K F Y G A G G E
              70      80      90      100     110     120

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:08 2010 done: Fri Feb 5 12:56:08 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-l2: 120 - 199 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

opt      E()
+ADw- 20    2     0:+AD0-
   22    0     0:           one +AD0- represents 4 library sequences
   24    0     0:
   26    0     0:
   28    7     0:+AD0APQ-
   30    8     2:+ACoAPQ-
   32   15     8:+AD0AKgA9AD0-
   34   25    21:+AD0APQA9AD0APQAqAD0-
   36   30    44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
   38   43    72:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-       +ACo-
   40   84
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
   42  109
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP QA9AD0- +ACo-
   44  120
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP QA9AD0APQA9- +ACo-
   46  122  138:+AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
   48  184
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
   50  138
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP QA9AD0APQA9ACoAPQA9AD0APQ-
   52  107
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP QAq-
   54   71   91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
   56   83   76:+AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
   58   61   62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
   60   60   50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
   62   65   40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
   64   24   32:+AD0APQA9AD0APQA9- +ACo-
   66   29   25:+AD0APQA9AD0APQA9ACoAPQ-
   68   21   20:+AD0APQA9AD0AKgA9-
   70   14   16:+AD0APQA9ACo-
   72    7   12:+AD0APQAq-
   74    4   10:+AD0- +ACo-
   76    8    7:+AD0AKg-
   78    4    6:+AD0AKg-
   80    3    4:+ACo-
   82    7    3:+ACoAPO-

```



```

84      1      3:+ACo-
86      2      2:+ACo-
88      6      2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      1      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      3      1:+ACo-          :+ACoAPQA9-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     1      0:+AD0-          +ACoAPQ-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     1      0:+AD0-          +ACoAPQ-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120    0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.21610.00345+ADs- mu+AD0- 4.7967
0.179
mean+AF8-var+AD0-35.3882 8.775, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.215598
Kolmogorov-Smirnov statistic: 0.0556 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  74 27.6      0.23
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  64 24.7      0.58
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.8      1.9
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.9      2.1
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.9      2.1
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.4      4.1
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.4      4.2
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)  57 22.4      6.1
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.4      6.2
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.3      6.2
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  53 21.3      6.2

```

gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 (295)
 57 22.4 6.4
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.0 6.8
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.9 6.9
 gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-Actinidi (116)
 51 20.7 8.2
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152)
 52 20.9 8.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 113.9 bits: 27.6 E(): 0.23
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (14-74:309-363)

```

                                10      20      30      40
AAD-12      QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                : : : : : : : : : : : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
      280      290      300      310      320      330

```

```

                    50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVK
      : : : : : : : : : : : :
gi+AHw-113  ESMKWNWRTNKKDVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
      340      350      360      370      380      390

```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs- Blomia t (134 aa)
 initn: 38 initl: 38 opt: 64 Z-score: 106.6 bits: 24.7 E(): 0.58
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (3-61:9-65)

```

                                10      20      30      40      50
AAD-12      QGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                                : : : : : : : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLYLQHQ
      10      20      30      40      50

```

```

                    60      70      80
AAD-12  LGHVQQAGSAYIGYMDTTATPLRPLVK
      : : : : :
gi+AHw-111  LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 97.4 bits: 22.8 E(): 1.9

Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (19-70:26-77)

```

                10      20      30      40      50
AAD-12      QGAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                :::      :. . . : . . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKQNVN
                10      20      30      40      50      60

                60      70      80
AAD-12      GHVQQAGSAYIGYGMDTTATPLRPLVK
                : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGGLAQKRVAG
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)

initn: 39 initl: 39 opt: 62 Z-score: 96.7 bits: 23.9 E(): 2.1
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (3-73:183-265)

```

                10      20
AAD-12      QGAVFSAEVVPAVGG----RTCFADMRAAYDA
                : : . . . : : : : :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                160      170      180      190      200      210

                30      40      50      60      70      80
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVK
                : : : . : . : . . . . : : : : : : : : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                220      230      240      250      260      270

gi+AHw-168 TVAAGGYKV
                280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)

initn: 39 initl: 39 opt: 62 Z-score: 96.4 bits: 23.9 E(): 2.1
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (3-73:192-274)

```

                10      20
AAD-12      QGAVFSAEVVPAVGG----RTCFADMRAAYDA
                : : . . . : : : : :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                170      180      190      200      210      220

                30      40      50      60      70      80
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVK
                : : : . : . : . . . . : : : : : : : : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230      240      250      260      270      280

```

AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLVK

 ::: ::: ::: ::: ::: ::: ::: :::

10
20
30
40
50
 AAD-12 QGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
 : : : : : : : : : : : : : : : : : : : : : : : :

gi+AHw-111 MKFAIVLIACFAASVL-AQECHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
 10 20 30 40 50

 60 70 80
 AAD-12 LGHVQQAGSAYIGYMDTTATPLRPLVK
 : : :

gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
 60 70 80 90 100 110

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
 5.020 (295 aa)

initn: 34 init1: 34 opt: 57 Z-score: 87.9 bits: 22.4 E(): 6.4
 Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
 in 82 aa overlap (3-72:197-278)

 10 20
 AAD-12 QGAVFSAEVVPAVGG----RTCFADMRAAYDA
 :.. : :. ...:
 gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
 170 180 190 200 210 220

 30 40 50 60 70 80
 AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYMDTTATPLRPLVK
 :: : . : ..: : : : : : : :
 gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
 230 240 250 260 270 280

gi+AHw-330 TVAAGGYKV
 290

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)

initn: 38 init1: 38 opt: 52 Z-score: 87.4 bits: 21.0 E(): 6.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (21-61:11-50)

 10 20 30 40 50
 AAD-12 QGAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQ
 :.. : : : : : : : :
 gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLNE
 10 20 30 40

 60 70 80
 AAD-12 AGSAYIGYMDTTATPLRPLVK
 :

gi+AHw-160 NSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLKILLKDLK
 50 60 70 80 90 100

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)

initn: 47 init1: 47 opt: 59 Z-score: 87.3 bits: 22.9 E(): 6.9
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (39-76:198-242)

```
      10      20      30      40      50      60
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
      ... ..: ...: ...: ...:
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
      170      180      190      200      210      220
```

```
      70      80
AAD-12 YIGYGMDT-TATPLRPLVK
      .....: ..:
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230      240      250      260      270      280
```

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytoctystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 51 Z-score: 86.0 bits: 20.7 E(): 8.2
Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
in 63 aa overlap (3-63:19-80)

```
      10      20      30      40
AAD-12 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
      :: ... .: ::: . . .: . .: : : : : : : : : : : :
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
      10      20      30      40      50
```

```
      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTATPLRPLVK
      : ...: ...: ...:
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMWHFRNLTSFRKV
      60      70      80      90      100      110
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 85.3 bits: 20.9 E(): 8.9
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (26-49:29-52)

```
      10      20      30      40      50
AAD-12 QGAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
      : : ::: : . .: .: .:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
      10      20      30      40      50      60
```

```
      60      70      80
AAD-12 QAGSAYIGYGMDTTATPLRPLVK
gi+AHw-144 KVDEKLDAGDKQKLTAIEIDKTQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAGGE
      70      80      90      100      110      120
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:08 2010 done: Fri Feb 5 12:56:09 2010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 121 - 200 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]


```

56      82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58      60
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60      67
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
62      62      40:+AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
64      23      32:+AD0APQA9AD0APQA9AD0APQ- +ACo-
66      26      25:+AD0APQA9AD0APQA9AD0APQAq-
68      18      20:+AD0APQA9AD0APQA9ACo-
70      16      16:+AD0APQA9AD0APQAq-
72      5       12:+AD0APQ- +ACo-
74      9       10:+AD0APQA9ACo-
76      8       7:+AD0APQAq-
78      2       6:+AD0AKg-
80      4       4:+AD0AKg-
82      6       3:+ACoAPQ-
84      1       3:+ACo-
86      3       2:+ACo-
88      5       2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      2       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      3       1:+ACo-          :+ACoAPQA9-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     1       0:+AD0-          +ACoAPQ-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     1       0:+AD0-          +ACoAPQ-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.08520.00338+ADs- mu+AD0- 5.5129
0.175
mean+AF8-var+AD0-35.8947 9.001, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.214072
Kolmogorov-Smirnov statistic: 0.0474 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 74 27.5 0.24

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 64 Z-score: 106.0 bits: 24.6 E(): 0.62
 Smith-Waterman score: 64+ADs- 29.508+ACU- identity (63.934+ACU- similar)
 in 61 aa overlap (2-60:9-65)

```

              10      20      30      40      50
AAD-12      GAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
              : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
              10      20      30      40      50

```

```

              60      70      80
AAD-12      LGHVQQAGSAYIGYGMDDTTATPLRPLVKV
              : : : : :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 96.9 bits: 22.8 E(): 2
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (18-69:26-77)

```

              10      20      30      40      50
AAD-12      GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
              : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAIPVYEQSLTKHSPDVLAFKVN
              10      20      30      40      50      60

```

```

              60      70      80
AAD-12      GHVQQAGSAYIGYGMDDTTATPLRPLVKV
              : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRVAG
              70      80      90      100      110      120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
 +AFs-Phl (281 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 96.4 bits: 23.9 E(): 2.1
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (2-72:183-265)

```

              10      20
AAD-12      GAVFSAEVVPAVGG----RTCFADMRAAYDA
              : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
              160      170      180      190      200      210

```

```

              30      40      50      60      70
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLVK
              : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
              220      230      240      250      260      270

```

80
 AAD-12 V

gi+AHw-168 TVAAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)

initn: 39 initl: 39 opt: 62 Z-score: 96.2 bits: 23.9 E(): 2.2
Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
in 83 aa overlap (2-72:192-274)

```

                                10          20
AAD-12                      GAVFSAEVVPAVGG----RTCFADMRAAYDA
                                :... . ...: .. ...:
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                170          180          190          200          210          220
```

```

                30          40          50          60          70
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVK
                :: : . : ..: . . .... :.: :.: .. : :.:
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230          240          250          260          270          280
```

80
AAD-12 V

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)

initn: 41 initl: 41 opt: 57 Z-score: 91.0 bits: 22.4 E(): 4.3
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (19-71:93-149)

```

                                10          20          30          40
AAD-12                      GAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....: :.: :. . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70          80          90          100          110          120
```

```

                50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKV
                .. : ..: .: .....: : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130          140          150          160          170          180
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)

initn: 41 initl: 41 opt: 57 Z-score: 90.8 bits: 22.4 E(): 4.4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (19-71:97-153)

```

                                10          20          30          40
AAD-12                      GAVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
```

```
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70          80          90          100          110          120
```

```
50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKV
      .. :   .. :   ..... :   :   :
```

```
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130          140          150          160          170          180
```

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 initl: 34 opt: 57 Z-score: 88.0 bits: 22.3 E(): 6.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (2-71:186-267)

```
10          20
AAD-12 GAVFSAEVVPAVGG----RTCFADMRAAYDA
      :... . .... :.. ..:::
gi+AHw-285 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
              160          170          180          190          200          210
```

```
30          40          50          60          70
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTATPLRPLVK
      :: : . :   ..: . . .... ::: :.. : :::
gi+AHw-285 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
              220          230          240          250          260          270
```

```
80
AAD-12 V
```

```
gi+AHw-285 TVAAGGYKV
              280
```

+AD4APg-gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p
5.020 (287 aa)
initn: 34 initl: 34 opt: 57 Z-score: 87.9 bits: 22.3 E(): 6.4
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (2-71:189-270)

```
10          20
AAD-12 GAVFSAEVVPAVGG----RTCFADMRAAYDA
      :... . .... :.. ..:::
gi+AHw-330 GELQIIDKIDAAFKVAATAAATAPADTVFEAAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
              160          170          180          190          200          210
```

```
30          40          50          60          70
AAD-12 LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTATPLRPLVK
      :: : . :   ..: . . .... ::: :.. : :::
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
              220          230          240          250          260          270
```

```
80
AAD-12 V
```

gi+AHw-330 TVAAGGYKV
280

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (2-60:9-65)

	10	20	30	40	50
AAD-12	GAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK				
	:	:::	:	:	:
gi+AHw-420	MKFAIVLIACFAASVL-AQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ				
	10	20	30	40	50

	60	70	80
AAD-12	LGHVQQAGSAYIGYGMDDTTATPLRPLVKV		
	:	:
gi+AHw-420	LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI		
	60	70	80

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (2-60:9-65)

	10	20	30	40	50
AAD-12	GAVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK				
	:	:::	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ				
	10	20	30	40	50

	60	70	80
AAD-12	LGHVQQAGSAYIGYGMDDTTATPLRPLVKV		
	:	:
gi+AHw-111	LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI		
	60	70	80

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)
initn: 34 initl: 34 opt: 57 Z-score: 87.7 bits: 22.3 E(): 6.6
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (2-71:197-278)

	10	20
AAD-12	GAVFSAEVVPAVGG----RTCFADMRAAYDA	
	:
gi+AHw-330	QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ	
	170	220

	30	40	50	60	70
AAD-12	LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLVK				

AAD-12 10 20 30 40
GAVFSAEVPVAVGGRTCFADMRAAYDALDEATRALV-HORSAR

```

      :: ... . :...: . . .: . . : : :. ....:
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMDTTATPLRPLVKV
      : ... :...: ...:

```

```

gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 85.0 bits: 20.9 E(): 9.3
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (25-48:29-52)

```

      10      20      30      40      50
AAD-12 GAVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
      : : ...: . . ...: . . ...:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
      10      20      30      40      50      60

```

```

      60      70      80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKV

```

```

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
      70      80      90      100      110      120

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:10 2010 done: Fri Feb 5 12:56:10 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 122 - 201 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:

```

one +AD0- represents 3 library sequences

[illegible]

```

88      5      2: +ACoAPQ-          inset +AD0- represents 1 library
sequences
90      2      1: +ACo-
92      0      1: +ACo-          : +ACo-
94      0      1: +ACo-          : +ACo-
96      3      1: +ACo-          : +ACoAPQA9-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     1      0: +AD0-          +ACoAPQ-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0: +AD0-          +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.19250.0032+ADs- mu+AD0- 4.9319
0.166
mean+AF8-var+AD0-35.7991 8.999, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.214357
Kolmogorov-Smirnov statistic: 0.0474 (N+AD0-29) at 46

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   74 27.5      0.24
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   64 24.6      0.61
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 22.8      2
gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 ( 281)
62 23.9      2.1
gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 ( 290)
62 23.9      2.2
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.4      4.3
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.4      4.4
gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName: Full+AD0-P
( 284)   57 22.3      6.3
gi+AHw-3309047+AHw-gb+AHw-AAC25998.1+AHw- group V allergen Phl p 5 ( 287)
57 22.3      6.4
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
53 21.2      6.5
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   53 21.2      6.5
gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p 5 ( 295)
57 22.3      6.6

```

```
+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
  initn: 58 initl: 58 opt: 58 Z-score: 97.1 bits: 22.8 E(): 2
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (17-68;26-77)
```

```

                10      20      30      40      50
AAD-12      AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                :::      :. . . : . . . . . . . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQQLSTKHSVPDVLAFKVN
                10      20      30      40      50      60

```

```

                60      70      80
AAD-12      GHVQQAGSAYIGYGMDTTATPLRPLVKH
                : : : : : : : : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGKLGGLAQKRVAG
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
 +AFs-Phl (281 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 96.4 bits: 23.9 E(): 2.1
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (1-71:183-265)

```

                10      20
AAD-12      AVFSAEVVPAVGG----RTCFADMRAAYDA
                : : . . . : : : : : : :
gi+AHw-168 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                160      170      180      190      200      210

```

```

                30      40      50      60      70
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVK
                : : : . : . : . . . . . : : : : : : : : : :
gi+AHw-168 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                220      230      240      250      260      270

```

```

                80
AAD-12      VH

```

```

gi+AHw-168 TVAAGGYKV
                280

```

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
 5.020 (290 aa)
 initn: 39 initl: 39 opt: 62 Z-score: 96.2 bits: 23.9 E(): 2.2
 Smith-Waterman score: 62+ADs- 26.506+ACU- identity (55.422+ACU- similar)
 in 83 aa overlap (1-71:192-274)

```

                10      20
AAD-12      AVFSAEVVPAVGG----RTCFADMRAAYDA
                : : . . . : : : : : : :
gi+AHw-330 QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
                170      180      190      200      210      220

```

```

                30      40      50      60      70
AAD-12      LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVK
                : : : . : . : . . . . . : : : : : : : : : :
gi+AHw-330 AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAA
                230      240      250      260      270      280

```

80
AAD-12 VH

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.0 bits: 22.4 E(): 4.3
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (18-70:93-149)

	10	20	30	40
AAD-12	AVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH			
		::: ::
gi+AHw-144	AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE			
	70	80	90	100 110 120
	50	60	70	80
AAD-12	SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVH			
	.. : ... : : : : : : : :			
gi+AHw-144	TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK			
	130	140	150	160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 90.9 bits: 22.4 E(): 4.4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (18-70:97-153)

	10	20	30	40
AAD-12	AVFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH			
		::: ::
gi+AHw-622	AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE			
	70	80	90	100 110 120
	50	60	70	80
AAD-12	SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVH			
	.. : ... : : : : : : : :			
gi+AHw-622	TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK			
	130	140	150	160 170 180

+AD4APg-gi+AHw-2851457+AHw-sp+AHw-Q40963.2+AHw-MPA5B+AF8-PHLPR RecName:
Full+AD0-Polle (284 aa)
initn: 34 initl: 34 opt: 57 Z-score: 88.0 bits: 22.3 E(): 6.3
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (1-70:186-267)

	10	20
AAD-12	AVFSAEVVPAVGG----RTCFADMRAAYDA	

gi+AHw-285	QIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDITYKCIPSLEAAVKQ	
	160	170 180 190 200 210

```

          60          70          80
AAD-12 LGHVQQAGSAYIGYGMDDTATPLRPLVKVH
      : . . . :
gi+AHw-420 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKI
          60          70          80          90         100         110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 53 Z-score: 87.8 bits: 21.2 E(): 6.5
Smith-Waterman score: 53+ADs- 27.869+ACU- identity (62.295+ACU- similar)
in 61 aa overlap (1-59:9-65)

```

                10         20         30         40         50
AAD-12      AVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
              : : : : : . : : : : : : : : : : : : : : : : :
gi+AHw-111  MKFAIVLIACFAASVL-AQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
              10         20         30         40         50

```

```

                60         70         80
AAD-12  LGHVQQAGSAYIGYGMDDTTATPLRPLVKVH
              : : : : :
gi+AHw-111  LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
              60         70         80         90        100        110

```

+AD4APg-gi+AHw-3309041+AHw-gb+AHw-AAC25995.1+AHw- group V allergen Phl p
5.020 (295 aa)

initn: 34 initl: 34 opt: 57 Z-score: 87.7 bits: 22.3 E(): 6.6
Smith-Waterman score: 57+ADs- 25.610+ACU- identity (54.878+ACU- similar)
in 82 aa overlap (1-70:197-278)

```

                                10         20
AAD-12      AVFSAEVVPAVGG----RTCFADMRAAYDA
                                : : . : : : : : : : : :
gi+AHw-330  QIIDKIDAAFKAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQ
              170        180        190        200        210        220

```

```

                30         40         50         60         70
AAD-12  LDEATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDDTTATPLRPLVK
              : : : . : : : : : : : : : : : : : : : : :
gi+AHw-330  AYAATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAA
              230        240        250        260        270        280

```

80
AAD-12 VH

gi+AHw-330 TVAAGGYKV
290

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.2 bits: 20.9 E(): 7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (19-59:11-50)

```

                10         20         30         40         50
AAD-12  AVFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAG
              : : : : : : : : : : : : : : : : : : : :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQDELNENK
              10         20         30         40

```

60 70 80
AAD-12 SAYIGYGMTTATPLRPLVKVH
:
gi+AHw-160 SKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKILLKDLKET
50 60 70 80 90 100

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 87.1 bits: 22.9 E(): 7.1
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (37-74:198-242)

10 20 30 40 50 60
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
::: :::: :::: : : :::
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
170 180 190 200 210 220

70 80
AAD-12 YIGYGMT-TATPLRPLVKVH
::: :::
gi+AHw-303 VLGFGMTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
230 240 250 260 270 280

+AD4APg-gi+AHw-40807635+AHw-gb+AHw-AAR92223.1+AHw- phytocystatin +AFs-
Actinidia de (116 aa)
initn: 34 initl: 34 opt: 51 Z-score: 85.7 bits: 20.6 E(): 8.4
Smith-Waterman score: 51+ADs- 28.571+ACU- identity (60.317+ACU- similar)
in 63 aa overlap (1-61:19-80)

10 20 30 40
AAD-12 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALV-HQRSAR
::: :::: :::: : : :::
gi+AHw-408 MVPKPLSLLLFLLLALSAAVVGGRKLVAAGGWRPIESLNSA-EVQDVAQFAVSEHNKQAN
10 20 30 40 50

50 60 70 80
AAD-12 HSLVYSQSKLGHVQQ-AGSAYIGYGMTTATPLRPLVKVH
: :::: :::: :
gi+AHw-408 DELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPWMHFRNLTSFRKV
60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 85.1 bits: 20.9 E(): 9.2
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (24-47:29-52)

10 20 30 40 50
AAD-12 AVFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
: : :::: : . :::: : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSRLNTLSDS
10 20 30 40 50 60

60 70 80
AAD-12 QAGSAYIGYMDTTATPLRPLVKVH

gi+AHw-144 KVDEKLDAGDKQLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAGGE

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:10 2010 done: Fri Feb 5 12:56:10 2010
Total Scan time: 0.080 Total Display time: 0.010

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 123 - 202 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

Kolmogorov-Smirnov statistic: 0.0578 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 74 27.5 0.25

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
60 23.4 1.4

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 58 22.9 1.9

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
57 22.5 4

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
(204) 57 22.5 4.1

gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281)
57 22.4 5.9

gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290)
57 22.4 6.1

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
52 21.0 6.5

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
59 22.9 6.8

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
52 21.0 7.4

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
52 21.0 7.4

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
(152) 52 21.0 8.5

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 57 initl: 57 opt: 74 Z-score: 113.3 bits: 27.5 E(): 0.25

Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
in 61 aa overlap (11-71:309-363)

			10	20	30	40
AAD-12			VFSAEVVPAVGGR	TCFADMRAAYDALDE	ATRALVHQ	SAR
			:: :	: :.	... :	...
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR					-----HGEAAA
	280	290	300	310	320	330

		50	60	70	80
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYGM	TTATPLRPLVKVHP			
	: :: . ::
gi+AHw-113	ESMKWNWRTNKDVL	ENGAI	FV	ASGVDPVLTPEQSAGMIP	AE
	340	350	360	370	380

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 60 Z-score: 99.8 bits: 23.4 E(): 1.4
 Smith-Waterman score: 60+ADs- 28.814+ACU- identity (64.407+ACU- similar)
 in 59 aa overlap (2-58:11-65)

```

                10      20      30      40
AAD-12      VFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK
                :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi+AHw-111 MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                10      20      30      40      50

                50      60      70      80
AAD-12 LGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
                : .... :
gi+AHw-111 LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKI
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 97.5 bits: 22.9 E(): 1.9
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (16-67:26-77)

```

                10      20      30      40      50
AAD-12      VFSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                :: :: :: :: :: :: :: :: :: :: ::
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAIPVYQLSTKHSVPDVLAFKVN
                10      20      30      40      50      60

                60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
                ::::: : :: :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAEKLGGLAQKRVAG
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 91.5 bits: 22.5 E(): 4
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (17-69:93-149)

```

                10      20      30      40
AAD-12      VFSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                ::::: :: :: :: :: ::
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120

                50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
                .. : .. : ::::: : :: :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)

30 40 50 60 70
AAD-12 EATRALVHO-----RSARHSLVYSOSKLGHVQ--AGSAYIGYGMDDTTATPLRPLVKVH

10 20 30 40 50
AAD-12 VFSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHORSARHSLVYSOSKL

```
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
              10      20      30      40      50
```

```
60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
      .... :
```

```
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
              60      70      80      90      100      110
```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 86.8 bits: 21.0 E(): 7.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (18-58:26-65)

```
10      20      30      40      50
AAD-12 VFSAEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
              .... :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
              10      20      30      40      50
```

```
60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
              60      70      80      90      100      110
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)

initn: 52 initl: 52 opt: 52 Z-score: 85.7 bits: 21.0 E(): 8.5
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (23-46:29-52)

```
10      20      30      40      50
AAD-12 VFSAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
              : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAAARISAKNALESYAYSLRNTLSDS
              10      20      30      40      50      60
```

```
60      70      80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHP
```

```
gi+AHw-144 KVDEKLDAGDKQKLTAIEDKTVQWLLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
              70      80      90      100      110      120
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:10 2010 done: Fri Feb 5 12:56:11 2010

Total Scan time: 0.080 Total Display time: 0.010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]


```

60      68
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
62      60      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      48      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66      22      25:+AD0APQA9AD0APQA9AD0APQAq-
68      20      20:+AD0APQA9AD0APQA9ACo-
70      24      16:+AD0APQA9AD0APQAqAD0APQ-
72      11      12:+AD0APQA9ACo-
74      5       10:+AD0APQ- +ACo-
76      11      7:+AD0APQAqAD0-
78      6       6:+AD0AKg-
80      7       4:+AD0AKgA9-
82      4       3:+ACoAPQ-
84      2       3:+ACo-
86      1       2:+ACo-
88      5       2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      1       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     1       0:+AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     1       0:+AD0-          +ACoAPQ-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.39720.00318+ADs- mu+AD0- 2.8909
0.165
mean+AF8-var+AD0-36.1929 9.478, 0's: 2 Z-trim: 3 B-trim: 30 in 1/42
Lambda+AD0- 0.213188
Kolmogorov-Smirnov statistic: 0.0612 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 74 27.7 0.21
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 60 23.7 1.2
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 58 23.1 1.6
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6 3.6

```

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
 (204) 57 22.6 3.7
 gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5 (281)
 57 22.6 5.3
 gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p 5 (290)
 57 22.6 5.5
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.2 5.7
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 23.1 6.2
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 52 21.2 6.6
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.2 6.6
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.2 7.6

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 114.5 bits: 27.7 E(): 0.21
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (10-70:309-363)

	10	20	30	
AAD-12	FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR			
	:	:	:	:
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA			
	280	290	300	310
	40	50	60	70
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPE			
	:	:	:	:
gi+AHw-113	ESMKWNWRTNKKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP			
	340	350	360	370

gi+AHw-113 GAPC

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 60 Z-score: 101.0 bits: 23.7 E(): 1.2
 Smith-Waterman score: 60+ADs- 28.814+ACU- identity (64.407+ACU- similar)
 in 59 aa overlap (1-57:11-65)

	10	20	30	40
AAD-12	FSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSK			
	:	:	:	:
gi+AHw-111	MKFAIVLIACFAASVL-AQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ			
	10	20	30	40
	50	60	70	80
AAD-12	LGHVQQAGSAYIGYMDTTATPLRPLVKVHPE			
	:	:	:	:
gi+AHw-111	LDELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEAAQTLSKI			

60 70 80 90 100 110

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 98.6 bits: 23.1 E(): 1.6
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (15-66:26-77)

AAD-12 10 20 30 40
FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
::: . . . : . . . :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFAKVN
10 20 30 40 50 60

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE
: : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAG
70 80 90 100 110 120

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 92.4 bits: 22.6 E(): 3.6
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (16-68:93-149)

AAD-12 10 20 30 40
FSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
: : : : : :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE
: : : : : : : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 92.2 bits: 22.6 E(): 3.7
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (16-68:97-153)

AAD-12 10 20 30 40
FSAEVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
: : : : : :
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE
: : : : : : : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK

130 140 150 160 170 180

+AD4APg-gi+AHw-1684718+AHw-emb+AHw-CAB05371.1+AHw- major allergen Phl p 5
+AFs-Phl (281 aa)

initn: 39 initl: 39 opt: 57 Z-score: 89.4 bits: 22.6 E(): 5.3
Smith-Waterman score: 57+ADs- 25.926+ACU- identity (54.321+ACU- similar)
in 81 aa overlap (1-69:185-265)

AAD-12 10 20
FSAEVVPAVGG----RTCFAADMRAAYDALD
:. . .: :. .: :
gi+AHw-168 160 170 180 190 200 210
IDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQAY

30 40 50 60 70
AAD-12 EATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVKVH
:: : . : ..: . . .: :. : : : :
gi+AHw-168 220 230 240 250 260 270
AATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAATV

80
AAD-12 PE

gi+AHw-168 AAGGYKV
280

+AD4APg-gi+AHw-3309045+AHw-gb+AHw-AAC25997.1+AHw- group V allergen Phl p
5.020 (290 aa)

initn: 39 initl: 39 opt: 57 Z-score: 89.1 bits: 22.6 E(): 5.5
Smith-Waterman score: 57+ADs- 25.926+ACU- identity (54.321+ACU- similar)
in 81 aa overlap (1-69:194-274)

AAD-12 10 20
FSAEVVPAVGG----RTCFAADMRAAYDALD
:. . .: :. .: :
gi+AHw-330 170 180 190 200 210 220
IDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKESTGGAYDTYKCIPSLEAAVKQAY

30 40 50 60 70
AAD-12 EATRALVHQ-----RSARHSLVYSQSKLGHVQQ--AGSAYIGYGMDTTATPLRPLVKVH
:: : . : ..: . . .: :. : : : :
gi+AHw-330 230 240 250 260 270 280
AATVAAAPQVKYAVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAATV

80
AAD-12 PE

gi+AHw-330 AAGGYKV
290

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 88.8 bits: 21.2 E(): 5.7

Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (17-57:11-50)

```

      10      20      30      40      50
AAD-12 FSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSA
      ::  :: :  :::::  :::::  ::  ::  ::
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLENENKSK
      10      20      30      40      50

```

```

      60      70      80
AAD-12 YIGYGMDTTATPLRPLVKVHPE

gi+AHw-160 ELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLISKILLKDLKETEQ
      60      70      80      90     100     110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 88.2 bits: 23.1 E(): 6.2
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (35-72:198-242)

```

      10      20      30      40      50
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
      ::  :::  :::  ::  ::  ::  ::
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQGERYGLRGGQQILADNVFKGFNMEALAD
      170     180     190     200     210     220

```

```

      60      70      80
AAD-12 YIGYGMDT-TATPLRPLVKVHPE
      :::::  ::  ::
gi+AHw-303 VLGFGMDTETARKVVRGDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230     240     250     260     270     280

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (17-57:26-65)

```

      10      20      30      40
AAD-12 FSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      ::  :: :  :::::  :::::  ::  ::
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPE
      .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLISKIL
      60      70      80      90     100     110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.7 bits: 21.2 E(): 6.6

Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (17-57:26-65)

```

                10         20         30         40
AAD-12          FSAEVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                ::  ::  :  :::::  :::::  ::  ::
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50

                50         60         70         80
AAD-12          GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPE
                ....  :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 init1: 52 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (22-45:29-52)

```

                10         20         30         40         50
AAD-12          FSAEVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                :  :  ::  :  .  .::  ::  ::
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10         20         30         40         50         60

                60         70         80
AAD-12          QAGSAYIGYGMDDTTATPLRPLVKVHPE

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAGGE
                70         80         90         100         110         120

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:11 2010 done: Fri Feb 5 12:56:11 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 125 - 204 80 aa - 80 aa

[illegible]

```

82      5      3:+ACoAPQ-
84      3      3:+ACo-
86      1      2:+ACo-
88      4      2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      1      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     1      0:+AD0-          +ACoAPQ-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120    0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.25560.00328+ADs- mu+AD0- 3.5122
0.170
mean+AF8-var+AD0-36.6945 9.509, 0's: 2 Z-trim: 3 B-trim: 30 in 1/42
Lambda+AD0- 0.211726
Kolmogorov-Smirnov statistic: 0.0604 (N+AD0-29) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   74 27.7      0.21
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 23.0      1.7
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   56 22.4      2.9
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6      3.6
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.6      3.7
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2      5.9
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.1      6.1
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.2      6.7
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2      6.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.1      7.7

```


+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 57 initl: 57 opt: 74 Z-score: 114.5 bits: 27.7 E(): 0.21
 Smith-Waterman score: 74+ADs- 24.590+ACU- identity (54.098+ACU- similar)
 in 61 aa overlap (9-69:309-363)

```

                                10      20      30
AAD-12      SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                ::: : : : . . . : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
          280      290      300      310      320      330

          40      50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPET
          :. . . : . :. . . :. :. :
gi+AHw-113  ESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
          340      350      360      370      380      390

gi+AHw-113  GAPC

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 98.3 bits: 23.0 E(): 1.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (14-65:26-77)

```

                                10      20      30      40
AAD-12      SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                ::: :. . . : . . . : . . .
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVN
          10      20      30      40      50      60

          50      60      70      80
AAD-12  GHVQQAGSAYIGYMDTTATPLRPLVKVHPET
          :. . . . : . :
gi+AHw-527  DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRVAG
          70      80      90      100      110      120

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 56 Z-score: 94.2 bits: 22.4 E(): 2.9
 Smith-Waterman score: 56+ADs- 28.070+ACU- identity (61.404+ACU- similar)
 in 57 aa overlap (2-56:12-65)

```

                                10      20      30      40
AAD-12      SAEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                : : : : . :. : : . . . . . : :
gi+AHw-111  MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
          10      20      30      40      50

          50      60      70      80
AAD-12  GHVQQAGSAYIGYMDTTATPLRPLVKVHPET
          . . . :

```

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLISKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 92.3 bits: 22.6 E(): 3.6
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (15-67:93-149)

10 20 30
AAD-12 SAEVVPVAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
.:.:.: :.:.: .:.
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

40 50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
.:. :.:. :.:. :.:. :.:. :.
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 92.2 bits: 22.6 E(): 3.7
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (15-67:97-153)

10 20 30
AAD-12 SAEVVPVAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
.:.:.: :.:.: .:.
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

40 50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
.:. :.:. :.:. :.:. :.:. :.
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 88.6 bits: 21.2 E(): 5.9
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (16-56:11-50)

10 20 30 40 50
AAD-12 SAEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAY
.:. :. :. :. :. :. :. :. :. :.
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQDELNENKSKE
10 20 30 40 50

60 70 80
AAD-12 IGYGMDDTTATPLRPLVKVHPET

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
 ::: :

```
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLISKIL
          60          70          80          90         100         110
```

```
+AD4-+AD4-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
```

```
  initn: 52 initl: 52 opt: 52 Z-score: 86.5 bits: 21.1 E(): 7.7
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (21-44:29-52)
```

```

          10          20          30          40          50
AAD-12      SAEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
              : : : : : : : : : : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
          10          20          30          40          50          60
```

```

          60          70          80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKVHPET
```

```
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
          70          80          90         100         110         120
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:12 2010 done: Fri Feb 5 12:56:12 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 126 - 205 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      3      2:+ACo-
      32      8      8:+AD0APQAq-
      34      28     21:+AD0APQA9AD0APQA9ACoAPQA9AD0-
      36      24     44:+AD0APQA9AD0APQA9AD0APQ-      +ACo-
```

inset +AD0- represents 1 library

```

106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      1      0: +AD0-      +ACoAPQ-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.30480.00328+ADs- mu+AD0- 3.0729
0.170
mean+AF8-var+AD0-37.1335 9.635, 0's: 2 Z-trim: 3 B-trim: 30 in 1/42
Lambda+AD0- 0.210471
Kolmogorov-Smirnov statistic: 0.0694 (N+AD0-29) at 48

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   77 28.6      0.11
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 23.0      1.7
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   56 22.4      2.8
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6      3.6
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.6      3.7
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2      5.8
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.1      6.1
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.2      6.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2      6.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.2      7.6

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 60 initl: 60 opt: 77 Z-score: 119.2 bits: 28.6 E(): 0.11
Smith-Waterman score: 77+ADs- 23.288+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (8-80:309-375)

```

```

                                10      20      30
AAD-12      AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                : : : : : : : : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
      280      290      300      310      320      330

      40      50      60      70      80

```

AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG

... .. : . : . . . : : . : :

gi+AHw-113 ESMKWNWRTNKNVDLENGAIFVASGVDPVLTPEQSAGMIPAEPEGESALSLTSSAGVLSCQP
340 350 360 370 380 390

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:

Full+AD0-Thior (121 aa)

initn: 58 initl: 58 opt: 58 Z-score: 98.4 bits: 23.0 E(): 1.7

Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)

in 52 aa overlap (13-64:26-77)

AAD-12 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
::: . . . : . . . :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFKVN
10 20 30 40 50 60

AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
: : : : : : : : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGGGLAQKRVAG
70 80 90 100 110 120

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 56 Z-score: 94.2 bits: 22.4 E(): 2.8

Smith-Waterman score: 56+ADs- 28.070+ACU- identity (61.404+ACU- similar)

in 57 aa overlap (1-55:12-65)

AAD-12 AEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
: : : : . :
gi+AHw-111 MKFAIVLIACFAASVLAQGHPKPKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
10 20 30 40 50

AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETG
: : : : : : : : : : : : : : : :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLISKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)

initn: 41 initl: 41 opt: 57 Z-score: 92.4 bits: 22.6 E(): 3.6

Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)

in 58 aa overlap (14-66:93-149)

AAD-12 AEVVPVAVGGRTCFADMRAA----YDALDEATRALVHQRSARH
: : : : : : : : : : : : : : : :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE

```

              70          80          90          100          110          120
      40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETG
      .. :   .. :   ..... :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 92.2 bits: 22.6 E(): 3.7
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (14-66:97-153)

```

              10          20          30
AAD-12          AEVVPVAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
              ..... :   :   :   :
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70          80          90          100          110          120

```

```

      40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETG
      .. :   .. :   ..... :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.7 bits: 21.2 E(): 5.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (15-55:11-50)

```

              10          20          30          40          50
AAD-12 AEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYI
              :   :   :   ..... :   :   :   :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDDELNENKSKEL
              10          20          30          40          50

```

```

      60          70          80
AAD-12 GYGMDTTATPLRPLVKVHPETG
gi+AHw-160 QEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKV
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 88.3 bits: 23.1 E(): 6.1
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (33-70:198-242)

```

              10          20          30          40          50
AAD-12 VVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
              :   :   :   ..... :   :   :   :
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD

```


170 180 190 200 210 220

60 70 80
AAD-12 YIGYGMT-TATPLRPLVKVHPETG
..... :: ::
gi+AHw-303 VLGFMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
230 240 250 260 270 280

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (15-55:26-65)

10 20 30 40
AAD-12 AEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETG
.... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.7 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (15-55:26-65)

10 20 30 40
AAD-12 AEVVPVAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : :
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETG
.... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 86.6 bits: 21.2 E(): 7.6
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (20-43:29-52)

10 20 30 40 50
AAD-12 AEVVPVAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
: : :: : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAAARISAKNALESYAYSLRNTLSDS

```

                10             20             30             40             50             60
        60             70             80
AAD-12  QAGSAYIGYGMDDTTATPLRPLVKVHPETG

gi+AHw-144  KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
                70             80             90             100             110             120

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:12 2010 done: Fri Feb 5 12:56:12 2010
Total Scan time: 0.080 Total Display time: 0.000

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 127 - 206 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      4      2: +ACoAPQ-
      32      8      8: +AD0APQAq-
      34     12     21: +AD0APQA9AD0- +ACo-
      36     31     44: +AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      38     43     72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      40     90
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9- +ACo-
      42     100
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0- +ACo-
      44     143
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0- +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
      46     114
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-

```

inset +AD0- represents 1 library sequences

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po

(396) 77 28.4 0.13

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T

(121) 58 22.9 1.8

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)

57 22.6 3.8

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl

(204) 57 22.6 3.9

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (

134) 54 21.7 4.6

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)

52 21.1 6.1

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (

465) 59 23.0 6.4

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (

134) 52 21.1 6.9

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)

52 21.1 6.9

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-

(152) 52 21.1 7.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:

Full+AD0-Pollen (396 aa)

initn: 60 initl: 60 opt: 77 Z-score: 118.4 bits: 28.4 E(): 0.13

Smith-Waterman score: 77+ADs- 23.288+ACU- identity (50.685+ACU- similar)

in 73 aa overlap (7-79:309-375)

			10	20	30	
AAD-12			EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR			
			:: :	: :	... :	: ...
gi+AHw-113	HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA					
	280 290 300 310 320 330					

	40	50	60	70	80	
AAD-12	HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR					
	: ::	. ::	. :	:
gi+AHw-113	ESMKWNWRTNKNVDLENGAIFVASGVDPVLTPEQSAGMIPAEPEGESALSLTSSAGVLSCQP					
	340 350 360 370 380 390					

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:

Full+AD0-Thior (121 aa)

initn: 58 initl: 58 opt: 58 Z-score: 97.9 bits: 22.9 E(): 1.8

Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)

in 52 aa overlap (12-63:26-77)

```

                10          20          30          40
AAD-12          EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                :::          :. . . : . . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVN
                10          20          30          40          50          60

```

```

                50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR
                : . . . . : . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGGLAQKRVAG
                70          80          90          100          110          120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.9 bits: 22.6 E(): 3.8
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (13-65:93-149)

```

                10          20          30
AAD-12          EVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                . . . . . : : : : . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70          80          90          100          110          120

```

```

                40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR
                . . : . . . : . . . . . : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130          140          150          160          170          180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.8 bits: 22.6 E(): 3.9
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (13-65:97-153)

```

                10          20          30
AAD-12          EVVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                . . . . . : : : : . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70          80          90          100          110          120

```

```

                40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGR
                . . : . . . : . . . . . : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130          140          150          160          170          180

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 54 Z-score: 90.5 bits: 21.7 E(): 4.6
Smith-Waterman score: 54+ADs- 27.778+ACU- identity (62.963+ACU- similar)
in 54 aa overlap (3-54:15-65)

```

                10         20         30         40
AAD-12      EVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
              : : : .   : :   : :   : :   : :   : :   : :
gi+AHw-111  MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
              10         20         30         40         50

```

```

                50         60         70         80
AAD-12      GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR
              .... :
gi+AHw-111  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
              60         70         80         90        100        110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.3 bits: 21.1 E(): 6.1
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (14-54:11-50)

```

                10         20         30         40         50
AAD-12      EVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIG
              : : : .   : :   : :   : :   : :   : :   : :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDELNENKSKELQ
              10         20         30         40         50

```

```

                60         70         80
AAD-12      YGMDDTTATPLRPLVKVHPETGR
gi+AHw-160  EKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVK
              60         70         80         90        100        110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 87.9 bits: 23.0 E(): 6.4
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (32-69:198-242)

```

                10         20         30         40         50
AAD-12      VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
              : : : : : : : : : : : : : : : :
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
              170        180        190        200        210        220

```

```

                60         70         80
AAD-12      YIGYGMDDTTATPLRPLVKVHPETGR
              : : : : : : : : : : : :
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230        240        250        260        270        280

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.3 bits: 21.1 E(): 6.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (14-54:26-65)

```

                10         20         30         40
AAD-12          EVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  :  :::::  :::::  :::  ::
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR
                .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.3 bits: 21.1 E(): 6.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (14-54:26-65)

```

                10         20         30         40
AAD-12          EVVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  :  :::::  :::::  :::  ::
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10         20         30         40         50

```

```

                50         60         70         80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGR
                .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.2 bits: 21.1 E(): 7.9
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (19-42:29-52)

```

                10         20         30         40         50
AAD-12          EVVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                : : :::  : .  ..:  ::  :::
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10         20         30         40         50         60

```

```

                60         70         80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGR
gi+AHw-144 KVDEKLDAGDKQKLTAIEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
                70         80         90         100         110         120

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:12 2010 done: Fri Feb 5 12:56:13 2010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 128 - 207 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]


```

58      72
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-+AD0-
60      67
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
62      49      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64      47      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66      17      25:+AD0APQA9AD0APQA9- +ACo-
68      28      20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
70      36      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
72          6      12:+AD0APQ- +ACo-
74      10      10:+AD0APQA9ACo-
76      12          7:+AD0APQAqAD0-
78      11          6:+AD0AKgA9AD0-
80          1          4:+AD0AKg-
82          7          3:+ACoAPQA9-
84          1          3:+ACo-
86          4          2:+ACoAPQ-
88          1          2:+ACo- inset +AD0- represents 1 library sequences
90          2          1:+ACo-
92          1          1:+ACo- :+ACo-
94          0          1:+ACo- :+ACo-
96          1          1:+ACo- :+ACo-
98          0          0: +ACo-
100         0          0: +ACo-
102         0          0: +ACo-
104         0          0: +ACo-
106         0          0: +ACo-
108         0          0: +ACo-
110         0          0: +ACo-
112         0          0: +ACo-
114         0          0: +ACo-
116         1          0:+AD0- +ACoAPQ-
118         0          0: +ACo-
+AD4-120     0       0: +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.53110.00328+ADs- mu+AD0- 1.6975
0.170
mean+AF8-var+AD0-39.436710.129, 0's: 2 Z-trim: 3 B-trim: 5 in 1/42
Lambda+AD0- 0.204232
Kolmogorov-Smirnov statistic: 0.0760 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are: opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   77 28.2    0.15
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 22.8    1.9
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.5      4.1
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.5    4.2

```

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 54 21.6 4.8
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119) 52 21.1 6.3
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.9 7
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 52 21.1 7.2
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 52 21.1 7.2
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.0 8.3

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 60 initl: 60 opt: 77 Z-score: 117.2 bits: 28.2 E(): 0.15
 Smith-Waterman score: 77+ADs- 23.288+ACU- identity (50.685+ACU- similar)
 in 73 aa overlap (6-78:309-375)

```

                                10      20      30
AAD-12      VVPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :: : : : : : : : :
gi+AHw-113  HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
      280      290      300      310      320      330

```

```

      40      50      60      70      80
AAD-12  HSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRP
      .. . : . : . : : : : : : :
gi+AHw-113  ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
      340      350      360      370      380      390

```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 97.4 bits: 22.8 E(): 1.9
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (11-62:26-77)

```

                                10      20      30      40
AAD-12      VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                :: : : : : : : : :
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQ LSTKHSVPDVLAFKVN
      10      20      30      40      50      60

```

```

      50      60      70      80
AAD-12  GHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRP
      : : : : : : : :
gi+AHw-527  DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAEKLGGLAQKRVAG
      70      80      90      100      110      120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)

initn: 41 initl: 41 opt: 57 Z-score: 91.4 bits: 22.5 E(): 4.1
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (12-64:93-149)

```

                                10          20          30
AAD-12          VVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....    ::: :: .. .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70          80          90          100          110          120

```

```

              40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRP
              .. :   ... .. : ..... :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 91.2 bits: 22.5 E(): 4.2
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (12-64:97-153)

```

                                10          20          30
AAD-12          VVPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....    ::: :: .. .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70          80          90          100          110          120

```

```

              40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRP
              .. :   ... .. : ..... :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 54 Z-score: 90.1 bits: 21.6 E(): 4.8
 Smith-Waterman score: 54+ADs- 27.778+ACU- identity (62.963+ACU- similar)
 in 54 aa overlap (2-53:15-65)

```

                                10          20          30          40
AAD-12          VVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                : : : .   ::  : : :   .....   ..... : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
              10          20          30          40          50

```

```

              50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRP
              .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRDTLNILERFNYYEEAQTLISKIL
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)

initn: 38 initl: 38 opt: 52 Z-score: 88.0 bits: 21.1 E(): 6.3
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (13-53:11-50)

```

      10      20      30      40      50
AAD-12 VVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
      ::  ::  :  .....  .....  :  ::  ....  :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLNLNENKSKELQE
      10      20      30      40      50

```

```

      60      70      80
AAD-12 GMDTTATPLRPLVKVHPETGRP

```

```

gi+AHw-160 KIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKILLKDLKETEQKVVD
      60      70      80      90     100     110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)

initn: 47 initl: 47 opt: 59 Z-score: 87.2 bits: 22.9 E(): 7
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (31-68:198-242)

```

      10      20      30      40      50
AAD-12 VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
      ::  :::  :::  :  :  :  :  :  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
      170     180     190     200     210     220

```

```

      60      70      80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRP
      .....  ::  ::
gi+AHw-303 VLGFGMDTETARKVVRGDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230     240     250     260     270     280

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.0 bits: 21.1 E(): 7.2
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (13-53:26-65)

```

      10      20      30      40
AAD-12 VVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      ::  ::  :  .....  .....  :  ::
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRP
      ....  :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLKIL
      60      70      80      90     100     110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein B1 (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.0 bits: 21.1 E(): 7.2
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (13-53:26-65)

```

                        10      20      30      40
AAD-12      VVPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                        ::  :: :  .....  .....  ::
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                        10      20      30      40      50

                        50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRP
                        .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKIL
                        60      70      80      90      100      110

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)

initn: 52 initl: 52 opt: 52 Z-score: 85.9 bits: 21.0 E(): 8.3
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (18-41:29-52)

```

                        10      20      30      40
AAD-12      VVPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                        : : ::: : .  .:: : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                        10      20      30      40      50      60

                        50      60      70      80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRP

gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAGGE
                        70      80      90      100      110      120

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:13 2010 done: Fri Feb 5 12:56:13 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

[illegible]

```

76      13      7:+AD0APQAqAD0APQ-
78      4      6:+AD0AKg-
80      4      4:+AD0AKg-
82      5      3:+ACoAPQ-
84      1      3:+ACo-
86      3      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     1      0:+AD0-          +ACoAPQ-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120 0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.72930.00338+ADs- mu+AD0- 0.5494
0.175
mean+AF8-var+AD0-41.562910.663, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.198940
Kolmogorov-Smirnov statistic: 0.0856 (N+AD0-29) at 46

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  77 27.9    0.19
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 22.7    2.1
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.3    4.6
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.3    4.7
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  54 21.5    5.3
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.0    6.9
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 20.9    7.9
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 20.9    7.9
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 22.7    8.1

```

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
(152) 52 20.9 9.1

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 60 initl: 60 opt: 77 Z-score: 115.4 bits: 27.9 E(): 0.19
Smith-Waterman score: 77+ADs- 23.288+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (5-77:309-375)

```

                                10      20      30
AAD-12                        VPAVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                ::: : : : . . . . : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
                280      290      300      310      320      330
```

```

                40      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPS
                .:. . . : . : . . . :. : . : . : :
gi+AHw-113 ESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
                340      350      360      370      380      390
```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 96.5 bits: 22.7 E(): 2.1
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (10-61:26-77)

```

                                10      20      30      40
AAD-12                        VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                ::: : . . : : . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPCPKAIAPVYEQLSTKHSVPDVLAFKVN
                10      20      30      40      50      60
```

```

                50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPS
                :. : . : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAEKLGGLAQKRVAG
                70      80      90      100      110      120
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 90.5 bits: 22.3 E(): 4.6
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (11-63:93-149)

```

                                10      20      30
AAD-12                        VPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                . : : : : : : : : : : : :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120
```



```

      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPS
      .. :   .. :   ..... :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
      130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 90.3 bits: 22.3 E(): 4.7
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (11-63:97-153)

```

                        10      20      30
AAD-12                VPAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                        ..... :   :   :   :
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
      70      80      90      100      110      120

```

```

      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPS
      .. :   .. :   ..... :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
      130      140      150      160      170      180

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 54 Z-score: 89.4 bits: 21.5 E(): 5.3
Smith-Waterman score: 54+ADs- 27.778+ACU- identity (62.963+ACU- similar)
in 54 aa overlap (1-52:15-65)

```

                        10      20      30      40
AAD-12                VPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                        : : : .   : :   :   ..... :   :
gi+AHw-111 MKFAIVLIACFAASVLAQGHPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPS
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.3 bits: 21.0 E(): 6.9
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (12-52:11-50)

```

      10      20      30      40      50
AAD-12 VPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
      : :   :   :   ..... :   :   :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDELNENKSKELQEK
      10      20      30      40      50

```

60 70 80
AAD-12 MDTTATPLRPLVKVHPETGRPS

gi+AHw-160 IIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKILLKDLKETEQKV KDI
60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 86.3 bits: 20.9 E(): 7.9
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (12-52:26-65)

10 20 30 40
AAD-12 VPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
::: :: : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQEHEKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ L
10 20 30 40 50

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPS
.... :
gi+AHw-111 DELNENKSKELQEKI IIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 86.3 bits: 20.9 E(): 7.9
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (12-52:26-65)

10 20 30 40
AAD-12 VPAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
::: :: : : : : : : : : : : : : :
gi+AHw-420 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ L
10 20 30 40 50

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPS
.... :
gi+AHw-420 DELNENKSKELQEKI IIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 86.1 bits: 22.7 E(): 8.1
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (30-67:198-242)

10 20 30 40 50
AAD-12 VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
::: :: : : : : : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
170 180 190 200 210 220

```

          60          70          80
AAD-12  YIGYGMTD-TATPLRPLVKVHPETGRPS
          .:.:.:.: :. :.
gi+AHw-303 VLGFGMTDTETARKVRGEDDQQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
          230          240          250          260          270          280

```

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
  initn: 52 initl: 52 opt: 52 Z-score: 85.2 bits: 20.9 E(): 9.1
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (17-40:29-52)

```

```

          10          20          30          40
AAD-12          VPAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
          : : :. : . :. :. :. :.
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
          10          20          30          40          50          60

```

```

          50          60          70          80
AAD-12  QAGSAYIGYGMTTATPLRPLVKVHPETGRPS
          50          60          70          80          90          100          110          120
gi+AHw-144 KVDEKLDAGDKQKLTAIEDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
          70          80          90          100          110          120

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:13 2010 done: Fri Feb 5 12:56:14 2010
Total Scan time: 0.080 Total Display time: 0.000

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 130 - 209 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      1      2:+ACo-

```

[illegible]

```

  96      1      1:+ACo-      :+ACo-
  98      0      0:      +ACo-
 100      0      0:      +ACo-
 102      0      0:      +ACo-
 104      0      0:      +ACo-
 106      0      0:      +ACo-
 108      0      0:      +ACo-
 110      0      0:      +ACo-
 112      0      0:      +ACo-
 114      0      0:      +ACo-
 116      0      0:      +ACo-
 118      0      0:      +ACo-
+AD4-120      1      0:+AD0-      +ACoAPQ-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.81420.00334+ADs- mu+AD0- -
0.0666 0.173
mean+AF8-var+AD0-41.723610.600, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.198556
Kolmogorov-Smirnov statistic: 0.0902 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 82 29.3 0.069
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 58 22.7 2.1
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.3 4.5
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204) 57 22.3 4.6
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 53 21.3 6.3
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.0 6.7
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 52 21.0 7.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.0 7.6
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 22.7 8
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 20.9 8.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 initl: 65 opt: 82 Z-score: 123.2 bits: 29.3 E(): 0.069
Smith-Waterman score: 82+ADs- 23.377+ACU- identity (51.948+ACU- similar)
in 77 aa overlap (4-80:309-379)

10 20 30
AAD-12 PAVGGRTCFADMRAAYDALDEATRALVHQRSAR
```

```

                                : : : : : : : : : : : : : : :
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
          280          290          300          310          320          330

```

```

          40          50          60          70          80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSL
          : : : : : : : : : : : : : : : : : : : : :
gi+AHw-113 ESMKWNWRTNKNVDLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
          340          350          360          370          380          390

```

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 init1: 58 opt: 58 Z-score: 96.7 bits: 22.7 E(): 2.1
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (9-60:26-77)

```

          10          20          30          40
AAD-12 PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
          : : : : : : : : : : : : : : : : : :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPCPKAIAIPVYEQLSTKHSVPDVLAFAKVN
          10          20          30          40          50          60

```

```

          50          60          70          80
AAD-12 GHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSL
          : : : : : : : : : : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAG
          70          80          90          100          110          120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 init1: 41 opt: 57 Z-score: 90.7 bits: 22.3 E(): 4.5
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (10-62:93-149)

```

          10          20          30
AAD-12 PAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
          : : : : : : : : : : : : : : : : : :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
          70          80          90          100          110          120

```

```

          40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSL
          : : : : : : : : : : : : : : : : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
          130          140          150          160          170          180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 init1: 41 opt: 57 Z-score: 90.5 bits: 22.3 E(): 4.6
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (10-62:97-153)

```

                                10          20          30
AAD-12          PAVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....   :::  ::  .  ..
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70          80          90          100          110          120

```

```

              40          50          60          70          80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL
              .. :   ...  ::  .....  :   :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 init1: 38 opt: 53 Z-score: 88.1 bits: 21.3 E(): 6.3
 Smith-Waterman score: 53+ADs- 26.923+ACU- identity (63.462+ACU- similar)
 in 52 aa overlap (2-51:17-65)

```

                                10          20          30          40
AAD-12          PAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                : : .   ::  ::  :   .....   .....  : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
              10          20          30          40          50

```

```

              50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL
              .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 init1: 38 opt: 52 Z-score: 87.6 bits: 21.0 E(): 6.7
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (11-51:11-50)

```

              10          20          30          40          50
AAD-12 PAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
              ::  ::  :   .....   .....  : :   .... :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQLDELNENKSKELQEKI
              10          20          30          40          50

```

```

              60          70          80
AAD-12 DTTATPLRPLVKVHPETGRPSL

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVVDIQ
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 init1: 38 opt: 52 Z-score: 86.5 bits: 21.0 E(): 7.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (11-51:26-65)

```

                10          20          30          40
AAD-12          PAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  :  :::::  :::::  :::  :::
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL
                .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 86.5 bits: 21.0 E(): 7.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (11-51:26-65)

```

                10          20          30          40
AAD-12          PAVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  :  :::::  :::::  :::  :::
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10          20          30          40          50

```

```

                50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL
                .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs- Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 86.2 bits: 22.7 E(): 8
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (29-66:198-242)

```

                10          20          30          40          50
AAD-12          PAVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                :::  :::  :  :::  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
                170          180          190          200          210          220

```

```

                60          70          80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSL
                ..... :::  :::
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230          240          250          260          270          280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 85.4 bits: 20.9 E(): 8.8
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (16-39:29-52)

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-l2: 131 - 210 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

44      121
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
    46     118
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
    48     115
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
    50     119
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
    52     140
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
    54     106
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9-
    56     80
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9-
    58     80
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9-
    60     59       50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
    62     57       40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
    64     57       32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
    66     21       25:+AD0APQA9AD0APQA9AD0- +ACo-
    68     25       20:+AD0APQA9AD0APQA9ACoAPQA9-
    70     22       16:+AD0APQA9AD0APQAqAD0APQ-
    72     24       12:+AD0-+AD0APQAqAD0APQA9AD0-
    74     10       10:+AD0APQA9ACo-
    76     11        7:+AD0APQAqAD0-
    78         6        6:+AD0AKg-
    80         5        4:+AD0AKg-
    82         5        3:+ACoAPQ-
    84         2        3:+ACo-
    86         3        2:+ACo-
    88         2        2:+ACo- inset +AD0- represents 1 library sequences
    90         2        1:+ACo-
    92         0        1:+ACo- :+ACo-
    94         0        1:+ACo- :+ACo-
    96         1        1:+ACo- :+ACo-
    98         0        0:          +ACo-
   100         0        0:          +ACo-
   102         0        0:          +ACo-
   104         0        0:          +ACo-
   106         0        0:          +ACo-
   108         0        0:          +ACo-
   110         0        0:          +ACo-
   112         0        0:          +ACo-
   114         0        0:          +ACo-
   116         0        0:          +ACo-
   118         0        0:          +ACo-
```

```
+AD4-120      1      0:+AD0-      +ACoAPQ-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.84200.00329+ADs- mu+AD0- -
0.4717 0.171
mean+AF8-var+AD0-41.992010.518, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.197921
Kolmogorov-Smirnov statistic: 0.1001 (N+AD0-28) at 50
```

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
```

```
join: 42, opt: 30, open/ext: -10/-2, width: 32
```

```
Scan time: 0.090
```

```
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   82 29.4   0.068
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 22.8     2
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.4     4.3
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-G1
( 204)   57 22.4     4.4
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   53 21.3     6
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.1     6.4
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.0     7.3
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.0     7.3
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 22.8     7.7
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.0     8.5
```

```
+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 82 Z-score: 123.3 bits: 29.4 E(): 0.068
Smith-Waterman score: 82+ADs- 23.377+ACU- identity (51.948+ACU- similar)
in 77 aa overlap (3-79:309-379)
```

```
                                10      20      30
AAD-12                        AVGGRTCFADMRAAYDALDEATRALVHQRSAR
                                :: : : :: . . . . : . . .
gi+AHw-113 HGFFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAA
                280      290      300      310      320      330
```

```
                                40      50      60      70      80
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLL
                . . . . : . . . . . . . . . . . . . . . .
gi+AHw-113 ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
                340      350      360      370      380      390
```

```
gi+AHw-113 GAPC
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:

Full+AD0-Thior (121 aa)

initn: 58 initl: 58 opt: 58 Z-score: 97.0 bits: 22.8 E(): 2
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (8-59:26-77)

```

                                10      20      30      40
AAD-12      AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                :::      . . . :      ....
gi+AHw-527  MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFAKVN
                                10      20      30      40      50      60
```

```

                                50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                ::::: :      : :
gi+AHw-527  DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAG
                                70      80      90      100      110      120
```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant

allergen +AFs- (200 aa)

initn: 41 initl: 41 opt: 57 Z-score: 90.9 bits: 22.4 E(): 4.3
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (9-61:93-149)

```

                                10      20      30
AAD-12      AVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                ..... : : : . . .
gi+AHw-144  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100      110      120
```

```

                                40      50      60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                .. :   . . . : ..... : : :
gi+AHw-144  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180
```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:

Full+AD0-Glutat (204 aa)

initn: 41 initl: 41 opt: 57 Z-score: 90.7 bits: 22.4 E(): 4.4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (9-61:97-153)

```

                                10      20      30
AAD-12      AVGGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                ..... : : : . . .
gi+AHw-622  AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100      110      120
```

```

                                40      50      60      70      80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                .. :   . . . : ..... : : :
gi+AHw-622  TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180
```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 53 Z-score: 88.4 bits: 21.3 E(): 6
Smith-Waterman score: 53+ADs- 26.923+ACU- identity (63.462+ACU- similar)
in 52 aa overlap (1-50:17-65)

```

                                10      20      30      40
AAD-12      AVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
              : : .      ::  : :  .....  .....: :
gi+AHw-111  MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
              10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
          .... :
gi+AHw-111  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.9 bits: 21.1 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (10-50:11-50)

```

                                10      20      30      40      50
AAD-12  AVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
              ::  : :  .....  .....: :  .... :
gi+AHw-160  GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQDELNENKSKELQEKI
              10      20      30      40      50

```

```

                    60      70      80
AAD-12  DTTATPLRPLVKVHPETGRPSLL
gi+AHw-160  IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVVDIQ
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 86.8 bits: 21.0 E(): 7.3
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (10-50:26-65)

```

                                10      20      30      40
AAD-12      AVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
              ::  : :  .....  .....: :
gi+AHw-111  MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
              10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
          .... :
gi+AHw-111  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein B1 (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 86.8 bits: 21.0 E(): 7.3
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (10-50:26-65)

```

                                10      20      30      40
AAD-12      AVGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                ::  ::  :  .....  .....  :  ::
gi+AHw-420  MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                                10      20      30      40      50

                                50      60      70      80
AAD-12  GHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL
                                .... :
gi+AHw-420  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                                60      70      80      90      100      110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs- Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 86.4 bits: 22.8 E(): 7.7
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (28-65:198-242)

```

                                10      20      30      40      50
AAD-12      AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ::  ::  :  ::  :  :  ::  .
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                                170      180      190      200      210      220

                                60      70      80
AAD-12  YIGYGMTTATPLRPLVKVHPETGRPSLL
                                ..... ::  .
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                                230      240      250      260      270      280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 85.7 bits: 21.0 E(): 8.5
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (15-38:29-52)

```

                                10      20      30      40
AAD-12      AVGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                                :  :  ::  :  .  ..  :  :  ::
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAAARISAKNALESYAYSRLNTLSDS
                                10      20      30      40      50      60

                                50      60      70      80
AAD-12  QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLL

gi+AHw-144  KVDEKLDAGDKQKLTAIEDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
                                70      80      90      100      110      120

```

Total Scan time: 0.090 Total Display time: 0.000

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenecity/FARRPV10/FARRPV10.fasta library
```

1+AD4APqA+-AAD-12: 132 - 211 80 aa - 80 aa

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

52      138
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
   54     109
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0-
   56     78
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
   58     80
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9-
   60     59    50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   62     56    40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
   64     54    32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
   66     24    25:+AD0APQA9AD0APQA9AD0APQAq-
   68     24    20:+AD0APQA9AD0APQA9ACoAPQ-
   70     22    16:+AD0APQA9AD0APQAqAD0APQ-
   72     25    12:+AD0APQA9ACoAPQA9AD0APQA9-
   74     12    10:+AD0APQA9ACo-
   76     11     7:+AD0APQAqAD0-
   78       7     6:+AD0AKgA9-
   80       1     4:+AD0AKg-
   82       6     3:+ACoAPQ-
   84       1     3:+ACo-
   86       4     2:+ACoAPQ-
   88       2     2:+ACo-                inset +AD0- represents 1 library sequences
   90       1     1:+ACo-
   92       1     1:+ACo-              :+ACo-
   94       0     1:+ACo-              :+ACo-
   96       1     1:+ACo-              :+ACo-
   98       0     0:                  +ACo-
  100       0     0:                  +ACo-
  102       0     0:                  +ACo-
  104       0     0:                  +ACo-
  106       0     0:                  +ACo-
  108       0     0:                  +ACo-
  110       0     0:                  +ACo-
  112       0     0:                  +ACo-
  114       0     0:                  +ACo-
  116       0     0:                  +ACo-
  118       0     0:                  +ACo-
+AD4-120      1        0:+AD0-          +ACoAPQ-
 331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.83470.00326+ADs- mu+AD0- -
0.4303 0.169
mean+AF8-var+AD0-41.141010.330, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.199957
Kolmogorov-Smirnov statistic: 0.0988 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
```


opt bits E(1471)

```
+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
  initn: 65 initl: 65 opt: 82 Z-score: 124.1 bits: 29.5 E(): 0.062
Smith-Waterman score: 82+ADs- 23.377+ACU- identity (51.948+ACU- similar)
in 77 aa overlap (2-78:309-379)
```

40 50 60 70 80
 AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLI
 .. . : . :. ... :. : . : : . : :
 gi+AHw-113 ESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQP
 340 350 360 370 380 390

```
+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
  initn: 58 initl: 58 opt: 58 Z-score: 97.5 bits: 22.9 E(): 1.9
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (7-58:26-77)
```

AAD-12 VGGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
::: : . . :

gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVVN
10 20 30 40 50 60

50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI
::: : : :

gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAG
70 80 90 100 110 120

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.3 bits: 22.4 E(): 4.1
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (8-60:93-149)

10 20 30
AAD-12 VGGRTCFADMRAA-----YDALDEATRALVHQRSARH
: : : : : : : : : : : : : : : :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

40 50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI
: : : : : : : : : : : : : : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.2 bits: 22.4 E(): 4.2
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (8-60:97-153)

10 20 30
AAD-12 VGGRTCFADMRAA-----YDALDEATRALVHQRSARH
: : : : : : : : : : : : : : : :
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70 80 90 100 110 120

40 50 60 70 80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLI
: : : : : : : : : : : : : : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
130 140 150 160 170 180

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 88.3 bits: 21.1 E(): 6.1
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (9-49:11-50)

10 20 30 40 50
AAD-12 VGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
: : : : : : : : : : : : : : : :

gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDENENKSKELQEKI
 10 20 30 40 50

 60 70 80
 AAD-12 DTTATPLRPLVKVHPETGRPSLLI

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKILLKDLKETEQKVVDIQ
 60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.2 bits: 21.1 E(): 7
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (9-49:26-65)

 10 20 30 40
 AAD-12 VGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
 ::: .: ::: : :
 gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
 10 20 30 40 50

 50 60 70 80
 AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI
 :
 gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKIL
 60 70 80 90 100 110

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.2 bits: 21.1 E(): 7
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (9-49:26-65)

 10 20 30 40
 AAD-12 VGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
 ::: .: ::: : :
 gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
 10 20 30 40 50

 50 60 70 80
 AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI
 :
 gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKIL
 60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
 protein Bl (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.2 bits: 21.1 E(): 7
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (9-49:26-65)

 10 20 30 40
 AAD-12 VGGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
 ::: .: ::: : :
 gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL

AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAQSAYIGYGMDTTATPLRPLVKVHP

AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
10 20 30

qi+AHw-462 LNSA

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

  1+AD4APgA+-AAD-12: 133 - 212 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

inset +AD0- represents 1 library sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 6.03020.00329+ADs- mu+AD0- -
 1.4547 0.171
 mean+AF8-var+AD0-40.831910.147, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
 Lambda+AD0- 0.200712
 Kolmogorov-Smirnov statistic: 0.0956 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 82 29.5 0.061
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 58 22.9 1.8
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
 57 22.5 4
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
 (204) 57 22.5 4.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.2 5.9
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.1 6.8
 gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.1 6.8
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 52 21.1 6.8
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.8 7.5
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.1 7.9
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 18.9 9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)

initn: 65 initl: 65 opt: 82 Z-score: 124.2 bits: 29.5 E(): 0.061
 Smith-Waterman score: 82+ADs- 23.377+ACU- identity (51.948+ACU- similar)
 in 77 aa overlap (1-77:309-379)

			10	20	30	
AAD-12			GGRTC	FADMRAAYDALDE	ATRALVHQ	SAR
			:: :	: :.	... :	...
gi+AHw-113	HGFFQ	VVNNNYDKWGSYAIGGSASPTILS	QGNRFCAP	DERSKKNVLGR	-----	HGEAAA
	280	290	300	310	320	330

	40	50	60	70	80	
AAD-12	HSLVYSQSKLGHVQQAGSAYIGY	GMDTTATPLRPLVKVHPETGRPS	LLIG			

gi+AHw-113	ESMKWNWRTNKDVL	ENGAI	FVASGVD	PVLTPEQSAGMIPAE	PGESALSLTSSAGVL	SCQP
	340	350	360	370	380	390

gi+AHw-113 GAPC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 97.8 bits: 22.9 E(): 1.8
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (6-57:26-77)

```

                                10      20      30      40
AAD-12                      GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                :::      . . . : . . . : . . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFKVN
                                10      20      30      40      50      60

                                50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG
                                : : : : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAG
                                70      80      90      100     110     120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.5 bits: 22.5 E(): 4
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (7-59:93-149)

```

                                10      20      30
AAD-12                      GGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                . . . . : : : : : . . . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100     110     120

                                40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG
                                . . : . . : . . . . . : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.3 bits: 22.5 E(): 4.1
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (7-59:97-153)

```

                                10      20      30
AAD-12                      GGRTCFADMRAA-----YDALDEATRALVHQRSARH
                                . . . . : : : : : . . . .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                                70      80      90      100     110     120

                                40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG
                                . . : . . : . . . . . : : :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                                130     140     150     160     170     180

```


+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.6 bits: 21.2 E(): 5.9
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (8-48:11-50)

```

      10      20      30      40      50
AAD-12  GGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
      ::  :: :  :::::  :::::  :: :  :: :  :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHLDELNENKSKELQEKI
      10      20      30      40      50

```

```

      60      70      80
AAD-12  DTTATPLRPLVKVHPETGRPSLLIG

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVKDIQ
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.4 bits: 21.1 E(): 6.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (8-48:26-65)

```

      10      20      30      40
AAD-12  GGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      ::  :: :  :::::  :::::  :: :  :: :  :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHL
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.4 bits: 21.1 E(): 6.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (8-48:26-65)

```

      10      20      30      40
AAD-12  GGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      ::  :: :  :::::  :::::  :: :  :: :  :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHL
      10      20      30      40      50

```

```

      50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein B1 (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.4 bits: 21.1 E(): 6.8
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (8-48:26-65)

```

                                10      20      30      40
AAD-12      GGRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                ::  ::  :  .....  .....  :  ::
gi+AHw-420  MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
                                10      20      30      40      50

                                50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG
                                .... :
gi+AHw-420  DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                                60      70      80      90      100      110
```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 86.6 bits: 22.8 E(): 7.5
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (26-63:198-242)

```

                                10      20      30      40
AAD-12      GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ::  :::  :::  :  :  :::  .
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                                170      180      190      200      210      220

                                50      60      70      80
AAD-12  YIGYGMDDT-TATPLRPLVKVHPETGRPSLLIG
                                ..... ::  .:
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                                230      240      250      260      270      280
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 86.2 bits: 21.1 E(): 7.9
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (13-36:29-52)

```

                                10      20      30      40
AAD-12      GGRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                                :  :  :::  :  .  ...  :  ::
gi+AHw-144  KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAAARISAKNALESYAYSLRNTLSDS
                                10      20      30      40      50      60

                                50      60      70      80
AAD-12  QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIG

gi+AHw-144  KVDEKLDAGDKQKLTAIEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
                                70      80      90      100      110      120
```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 85.2 bits: 18.9 E(): 9
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (41-61:5-25)

```

                20          30          40          50          60          70
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHP
                .....:..:..:..:..:
gi+AHw-462                AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
                        10          20          30

                80
AAD-12 ETGRPSLLIG

gi+AHw-462 LNSA

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:14 2010 done: Fri Feb 5 12:56:14 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 134 - 213 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8: +ACo-
      34      3     21:+AD0- +ACo-
      36     19     44:+AD0APQA9AD0APQA9AD0- +ACo-
      38     35     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-

```

sequences

```

112      1      0:+AD0-      +ACoAPQ-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.01930.00319+ADs- mu+AD0- -
1.5633 0.165
mean+AF8-var+AD0-41.013810.136, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.200267
Kolmogorov-Smirnov statistic: 0.0985 (N+AD0-28) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 74 27.2 0.3
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 58 22.9 1.8
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.5 4
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204) 57 22.5 4.1
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2 5.8
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 52 21.2 6.6
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134) 52 21.2 6.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2 6.6
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 22.8 7.3
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152) 52 21.1 7.7
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38) 43 19.0 8.8

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:

Full+AD0-Pollen (396 aa)

initn: 65 initl: 65 opt: 74 Z-score: 111.8 bits: 27.2 E(): 0.3

Smith-Waterman score: 74+ADs- 22.667+ACU- identity (50.667+ACU- similar)

in 75 aa overlap (2-76:311-379)

```

                                10      20      30
AAD-12                        GRTCFAADMRAAYDALDEATRALVHQRSARHS
                                : : : : . . . : : : :
gi+AHw-113 FFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAAES
                290      300      310      320      330

                40      50      60      70      80
AAD-12 LVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR

```

10
20
30
 AAD-12
 GRTCFADMRAA-----YDALDEATRALVHQRSARH
.:.:.:
::: :: ..
. ..
 gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
70
80
90
100
110
120

```

                40          50          60          70          80
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR
      .. :   ... .. : ..... :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                130          140          150          160          170          180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)
initn: 38 initl: 38 opt: 52 Z-score: 88.7 bits: 21.2 E(): 5.8
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (7-47:11-50)

```

                10          20          30          40          50
AAD-12  GRTCFCADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
      ... .. :   ... .. : ..... : ..... : ..... :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDLENENKSKELQEKI
                10          20          30          40          50

```

```

                60          70          80
AAD-12  DTTATPLRPLVKVHPETGRPSLLIGR

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLKILLKDLKETEQKVKDIQ
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (7-47:26-65)

```

                10          20          30
AAD-12  GRTCFCADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      ... .. :   ... .. : ..... : ..... : ..... :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10          20          30          40          50

```

```

                40          50          60          70          80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGR
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLKIL
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (7-47:26-65)

```

                10          20          30
AAD-12  GRTCFCADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      ... .. :   ... .. : ..... : ..... : ..... :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                10          20          30          40          50

```

```

      40      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR
      .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protein Bl (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (7-47:26-65)

```

                        10      20      30
AAD-12                GRTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                        :: : : ..... : ..... : :
gi+AHw-420 MKFAIVLIACFAASVLAQEHEKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                        10      20      30      40      50

```

```

      40      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGR
      .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLISKIL
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs- Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 86.8 bits: 22.8 E(): 7.3
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (25-62:198-242)

```

                        10      20      30      40
AAD-12                GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                        :: :: : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
      170      180      190      200      210      220

```

```

      50      60      70      80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGR
      ..... : :
gi+AHw-303 VLGFGMDTETARKVRGEDDQQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230      240      250      260      270      280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.4 bits: 21.1 E(): 7.7
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (12-35:29-52)

```

                        10      20      30      40
AAD-12                GRTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                        : : :: : . : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEEAARISAKNALESYAYSLRNTLSDS
      10      20      30      40      50      60

```


	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	0	0:	

sequences

```

  98      1      0:+AD0-      +ACoAPQ-
 100      0      0:      +ACo-
 102      0      0:      +ACo-
 104      0      0:      +ACo-
 106      0      0:      +ACo-
 108      0      0:      +ACo-
 110      0      0:      +ACo-
 112      1      0:+AD0-      +ACoAPQ-
 114      0      0:      +ACo-
 116      0      0:      +ACo-
 118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.95530.00322+ADs- mu+AD0- -
1.2225 0.167
mean+AF8-var+AD0-40.818610.074, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.200745
Kolmogorov-Smirnov statistic: 0.0937 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   74 27.3   0.29
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 23.0   1.8
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.5   3.9
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.5   4
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2   5.7
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.2   6.6
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.2   6.6
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2   6.6
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 22.9   7.2
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.2   7.7
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)   43 18.9   8.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 74 Z-score: 112.0 bits: 27.3 E(): 0.29
Smith-Waterman score: 74+ADs- 22.667+ACU- identity (50.667+ACU- similar)
in 75 aa overlap (1-75:311-379)

```

```

AAD-12                      RTCFADMRAAYDALDEATRALVHQRSARHS
                        : : : : . . . : : : :
gi+AHw-113 FFQVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAAES
                        290      300      310      320      330

```

```

                        40      50      60      70      80
AAD-12 LVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH
      . . . : . . . . : : . : : . : : :
gi+AHw-113 MKWNNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGA
                        340      350      360      370      380      390

```

gi+AHw-113 PC

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 initl: 58 opt: 58 Z-score: 98.0 bits: 23.0 E(): 1.8
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (4-55:26-77)

```

                        10      20      30
AAD-12          RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                        ::      : . . : . . : . . .
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFAKVVN
                        10      20      30      40      50      60

```

```

                        40      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH
      : : : : : : : : :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAG
                        70      80      90      100      110      120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.7 bits: 22.5 E(): 3.9
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (5-57:93-149)

```

                        10      20
AAD-12          RTCFADMRAA-----YDALDEATRALVHQRSARH
                        . . . : : : : : . .
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                        70      80      90      100      110      120

```

```

                        30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRH
      . . : . . : . . . . : : :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                        130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
Full+AD0-Glutat (204 aa)
initn: 41 initl: 41 opt: 57 Z-score: 91.6 bits: 22.5 E(): 4

Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (5-57:97-153)

```

                                10          20
AAD-12          RTCFADMRAA-----YDALDEATRALVHQRSARH
                                .....   ::: :: .. .
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
              70          80          90          100          110          120

              30          40          50          60          70          80
AAD-12 SLVYSQSKLGHVQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH
              .. :   ... .. : ..... :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
              130          140          150          160          170          180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
Structur (119 aa)

initn: 38 init1: 38 opt: 52 Z-score: 88.8 bits: 21.2 E(): 5.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (6-46:11-50)

```

              10          20          30          40          50
AAD-12      RTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQAGSAYIGYGM
              :::  :: :   .....   .....::: : :: .... :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDENENKSKELQEKI
              10          20          30          40          50

              60          70          80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRH

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVVDIQ
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 init1: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (6-46:26-65)

```

              10          20          30
AAD-12      RTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
              :::  :: :   .....   .....::: : ::
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
              10          20          30          40          50

              40          50          60          70          80
AAD-12 GHVQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH
              .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 init1: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6

Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (6-46:26-65)

```

                                10      20      30
AAD-12      RTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                :::  :::  :  .....  .....:  :::
gi+AHw-111  MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH
                                ....  :
gi+AHw-111  DELNENKSKELQEKKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.6
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (6-46:26-65)

```

                                10      20      30
AAD-12      RTCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                :::  :::  :  .....  .....:  :::
gi+AHw-420  MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH
                                ....  :
gi+AHw-420  DELNENKSKELQEKKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                                60      70      80      90      100     110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)

initn: 47 initl: 47 opt: 59 Z-score: 87.0 bits: 22.9 E(): 7.2
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (24-61:198-242)

```

                                10      20      30      40
AAD-12      RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :::  :::  :  :  :  :  :  :  :  :  :
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
                                170     180     190     200     210     220

                                50      60      70      80
AAD-12  YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH
                                .....:  :
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                                230     240     250     260     270     280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)

initn: 52 initl: 52 opt: 52 Z-score: 86.5 bits: 21.2 E(): 7.7

Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (11-34:29-52)

```

                        10      20      30      40
AAD-12                RTCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                        : : : : : : : : : : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSRLRNTLSDS
                        10      20      30      40      50      60

                        50      60      70      80
AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRH

gi+AHw-144 KVDEKLDAGDKQKLTAEDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
                        70      80      90      100     110     120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.3 bits: 18.9 E(): 8.9
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (39-59:5-25)

```

                        10      20      30      40      50      60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAYIGYGMDDTTATPLRPLVKVHP
                        : : : : : : : : : : : :
gi+AHw-462                AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
                        10      20      30

                        70      80
AAD-12 ETGRPSLLIGRH

gi+AHw-462 LNSA

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:15 2010 done: Fri Feb 5 12:56:15 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 136 - 215 80 aa - 80 aa

[illegible]


```

82      7      3:+ACoAPQA9-
84      1      3:+ACo-
86      2      2:+ACo-
88      4      2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.82030.00319+ADs- mu+AD0- -
0.4515 0.165
mean+AF8-var+AD0-40.128610.001, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.202464
Kolmogorov-Smirnov statistic: 0.1026 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   69 25.9   0.74
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   58 23.0   1.7
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6   3.8
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   57 22.6   3.9
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.2   5.6
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.2   6.5
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)   52 21.2   6.5
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2   6.5
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 22.9   6.8
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.2   7.5

```

gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(38) 43 18.9 9.1

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 69 Z-score: 104.7 bits: 25.9 E(): 0.74
Smith-Waterman score: 69+ADs- 21.918+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (2-74:313-379)

```

                                10      20      30
AAD-12                        TCFADMRAAYDALDEATRALVHQRSARHSLV
                                :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 QVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAAESMK
                290      300      310      320      330

```

```

                40      50      60      70      80
AAD-12 YSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHA
                ..      :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 WNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                340      350      360      370      380      390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 58 init1: 58 opt: 58 Z-score: 98.2 bits: 23.0 E(): 1.7
Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
in 52 aa overlap (3-54:26-77)

```

                                10      20      30
AAD-12                        TCFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                :::      :  :  :  :  :  :  :  :  :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAIPVYEQLSTKHSVPDVLAFKVN
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHA
                :::::  :  :  :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRVAG
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
allergen +AFs- (200 aa)
initn: 41 init1: 41 opt: 57 Z-score: 92.0 bits: 22.6 E(): 3.8
Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
in 58 aa overlap (4-56:93-149)

```

                                10      20
AAD-12                        TCFADMRAA-----YDALDEATRALVHQRSARH
                                .....  :  :  :  :  :  :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIAANYHYDA-DENSKQKKWDPLKKE
                70      80      90      100      110      120

```

```

                30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHA
                .. :  :  :  :  :  :  :  :  :

```

gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
 130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 91.8 bits: 22.6 E(): 3.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (4-56:97-153)

AAD-12 TCFADMRAA-----YDALDEATRALVHQRSARH
 : : : : :
 gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
 70 80 90 100 110 120

AAD-12 SLVYSQSKLGHVQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA
 . . : . . : : : : :
 gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
 130 140 150 160 170 180

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.9 bits: 21.2 E(): 5.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (5-45:11-50)

AAD-12 TCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQAGSAYIGYGM
 : : : : : : : : : : :
 gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQDELNENKSKELQEKI
 10 20 30 40 50

AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHA
 gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVKDIQ
 60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.8 bits: 21.2 E(): 6.5
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (5-45:26-65)

AAD-12 TCFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
 : : : : : : : : : : :
 gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQ
 10 20 30 40 50

AAD-12 GHVQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHA
 :

50 60 70 80
 AAD-12 YIGYGMTD-TATPLRPLVKVHPETGRPSLLIGRHA
 ::*:*:*:* * *

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

opt      E()
+ADw- 20    2      0:+AD0-
22      0      0:          one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      0      0:
30      0      2:+ACo-
32      0      8:   +ACo-
34      2      21:+AD0-       +ACo-
36     25     44:+AD0APQA9AD0APQA9AD0APQA9-         +ACo-
38     37     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-           +ACo-
40    121    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9A
D0-
42      76
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q-          +ACo-
44     124
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-        +ACo-
46     132
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
48     112    132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-        +ACo-
50     112
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
52     143
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9-
54     129
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
56      79
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQAqAD0-
58      78
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
-
60      59      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
62      45      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      43      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66      35      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      21      20:+AD0APQA9AD0APQA9ACo-
70      19      16:+AD0APQA9AD0APQAqAD0-

```

```

72      28      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      11      10:+AD0APQA9ACo-
76      9        7:+AD0APQAq-
78      10      6:+AD0AKgA9AD0-
80      2        4:+AD0AKg-
82      6        3:+ACoAPQ-
84      1        3:+ACo-
86      2        2:+ACo-
88      4        2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0        1:+ACo-
92      2        1:+ACo-          :+ACoAPQ-
94      0        1:+ACo-          :+ACo-
96      0        1:+ACo-          :+ACo-
98      1        0:+AD0-          +ACoAPQ-
100     0        0:              +ACo-
102     0        0:              +ACo-
104     1        0:+AD0-          +ACoAPQ-
106     0        0:              +ACo-
108     0        0:              +ACo-
110     0        0:              +ACo-
112     0        0:              +ACo-
114     0        0:              +ACo-
116     0        0:              +ACo-
118     0        0:              +ACo-
+AD4-120 0        0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.98500.00322+ADs- mu+AD0- -
1.2648 0.167
mean+AF8-var+AD0-40.0529 9.937, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.202655
Kolmogorov-Smirnov statistic: 0.1067 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  69 25.9      0.76
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  58 23.0      1.7
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6      3.8
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)  57 22.6      3.9
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.3      5.6
gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.2      6.4
gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (
134)  52 21.2      6.4
gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei ( 134)
52 21.2      6.4

```

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.9 7.1
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-(152) 52 21.2 7.5
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No (38) 43 19.0 8.7

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 65 initl: 65 opt: 69 Z-score: 104.5 bits: 25.9 E(): 0.76
 Smith-Waterman score: 69+ADs- 21.918+ACU- identity (50.685+ACU- similar)
 in 73 aa overlap (1-73:313-379)

```

                                10      20      30
AAD-12                        CFADMRAAYDALDEATRALVHQRSARHSLV
                                :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 QVVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGR-----HGEAAAESMK
                290          300          310          320          330

```

```

                40          50          60          70          80
AAD-12 YSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH
                ..      :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-113 WNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAE PGESALSLTSSAGVLSQPGAPC
                340          350          360          370          380          390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 initl: 58 opt: 58 Z-score: 98.3 bits: 23.0 E(): 1.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (2-53:26-77)

```

                                10      20      30
AAD-12                        CFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL
                                :::      :  :  :  :  :  :  :  :  :  :
gi+AHw-527 MVHHITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQ LSTKHSVPDVLAFKVN
                10          20          30          40          50          60

```

```

                40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAH
                :::::  :  :  :  :
gi+AHw-527 DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AA EKLGLAQKRVAG
                70          80          90          100          110          120

```

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 92.0 bits: 22.6 E(): 3.8
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (3-55:93-149)

```

                                10      20
AAD-12                        CFADMRAA-----YDALDEATRALVHQRSARH
                                .....  :  :  :  :  :  :  :  :  :
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAA IANYHYDA-DENSKQKKWDPLKKE
                70          80          90          100          110          120

```



```

      30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAH
      .. :   .. :   ..... :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
      130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 57 Z-score: 91.8 bits: 22.6 E(): 3.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (3-55:97-153)

```

                                10      20
AAD-12                      CFADMRAA-----YDALDEATRALVHQRSARH
                                ..... :   :   :   :   :
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
      70      80      90      100      110      120

```

```

      30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPETGRPSLLIGRHAH
      .. :   .. :   ..... :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
      130      140      150      160      170      180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 89.0 bits: 21.3 E(): 5.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (4-44:11-50)

```

      10      20      30      40      50
AAD-12      CFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
      :   :   :   ..... :   :   :   :   :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQLDENENKSKELQEKI
      10      20      30      40      50

```

```

      60      70      80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAH
gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVVDIQ
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 87.8 bits: 21.2 E(): 6.4
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (4-44:26-65)

```

      10      20      30
AAD-12      CFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
      :   :   :   ..... :   :   :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
      10      20      30      40      50

```

40 50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAH
.... :

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.8 bits: 21.2 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (4-44:26-65)

10 20 30
AAD-12 CFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

40 50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAH
.... :

gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.8 bits: 21.2 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (4-44:26-65)

10 20 30
AAD-12 CFADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : :
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

40 50 60 70 80
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAH
.... :

gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)

initn: 47 initl: 47 opt: 59 Z-score: 87.1 bits: 22.9 E(): 7.1
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (22-59:198-242)

10 20 30 40
AAD-12 CFADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
:: : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
170 180 190 200 210 220

```

      50      60      70      80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAH
      .:.:.:.: :. :.
gi+AHw-303 VLGFGMTTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230      240      250      260      270      280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 86.7 bits: 21.2 E(): 7.5
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (9-32:29-52)

```

      10      20      30      40
AAD-12 CFADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
      : : :. : . :. :. :.
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
      10      20      30      40      50      60

```

```

      50      60      70      80
AAD-12 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAH
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
      70      80      90      100      110      120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.5 bits: 19.0 E(): 8.7
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (37-57:5-25)

```

      10      20      30      40      50      60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAYIGYGMTTATPLRPLVKVHP
      :.:.:.: :. :. :. :.
gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
      10      20      30

```

```

      70      80
AAD-12 ETGRPSLLIGRHAH
gi+AHw-462 LNSA

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:15 2010 done: Fri Feb 5 12:56:15 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

[illegible]

```

62      48      40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
64      42      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      34      25: +AD0APQA9AD0- +AD0APQA9AD0AKgA9AD0APQ-
68      17      20: +AD0APQA9AD0APQA9ACo-
70      18      16: +AD0APQA9AD0APQAq-
72      28      12: +AD0APQA9ACoAPQA9AD0APQA9AD0-
74      10      10: +AD0APQA9ACo-
76      10      7: +AD0APQAqAD0-
78      9       6: +AD0AKgA9-
80      2       4: +AD0AKg-
82      5       3: +ACoAPQ-
84      1       3: +ACo-
86      2       2: +ACo-
88      4       2: +ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0       1: +ACo-
92      2       1: +ACo-          : +ACoAPQ-
94      0       1: +ACo-          : +ACo-
96      0       1: +ACo-          : +ACo-
98      1       0: +AD0-          +ACoAPQ-
100     1       0: +AD0-          +ACoAPQ-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.96790.00323+ADs- mu+AD0- -
1.1491 0.167
mean+AF8-var+AD0-39.9025 9.854, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.203036
Kolmogorov-Smirnov statistic: 0.0971 (N+AD0-29) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 67 25.3 1.1
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 58 23.0 1.7
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
57 22.6 3.8
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204) 57 22.6 3.9
gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru ( 119)
52 21.3 5.6

```

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134) 52 21.2 6.4
 gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134) 52 21.2 6.4
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134) 52 21.2 6.4
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465) 59 22.9 7
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0- (152) 52 21.2 7.5
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No (38) 43 19.0 8.7

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 65 init1: 65 opt: 67 Z-score: 101.4 bits: 25.3 E(): 1.1
 Smith-Waterman score: 67+ADs- 24.242+ACU- identity (53.030+ACU- similar)
 in 66 aa overlap (10-72:314-379)

		10	20	30	
AAD-12		FADMRAAYDALDEATRALV---HQRSARHSLVYSQSKLG			
		:	:	:	:
gi+AHw-113	VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNK				
	290 300 310 320 330 340				

	40	50	60	70	80
AAD-12	HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA				
	:	:	:	:	:
gi+AHw-113	DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC				
	350 360 370 380 390				

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 58 init1: 58 opt: 58 Z-score: 98.3 bits: 23.0 E(): 1.7
 Smith-Waterman score: 58+ADs- 26.923+ACU- identity (57.692+ACU- similar)
 in 52 aa overlap (1-52:26-77)

		10	20	30	
AAD-12		FADMRAAYDALDEATRALVHQRSARHSLVYSQSKL			
		:	:	:	:
gi+AHw-527	MVHHITSNDELQKLLSSTTYVVVDFFADWCPCPKAIAPVYEQSLTKHSVPDVLAFKVN				
	10 20 30 40 50 60				

	40	50	60	70	80
AAD-12	GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA				
	:	:	:	:	:
gi+AHw-527	DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAG				
	70 80 90 100 110 120				

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allergen +AFs- (200 aa)
 initn: 41 init1: 41 opt: 57 Z-score: 92.0 bits: 22.6 E(): 3.8
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (2-54:93-149)

```

                                10      20
AAD-12                      FADMRAA-----YDALDEATRALVHQRSARH
                                .....   ::: :: ..   .   ..
gi+AHw-144 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                        70      80      90      100      110      120

```

```

                30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA
                .. :   ... .. : ..... :   :   :
gi+AHw-144 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                        130      140      150      160      170      180

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 init1: 41 opt: 57 Z-score: 91.8 bits: 22.6 E(): 3.9
 Smith-Waterman score: 57+ADs- 29.310+ACU- identity (60.345+ACU- similar)
 in 58 aa overlap (2-54:97-153)

```

                                10      20
AAD-12                      FADMRAA-----YDALDEATRALVHQRSARH
                                .....   ::: :: ..   .   ..
gi+AHw-622 AISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKE
                        70      80      90      100      110      120

```

```

                30      40      50      60      70      80
AAD-12 SLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHA
                .. :   ... .. : ..... :   :   :
gi+AHw-622 TIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREK
                        130      140      150      160      170      180

```

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 init1: 38 opt: 52 Z-score: 89.0 bits: 21.3 E(): 5.6
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (3-43:11-50)

```

                10      20      30      40      50
AAD-12          FADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                :: : : : ..... : ..... : : : : :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQDELNENKSKELQEKI
                10      20      30      40      50

```

```

                60      70      80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHA

```

```

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQKVKDIQ
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
 Blomia t (134 aa)
 initn: 38 init1: 38 opt: 52 Z-score: 87.9 bits: 21.2 E(): 6.4
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (3-43:26-65)

```

                                10          20          30
AAD-12                      FADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                ::  ::  :  :::::  :::::  ::  ::
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                                10          20          30          40          50

```

```

                                40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA
                                .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                                60          70          80          90          100          110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.9 bits: 21.2 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (3-43:26-65)

```

                                10          20          30
AAD-12                      FADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                ::  ::  :  :::::  :::::  ::  ::
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                                10          20          30          40          50

```

```

                                40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA
                                .... :
gi+AHw-111 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                                60          70          80          90          100          110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)
initn: 38 init1: 38 opt: 52 Z-score: 87.9 bits: 21.2 E(): 6.4
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (3-43:26-65)

```

                                10          20          30
AAD-12                      FADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                                ::  ::  :  :::::  :::::  ::  ::
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
                                10          20          30          40          50

```

```

                                40          50          60          70          80
AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHA
                                .... :
gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
                                60          70          80          90          100          110

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 init1: 47 opt: 59 Z-score: 87.2 bits: 22.9 E(): 7
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (21-58:198-242)


```

                10      20      30      40
AAD-12          FADMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                        ...  ...:  ...  :      :  ...  .
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170      180      190      200      210      220

```

```

                50      60      70      80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHA
                .....:  ..  .:
gi+AHw-303 VLGFGMTETETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230      240      250      260      270      280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)
initn: 52 initl: 52 opt: 52 Z-score: 86.7 bits: 21.2 E(): 7.5
Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
in 24 aa overlap (8-31:29-52)

```

                10      20      30
AAD-12          FADMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                        :  :  :::  :  .  ...:  .:  ...:
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10      20      30      40      50      60

```

```

                40      50      60      70      80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHA
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQTATKDEYESQQKELEGVANPIMMKFYGAGGE
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.5 bits: 19.0 E(): 8.7
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (36-56:5-25)

```

                10      20      30      40      50      60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP
                        .....:  ..  ...:  .  ...:
gi+AHw-462          AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
                10      20      30

```

```

                70      80
AAD-12 ETGRPSLLIGRHAHA

```

```

gi+AHw-462 LNSA

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-

[illegible]

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
  join: 42, opt: 30, open/ext: -10/-2, width: 32
  Scan time: 0.080
The best scores are:
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)      67 25.2      1.2

```

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 56 22.4 2.6
 gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
 57 22.5 4
 gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
 (204) 57 22.5 4.1
 gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
 52 21.2 5.8
 gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.2 6.7
 gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
 52 21.2 6.7
 gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
 52 21.2 6.7
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 22.8 7.5
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.1 7.8
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 19.0 8.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 initl: 65 opt: 67 Z-score: 100.7 bits: 25.2 E(): 1.2
 Smith-Waterman score: 67+ADs- 24.242+ACU- identity (53.030+ACU- similar)
 in 66 aa overlap (9-71:314-379)

	10	20	30	
AAD-12	ADMRAAYDALDEATRALV---HQRSARHSLVYSQSKLG			
	:	::	..	:
gi+AHw-113	VVNNNYDKWGSYAIGGSASPTILS	QGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNK		
	290	300	310	320
	330	340		
	40	50	60	70
AAD-12	HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI			
	:	..	::	...
gi+AHw-113	DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC			
	350	360	370	380
	390			

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 50 initl: 50 opt: 56 Z-score: 94.8 bits: 22.4 E(): 2.6
 Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
 in 44 aa overlap (12-51:34-77)

	10	20	30	
AAD-12	ADMRAAYDALDEATRALVHQRSARHS----LVYSQSKLGHV			
	:	:	::	...
gi+AHw-527	HITSNDELQKLLSSTTYVVVDF	FADWCPPCKAIAPVYEQLSTKHSVPDVLAF	AKVNVDHV	
	10	20	30	40
	50	60	70	80
AAD-12	QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI			
	:	...	:	:

50 60 70 80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHAI

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKILLKDLKETEQKVKDIQ
60 70 80 90 100 110

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.5 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (2-42:26-65)

AAD-12 ADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
.... :
gi+AHw-111 DELNENKSKELQEKKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.5 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (2-42:26-65)

AAD-12 ADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : : : : : : : : : : : : : : :
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
.... :
gi+AHw-111 DELNENKSKELQEKKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKIL
60 70 80 90 100 110

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.5 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (2-42:26-65)

AAD-12 ADMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
:: : : : : : : : : : : : : : : : : :
gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
10 20 30 40 50

AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI
.... :

70 80
AAD-12 ETGRPSLLIGRHAHAI

[illegible]

Kolmogorov-Smirnov statistic: 0.0842 (N+AD0-29) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 67 25.2 1.2

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 56 22.4 2.6

gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg (200)
56 22.2 4.9

gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
(204) 56 22.2 5

gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution Stru (119)
52 21.2 5.8

gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-Blom (134)
52 21.2 6.7

gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-Blom (134)
52 21.2 6.7

gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding protei (134)
52 21.2 6.7

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
59 22.8 7.4

gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
(152) 52 21.1 7.8

gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(38) 43 19.0 8.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 65 initl: 65 opt: 67 Z-score: 100.8 bits: 25.2 E(): 1.2
Smith-Waterman score: 67+ADs- 24.242+ACU- identity (53.030+ACU- similar)
in 66 aa overlap (8-70:314-379)

	10	20	30	
AAD-12	DMRAAYDALDEATRALV---HQRSARHSLVYSQSKLG			
	:	::	..	:
gi+AHw-113	VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAE	SMKWNWRTNK		
	290	300	310	320
	330	340		
	40	50	60	70
AAD-12	HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIP			
	:	::
gi+AHw-113	DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC			
	350	360	370	380
	390			

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)

initn: 45 initl: 45 opt: 56 Z-score: 94.8 bits: 22.4 E(): 2.6
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (11-50:34-77)

AAD-12 DMRAAYDALDEATRALVHQRSARHS----LVYSQSKLGHV
 .: . :
 gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFQKVNVDHV
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP
 :
 gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGLGLAQKRVAGA
 70 80 90 100 110 120

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 56 Z-score: 90.0 bits: 22.2 E(): 4.9
 Smith-Waterman score: 56+ADs- 29.825+ACU- identity (59.649+ACU- similar)
 in 57 aa overlap (1-52:94-149)

AAD-12 10 20
 DMRAA-----YDALDEATRALVHQRSARHS
 :
 gi+AHw-144 ISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKET
 70 80 90 100 110 120

30 40 50 60 70 80
 AAD-12 LVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP
 . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
 gi+AHw-144 IPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREKV
 130 140 150 160 170 180

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)
 initn: 41 initl: 41 opt: 56 Z-score: 89.9 bits: 22.2 E(): 5
 Smith-Waterman score: 56+ADs- 29.825+ACU- identity (59.649+ACU- similar)
 in 57 aa overlap (1-52:98-153)

AAD-12 10 20
 DMRAA-----YDALDEATRALVHQRSARHS
 :
 gi+AHw-622 ISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKET
 70 80 90 100 110 120

30 40 50 60 70 80
 AAD-12 LVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP
 . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
 gi+AHw-622 IPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREKV
 130 140 150 160 170 180

+AD4APg-gi+AHw-160285626+AHw-pdb+AHw-2JMH+AHw-A Chain A, Nmr Solution
 Structur (119 aa)
 initn: 38 initl: 38 opt: 52 Z-score: 88.7 bits: 21.2 E(): 5.8
 Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
 in 43 aa overlap (1-41:11-50)

10 20 30 40

```

AAD-12          DMRAAYDAL--DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                :::  :::  .....  .....:  :::  ....  :
gi+AHw-160 GSQEHKPKKDDFRNEFDHLLIEQANHAI--EKGEHQLLYLQHLDELNENKSKELQEKI
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHAIP

```

```

gi+AHw-160 IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKILLKDLKETEQKVVDIQ
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-111120450+AHw-gb+AHw-ABH06359.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (1-41:26-65)

```

                10      20      30
AAD-12          DMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  .....  .....:  :::
gi+AHw-111 MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHL
                10      20      30      40      50

```

```

                40      50      60      70      80
AAD-12 GHVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGRHAHAIP

```

```

        ....  :
gi+AHw-111 DELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKIL
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-111120436+AHw-gb+AHw-ABH06352.1+AHw- Blo t 5 allergen +AFs-
Blomia t (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (1-41:26-65)

```

                10      20      30
AAD-12          DMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
                :::  :::  .....  .....:  :::
gi+AHw-111 MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHL
                10      20      30      40      50

```

```

                40      50      60      70      80
AAD-12 GHVQQAGSAYIGYGM DTTATPLRPLVKVHPETGRPSLLIGRHAHAIP

```

```

        ....  :
gi+AHw-111 DELNENKSKELQEKI IRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTL SKIL
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-4204917+AHw-gb+AHw-AAD10850.1+AHw- major IgE-binding
protein Bl (134 aa)

initn: 38 initl: 38 opt: 52 Z-score: 87.6 bits: 21.2 E(): 6.7
Smith-Waterman score: 52+ADs- 27.907+ACU- identity (69.767+ACU- similar)
in 43 aa overlap (1-41:26-65)

10 20 30

AAD-12 DMRAAYDAL--DEATRALVHQRSARHSLVYSQSKL
 :: : : : :
 gi+AHw-420 MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAI---EKGEHQLLYLQHQQL
 10 20 30 40 50

40 50 60 70 80
 AAD-12 GHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP
 :
 gi+AHw-420 DELNENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKIL
 60 70 80 90 100 110

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 86.7 bits: 22.8 E(): 7.4
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (19-56:198-242)

10 20 30 40
 AAD-12 DMRAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
 :: : : : : : : : :
 gi+AHw-303 LVQHTASDLNQLDQNPFRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
 170 180 190 200 210 220

50 60 70 80
 AAD-12 YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP
 : : : :
 gi+AHw-303 VLGFGMDDTETARKVVRGDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
 230 240 250 260 270 280

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 86.4 bits: 21.1 E(): 7.8
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (6-29:29-52)

10 20 30
 AAD-12 DMRAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
 : : :: : . : : : : : : :
 gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDAEAAARISAKNALESYAYSLRNTLSDS
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 QAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIP
 gi+AHw-144 KVDEKLDAGDKQKLTAIEDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
 70 80 90 100 110 120

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.4 bits: 19.0 E(): 8.8
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (34-54:5-25)

10 20 30 40 50 60

```

AAD-12  AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHP
          ..... :. .:: . .::
gi+AHw-462  AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
              10          20          30

          70          80
AAD-12  ETGRPSLLIGRHAHAIP
gi+AHw-462  LNSA

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:15 2010 done: Fri Feb 5 12:56:15 2010
Total Scan time: 0.080 Total Display time: 0.010

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 141 - 220 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      1      8:+AD0- +ACo-
      34      3     21:+AD0- +ACo-
      36     25     44:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38     59     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      40     104
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQ-
      42      91
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-

```

```

44      128
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
46      143
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
48      112
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
50      113
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
52      117
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
54      110
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
56      72
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
58      73
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
60      69      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0AKgA9AD0APQA9AD0APQ-
62      58      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      39      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66      35      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      17      20:+AD0APQA9AD0APQA9ACo-
70      21      16:+AD0APQA9AD0APQAqAD0-
72      30      12:+AD0APQA9ACoAPQA9AD0APQA9AD0-
74      12      10:+AD0APQA9ACo-
76      12       7:+AD0APQAqAD0-
78        8       6:+AD0AKgA9-
80        4       4:+AD0AKg-
82        6       3:+ACoAPQ-
84        2       3:+ACo-
86        3       2:+ACo-
88        0       2:+ACo-          inset +AD0- represents 1 library sequences
90        0       1:+ACo-
92        0       1:+ACo-          :+ACo-
94        0       1:+ACo-          :+ACo-
96        1       1:+ACo-          :+ACo-
98        0       0:              +ACo-
100       0       0:              +ACo-
102       0       0:              +ACo-
104       1       0:+AD0-         +ACoAPQ-
106       0       0:              +ACo-
108       0       0:              +ACo-
110       0       0:              +ACo-
112       0       0:              +ACo-
114       0       0:              +ACo-
116       0       0:              +ACo-
118       0       0:              +ACo-

```

```
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 6.00400.00326+ADs- mu+AD0- -
1.3123 0.169
mean+AF8-var+AD0-38.7001 9.412, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.206167
Kolmogorov-Smirnov statistic: 0.0808 (N+AD0-28) at 50
```

```
FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
```

```
join: 42, opt: 30, open/ext: -10/-2, width: 32
```

```
Scan time: 0.080
```

```
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   69 26.0   0.69
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   56 22.6   2.3
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.0   6.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.3   7
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)   43 19.1   8
```

```
+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
```

```
initn: 65 init1: 65 opt: 69 Z-score: 105.3 bits: 26.0 E(): 0.69
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (7-80:314-393)
```

```

                                10      20      30
AAD-12                        MRAAYDALDEATRALV---HQRSARHSLVYSQSKLG
                                : :: .. : : ... :.. ..
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEGAAESMKWNWRTNK
                290      300      310      320      330      340

                40      50      60      70      80
AAD-12 HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PG
                : . :. ... :: . :: . . : :. :. : : .. ::
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                350      360      370      380      390
```

```
+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
```

```
initn: 45 init1: 45 opt: 56 Z-score: 95.8 bits: 22.6 E(): 2.3
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (10-49:34-77)
```

```

                                10      20      30
AAD-12                        MRAAYDALDEATRALVHQRSARHS----LVYSQSKLGHV
                                .: . :. :...: :.... .. ::
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHV
                10      20      30      40      50      60
```



```

      10      20      30      40      50      60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP
      ..... :. .:: .  ::
gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
      10      20      30

```

[illegible]

inset +AD0- represents 1 library sequences

Kolmogorov-Smirnov statistic: 0.0815 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 69 26.1 0.65
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 56 22.6 2.2
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
59 23.1 6.2
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
(152) 52 21.3 6.8
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(38) 43 19.1 8.1

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 65 init1: 65 opt: 69 Z-score: 105.8 bits: 26.1 E(): 0.65
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (6-79:314-393)

			10		20		30
AAD-12			RAAYDALDEATRALV---		HQRSARHSLVYSQSKLG		
			:	:	:	:	:
gi+AHw-113	VVNNNYDKWGSYAIGGSASPTILS	QGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNK					
	290	300	310	320	330	340	
	40	50	60	70	80		
AAD-12	HVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---	PGM					
	:	:	:	:	:	:	:
gi+AHw-113	DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC						
	350	360	370	380	390		

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)

initn: 45 init1: 45 opt: 56 Z-score: 96.0 bits: 22.6 E(): 2.2
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (9-48:34-77)

			10		20		30
AAD-12			RAAYDALDEATRALVHQRSARHS----		LVYSQSKLGHV		
			:	:	:	:	:
gi+AHw-527	HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQ	LSTKHSVPDVLAFQKVNVDHV					
	10	20	30	40	50	60	
	40	50	60	70	80		
AAD-12	QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM						
	:	:	:	:	:	:	:
gi+AHw-527	QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA	AAEKLGLGGLAQKRVAGA					
	70	80	90	100	110	120	

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 88.1 bits: 23.1 E(): 6.2
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (17-54:198-242)

```

                10         20         30         40
AAD-12          RAAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                ...  ...:  ...:  :  :  :  :  :  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170         180         190         200         210         220

```

```

                50         60         70         80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGM
                .....:  :  :
gi+AHw-303 VLGFGMTDETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230         240         250         260         270         280

```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 87.4 bits: 21.3 E(): 6.8
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (4-27:29-52)

```

                10         20         30
AAD-12          RAAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                :  :  :::  :  .  ...:  :  :  :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
                10         20         30         40         50         60

```

```

                40         50         60         70         80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGM
gi+AHw-144 KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATATKDEYESQQKELEGVANPIMMKFYGAGGE
                70         80         90         100        110        120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 86.0 bits: 19.1 E(): 8.1
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (32-52:5-25)

```

                10         20         30         40         50         60
AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP
                .....:  :  ...:  .  ...:
gi+AHw-462          AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
                10         20         30

```

```

                70         80
AAD-12 ETGRPSLLIGRHAHAIPGM

```

gi+AHw-462 LNSA

[illegible]

```

54      122
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQ-
   56      78
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
   58      77
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
-
   60      53      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
   62      59      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
   64      42      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   66      27      25:+AD0APQA9AD0APQA9AD0APQAq-
   68      25      20:+AD0APQA9AD0APQA9ACoAPQA9-
   70      19      16:+AD0APQA9AD0APQAqAD0-
   72      23      12:+AD0APQA9ACoAPQA9AD0APQ-
   74      17      10:+AD0APQA9ACoAPQA9-
   76       8       7:+AD0APQAq-
   78       6       6:+AD0AKg-
   80      11      4:+AD0AKgA9AD0-
   82       3       3:+ACo-
   84       1       3:+ACo-
   86       2       2:+ACo-
   88       1       2:+ACo-          inset +AD0- represents 1 library sequences
   90       0       1:+ACo-
   92       0       1:+ACo-          :+ACo-
   94       0       1:+ACo-          :+ACo-
   96       1       1:+ACo-          :+ACo-
   98       0       0:              +ACo-
  100       0       0:              +ACo-
  102       0       0:              +ACo-
  104       0       0:              +ACo-
  106       1       0:+AD0-         +ACoAPQ-
  108       0       0:              +ACo-
  110       0       0:              +ACo-
  112       0       0:              +ACo-
  114       0       0:              +ACo-
  116       0       0:              +ACo-
  118       0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.67850.00322+ADs- mu+AD0- 0.7403
0.166
mean+AF8-var+AD0-36.5024 8.727, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.212282
Kolmogorov-Smirnov statistic: 0.0835 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)     6926.3     0.57

```

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 56 22.7 2.2
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholletia (465)
 59 23.2 5.8
 gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
 (152) 52 21.4 6.6
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 19.0 8.4

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 initl: 65 opt: 69 Z-score: 106.8 bits: 26.3 E(): 0.57
 Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
 in 80 aa overlap (5-78:314-393)

		10	20	30
AAD-12		AAYDALDEATRALV---HQRSARHSLVYSQSKLG		
		:	:	:
gi+AHw-113	VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNK			
	290 300 310 320 330 340			

	40	50	60	70	80
AAD-12	HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMD				
	:	:	:	:	:
gi+AHw-113	DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC				
	350 360 370 380 390				

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 initl: 45 opt: 56 Z-score: 96.4 bits: 22.7 E(): 2.2
 Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
 in 44 aa overlap (8-47:34-77)

		10	20	30
AAD-12		AAYDALDEATRALVHQRSARHS----LVYSQSKLGHV		
		:	:	:
gi+AHw-527	HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQSLTKHSVPDVLAFQKVNVDHV			
	10 20 30 40 50 60			

	40	50	60	70	80
AAD-12	QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD				
	:	:	:	:	:
gi+AHw-527	QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGKLGGLAQKRVAGA				
	70 80 90 100 110 120				

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 88.7 bits: 23.2 E(): 5.8
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (16-53:198-242)

		10	20	30
AAD-12		AAYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA		
		:	:	:

gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
 170 180 190 200 210 220

40 50 60 70 80
 AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD
 :: ..

gi+AHw-303 VLGFGMTTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
 230 240 250 260 270 280

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
 Full+AD0-Heat (152 aa)
 initn: 52 initl: 52 opt: 52 Z-score: 87.6 bits: 21.4 E(): 6.6
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (3-26:29-52)

10 20 30
 AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQ
 : : : : : . . . : : :
 gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
 10 20 30 40 50 60

40 50 60 70 80
 AAD-12 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMD

gi+AHw-144 KVDEKLDAGDKQKLTAIEDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
 70 80 90 100 110 120

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.8 bits: 19.0 E(): 8.4
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (31-51:5-25)

10 20 30 40 50 60
 AAD-12 AAYDALDEATRALVHQRSARHSLVYSQSKLGHVQAGSAYIGYGMTTATPLRPLVKVHP
 : . : :
 gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKN
 10 20 30

70 80
 AAD-12 ETGRPSLLIGRHAHAIPGMD

gi+AHw-462 LNSA

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:18 2010 done: Fri Feb 5 12:56:18 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 144 - 223 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      0      8:  +ACo-
      34      5      21: +AD0APQ-      +ACo-
      36      45      44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      38      68
72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      40      74
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      42      100
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0-      +ACo-
      44      144
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
      46      106
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
      48      125
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      50      109
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
      52      114
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
      54      124
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      56      82
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-

```

```

58      68
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      57      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      61
40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
64      40      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      26      25:+AD0APQA9AD0APQA9AD0APQAq-
68      27      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      20      16:+AD0APQA9AD0APQAqAD0-
72      18      12:+AD0APQA9ACoAPQA9-
74      22      10:+AD0APQA9ACoAPQA9AD0APQ-
76      13      7:+AD0APQAqAD0APQ-
78      6      6:+AD0AKg-
80      7      4:+AD0AKgA9-
82      1      3:+ACo-
84      2      3:+ACo-
86      1      2:+ACo-
88      2      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     0      0:          +ACo-
104     0      0:          +ACo-
106     1      0:+AD0-          +ACoAPQ-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120 0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.70930.00309+ADs- mu+AD0- 0.5536
0.160
mean+AF8-var+AD0-36.0156 8.639, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.213712
Kolmogorov-Smirnov statistic: 0.0828 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.070
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  69 26.4      0.54
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  56 22.7      2.1
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)  59 23.2      5.6
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)  52 21.4      6.4

```

gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(38) 43 19.1 8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 initl: 65 opt: 69 Z-score: 107.1 bits: 26.4 E(): 0.54
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (4-77:314-393)

```

                                10          20          30
AAD-12                      AYDALDEATRALV---HQRSARHSLVYSQSKLG
                                :  ::  .  :  :  ::  .  .  .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNK
                290          300          310          320          330          340

                40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAHAI---PGMDA
                :  .  ::  .  .  .  ::  .  ::  .  .  :  ::  .  :  .  ::
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                350          360          370          380          390
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 initl: 45 opt: 56 Z-score: 96.8 bits: 22.7 E(): 2.1
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (7-46:34-77)

```

                                10          20          30
AAD-12                      AYDALDEATRALVHQRSARHS----LVYSQSKLGHV
                                .:  .  .:  ::::  :....  .  ::
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFAKVNVDPHV
                10          20          30          40          50          60

                40          50          60          70          80
AAD-12 QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAHAIIPGMDA
                :...  :  .  :  :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGKLGGLAQKRVAGA
                70          80          90          100          110          120
```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 89.0 bits: 23.2 E(): 5.6
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (15-52:198-242)

```

                                10          20          30
AAD-12                      AYDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :..  :::  .  :  :  :  :  :  :
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
                170          180          190          200          210          220

                40          50          60          70          80
AAD-12 YIGYGMT-TATPLRPLVKVHPETGRPSLLIGRHAHAHAIIPGMDA
                .....  :  .  :
```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

opt      E()
+ADw- 20    2      0:+AD0-
22      0      0:          one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      0      0:
30      1      2:+ACo-
32      0      8:   +ACo-
34      5     21:+AD0APQ-   +ACo-
36     48    44:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-+AD0APQA9ACoAPQ-
38     70
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
40     54   101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42     109
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0-   +ACo-
44     126
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-   +ACo-
46     126   138:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0-   +ACo-
48     118
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-   +ACo-
50     106
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9-   +ACo-
52     126
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
54     122   91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQ-
56     70
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
58     56   62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
60     74
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
62     53   40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
64     43   32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66     33   25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68     23   20:+AD0APQA9AD0APQA9ACoAPQ-
70     24   16:+AD0APQA9AD0APQAqAD0APO-

```

```

72      16      12:+AD0APQA9ACoAPQA9-
74      22      10:+AD0APQA9ACoAPQA9AD0APQ-
76      11      7:+AD0APQAqAD0-
78      13      6:+AD0AKgA9AD0APQ-
80      6       4:+AD0AKg-
82      7       3:+ACoAPQA9-
84      2       3:+ACo-
86      1       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     1       0:+AD0-          +ACoAPQ-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.06930.00331+ADs- mu+AD0- 3.6737
0.170
mean+AF8-var+AD0-34.1757 8.340, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.219389
Kolmogorov-Smirnov statistic: 0.0917 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   69 26.9    0.38
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   56 22.9    1.8
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.7    4.1
gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName: Full+AD0-
( 152)   52 21.6    5.5
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)   43 19.0    8.5
gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant allerg ( 200)
51 21.3    9.3
gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName: Full+AD0-Gl
( 204)   51 21.3    9.5

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

```

initn: 65 initl: 65 opt: 69 Z-score: 109.9 bits: 26.9 E(): 0.38
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (3-76:314-393)

```

                                10          20
AAD-12                      YDALDEATRALV---HQRSARHSLVYSQSKLG
                                :  ::  .  :  :  ::  .  .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNK
                290          300          310          320          330          340
```

```

                30          40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAA
                :  .  ::  .  .  ::  .  .  :  ::  .  :  .  ::
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                350          360          370          380          390
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 initl: 45 opt: 56 Z-score: 97.9 bits: 22.9 E(): 1.8
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (6-45:34-77)

```

                                10          20          30
AAD-12                      YDALDEATRALVHQRSARHS----LVYSQSKLGHV
                                .:  .  .:  ::::  :....  .  ::
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFAKVNVDPHV
                10          20          30          40          50          60
```

```

                40          50          60          70          80
AAD-12 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
                :...  :  .  :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLAQKRVAGA
                70          80          90          100          110          120
```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 91.4 bits: 23.7 E(): 4.1
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (14-51:198-242)

```

                                10          20          30
AAD-12                      YDALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :..  :::  .:  :  :  :  ::
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
                170          180          190          200          210          220
```

```

                40          50          60          70          80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
                .:..:::  ::  .:
gi+AHw-303 VLGFGMDTETARKVRGEDDQQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230          240          250          260          270          280
```

+AD4APg-gi+AHw-14423730+AHw-sp+AHw-P78983.2+AHw-HSP70+AF8-ALTAL RecName:
Full+AD0-Heat (152 aa)

initn: 52 initl: 52 opt: 52 Z-score: 89.1 bits: 21.6 E(): 5.5
 Smith-Waterman score: 52+ADs- 41.667+ACU- identity (62.500+ACU- similar)
 in 24 aa overlap (1-24:29-52)

```

                                10      20      30
AAD-12                      YDALDEATRALVHQRSARHSLVYSQSKLGHVQ
                                : : : : : . . . : : :
gi+AHw-144 KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSRLRNTLSDS
              10      20      30      40      50      60

```

```

              40      50      60      70      80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA

gi+AHw-144 KVDEKLDAGDKQKLTAIEDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
              70      80      90      100      110      120

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.7 bits: 19.0 E(): 8.5
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (29-49:5-25)

```

              10      20      30      40      50      60
AAD-12 YDALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
                                : : : : : . . . : : :
gi+AHw-462                      AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLN
                                10      20      30

```

```

              70      80
AAD-12 GRPSLLIGRHAHAIPGMDAA

```

gi+AHw-462 SA

+AD4APg-gi+AHw-144952780+AHw-gb+AHw-ABP04044.1+AHw- Bla g 5 variant
 allergen +AFs- (200 aa)
 initn: 41 initl: 41 opt: 51 Z-score: 85.0 bits: 21.3 E(): 9.3
 Smith-Waterman score: 51+ADs- 27.660+ACU- identity (61.702+ACU- similar)
 in 47 aa overlap (1-47:104-149)

```

                                10      20      30
AAD-12                      YDALDEATRALVHQRSARHSLVYSQSKLGH
                                : : : : : . . . : : :
gi+AHw-144 LSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKETIPYYTKKFDE
              80      90      100      110      120      130

```

```

              40      50      60      70      80
AAD-12 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
              : : : : : : : :
gi+AHw-144 VVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREKVLGLPAIKAWV
              140      150      160      170      180      190

```

+AD4APg-gi+AHw-6225491+AHw-sp+AHw-O18598.3+AHw-GST1+AF8-BLAGE RecName:
 Full+AD0-Glutat (204 aa)

initn: 41 initl: 41 opt: 51 Z-score: 84.8 bits: 21.3 E(): 9.5
 Smith-Waterman score: 51+ADs- 27.660+ACU- identity (61.702+ACU- similar)
 in 47 aa overlap (1-47:108-153)

```

                                10      20      30
AAD-12                        YDALDEATRALVHQRSARHSLVYSQSKLGH
                                ::: :: .. . .... : ...
gi+AHw-622 LSGKDDWENLEIDMIVDTISDFRAAIANYHYDA-DENSKQKKWDPLKKETIPYYTKKFDE
                        80      90      100      110      120      130

                        40      50      60      70      80
AAD-12 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAA
                        : ..... : : :
gi+AHw-622 VVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALREKVLGLPAIKAWV
                        140      150      160      170      180      190

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:20 2010 done: Fri Feb 5 12:56:20 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 146 - 225 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      1      8:+AD0- +ACo-
      34      7      21:+AD0APQA9- +ACo-
      36      46      44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
      38      74
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
      40      55      101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-

```

[illegible]

```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.10760.0033+ADs- mu+AD0- 3.4677
0.170
mean+AF8-var+AD0-33.6122 8.210, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.221221
Kolmogorov-Smirnov statistic: 0.0903 (N+AD0-27) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 69 26.9 0.36
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 56 23.0 1.7
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 23.7 3.9
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38) 43 19.1 8

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 65 init1: 65 opt: 69 Z-score: 110.3 bits: 26.9 E(): 0.36
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (2-75:314-393)

```

                                10                20
AAD-12                        DALDEATRALV---HQRSARHSLVYSQSKLG
                                : :: .. : : ... :. :.
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEGAAAESMKWNWRTNK
                290          300          310          320          330          340

                30          40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAE
                : . :. ... :. :. :. :. :. :. :. :. :. :. :. :. :.
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                350          360          370          380          390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)

initn: 45 init1: 45 opt: 56 Z-score: 98.4 bits: 23.0 E(): 1.7
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (5-44:34-77)

```

                                10                20                30
AAD-12                        DALDEATRALVHQRSARHS----LVYSQSKLGHV
                                .: . :. :. :. :. :. :. :. :. :. :.
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHV
                10          20          30          40          50          60

```

```

                40          50          60          70          80
AAD-12 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE
      ..... :   :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAGA
                70          80          90          100          110          120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 91.7 bits: 23.7 E(): 3.9
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (13-50:198-242)

```

                        10          20          30
AAD-12                DALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                        ... :... :... :   :   :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
                170          180          190          200          210          220

```

```

                40          50          60          70          80
AAD-12 YIGYGMDDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAE
      ..... :   :
gi+AHw-303 VLGFGMDDTETARKVVRGDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230          240          250          260          270          280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 86.1 bits: 19.1 E(): 8
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (28-48:5-25)

```

                10          20          30          40          50          60
AAD-12 DALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETG
                        ..... :... :... :   :
gi+AHw-462                AITCGQVSSALSSCLGYLKNNGGAVPPGSSCGIKNLNS
                        10          20          30

```

```

                70          80
AAD-12 RPSLLIGRHAHAIPGMDAAE

```

gi+AHw-462 A

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:21 2010 done: Fri Feb 5 12:56:21 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

	opt	E()
+ADw-	20	2 0:+AD0-
22	0	0:
24	0	0:
26	0	0:
28	0	0:
30	0	2:+ACo-
32	1	8:+AD0- +ACo-
34	2	21:+AD0- +ACo-
36	21	44:+AD0APQA9AD0APQA9AD0- +ACo-
38	86	
72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ		
A9AD0APQ-		
40	77	
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
Q-		+ACo-
42	103	
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQ-		+ACo-
44	121	
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-		+ACo-
46	138	
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-		
48	105	
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQ-		+ACo-
50	112	
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-		+ACo-
52	115	
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP		
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-		
54	104	
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ		
A9AD0APQA9ACoAPQA9AD0APQ-		
56	96	
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg		
A9AD0APQA9AD0APQ-		
58	53	62:+AD0APQA9AD0APQA9AD0APOA9AD0APQA9AD0APQA9AD0APOA9- +ACo-

```

60      76
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ
-
62      44      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      43      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66      36      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      23      20:+AD0APQA9AD0APQA9ACoAPQ-
70      31      16:+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
72      14      12:+AD0APQA9ACoAPQ-
74      18      10:+AD0APQA9ACoAPQA9-
76      19      7:+AD0APQAqAD0APQA9AD0-
78      13      6:+AD0AKgA9AD0APQ-
80      5       4:+AD0AKg-
82      9       3:+ACoAPQA9-
84      0       3:+ACo-
86      1       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     1       0:+AD0-          +ACoAPQ-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.09990.0033+ADs- mu+AD0- 3.2779
0.170
mean+AF8-var+AD0-34.4388 8.386, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.218550
Kolmogorov-Smirnov statistic: 0.0896 (N+AD0-27) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  69 26.9      0.38
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  56 23.0      1.7
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.7      4
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)   43 19.1      8.1

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 initl: 65 opt: 69 Z-score: 110.0 bits: 26.9 E(): 0.38
Smith-Waterman score: 69+ADs- 23.750+ACU- identity (51.250+ACU- similar)
in 80 aa overlap (1-74:314-393)

```

                                10          20
AAD-12          ALDEATRALV---HQRSARHSLVYSQSKLG
                   : : . . : : . . . .
gi+AHw-113 VVNNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNK
              290          300          310          320          330          340
```

```

              30          40          50          60          70          80
AAD-12 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAES
           : . : . . . : : . : : . . : : . : . : : : : :
gi+AHw-113 DVLENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
              350          360          370          380          390
```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 initl: 45 opt: 56 Z-score: 98.2 bits: 23.0 E(): 1.7
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (4-43:34-77)

```

                                10          20
AAD-12          ALDEATRALVHQRSARHS----LVYSQSKLGHV
                   . : . . : : : : : : : : : :
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHV
              10          20          30          40          50          60
```

```

              30          40          50          60          70          80
AAD-12 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAES
           : : : : : : : : : : : :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGKLGGLAQKRVAGA
              70          80          90          100          110          120
```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 91.6 bits: 23.7 E(): 4
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (12-49:198-242)

```

                                10          20          30
AAD-12          ALDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                   : : . : : : . : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
              170          180          190          200          210          220
```

```

              40          50          60          70          80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAES
           : : : : : : : : : :
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230          240          250          260          270          280
```


+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 86.1 bits: 19.1 E(): 8.1
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (27-47:5-25)

```

                10         20         30         40         50         60
AAD-12 ALDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPETGR
                .....:..:..:
gi+AHw-462                AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
                        10         20         30

                70         80
AAD-12 PSLLLIGRHAHAIPGMDAAES

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:21 2010 done: Fri Feb 5 12:56:22 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 148 - 227 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      1      8:+AD0- +ACo-
      34      3     21:+AD0- +ACo-
      36     22     44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      38     76     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9ACoAPQA9-
      40     73
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-

```

```

42      126
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
44      113
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
46      142
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
48      112
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
50      105
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
52      112
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
54      100
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
56      95      76:+AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
58      57      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
60      71
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
62      41      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      47      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66      35      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      24      20:+AD0APQA9AD0APQA9ACoAPQ-
70      31      16:+AD0-+AD0APQA9AD0AKgA9AD0APQA9AD0-
72      16      12:+AD0APQA9ACoAPQA9-
74      20      10:+AD0APQA9ACoAPQA9AD0-
76      15      7:+AD0APQAqAD0APQ-
78      13      6:+AD0AKgA9AD0APQ-
80      7       4:+AD0AKgA9-
82      8       3:+ACoAPQA9-
84      0       3:+ACo-
86      1       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     1       0:+AD0-          +ACoAPQ-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-

```

```

116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.13440.00328+ADs- mu+AD0- 3.1328
0.170
mean+AF8-var+AD0-34.2358 8.315, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.219197
Kolmogorov-Smirnov statistic: 0.0849 (N+AD0-27) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 68 26.6 0.46
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 56 23.0 1.7
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 23.7 4
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38) 43 19.1 7.9

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 initl: 65 opt: 68 Z-score: 108.4 bits: 26.6 E(): 0.46
Smith-Waterman score: 68+ADs- 23.077+ACU- identity (51.282+ACU- similar)
in 78 aa overlap (2-73:316-393)

```

                                10      20
AAD-12                        LDEATRALV---HQRSARHSLVYSQSKLGHV
                                :: .. : : :: :: :: :: :: ::
gi+AHw-113 NNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDV
                290      300      310      320      330      340

                30      40      50      60      70      80
AAD-12 QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESE
                . :. ... :: . :: . . : :. :. : : .. ::
gi+AHw-113 LENGAIFVASGVDPVLTPEQSAGMIPAEPEGESALSLTSSAGVLSCQPGAPC
                350      360      370      380      390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 initl: 45 opt: 56 Z-score: 98.3 bits: 23.0 E(): 1.7
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (3-42:34-77)

```

                                10      20
AAD-12                        LDEATRALVHQRSARHS----LVYSQSKLGHV
                                .: . :. :: :: :: :: :: :: :: ::
gi+AHw-527 HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHV
                10      20      30      40      50      60

```

```

      30      40      50      60      70      80
AAD-12 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
      :...:  :  :
gi+AHw-527 QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAGAAEKLGLAQKRVAGA
      70      80      90      100      110      120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 91.6 bits: 23.7 E(): 4
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (11-48:198-242)

```

                        10      20      30
AAD-12                LDEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                        :...:  :  :
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
      170      180      190      200      210      220

```

```

      40      50      60      70      80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
      :...:  :  :
gi+AHw-303 VLGFMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230      240      250      260      270      280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 86.2 bits: 19.1 E(): 7.9
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (26-46:5-25)

```

      10      20      30      40      50      60
AAD-12 LDEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRP
      :...:  :  :
gi+AHw-462                AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
                        10      20      30

```

```

      70      80
AAD-12 SLLIGRHAHAIPGMDAAESE

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

opt      E()
+ADw- 20      2      0:+AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      0      0:
30      0      2:+ACo-
32      1      8:+AD0- +ACo-
34      3      21:+AD0- +ACo-
36      21     44:+AD0APQA9AD0APQA9AD0- +ACo-
38      59     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
40      95
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
42      116
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
44      112
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
46      165
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0-
48      116
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
50      96
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
52      114
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
54      111
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
56      84
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
58      59
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60      65
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
62      55      40:+AD0APQA9AD0APQA9AD0APQ-+AD0APQA9AD0APQAqAD0APQA9AD0APQ-
64      44      32:+AD0APOA9AD0APOA9AD0APOA9AD0AKgA9AD0APOA9-

```

```

66      28      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
68      26      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      20      16:+AD0APQA9AD0APQAqAD0-
72      18      12:+AD0APQA9ACoAPQA9-
74      26      10:+AD0APQA9ACoAPQA9AD0APQA9-
76      10      7:+AD0APQAqAD0-
78      11      6:+AD0AKgA9AD0-
80      7       4:+AD0AKgA9-
82      3       3:+ACo-
84      0       3:+ACo-
86      1       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      0       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     1       0:+AD0-          +ACoAPQ-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.57350.00325+ADs- mu+AD0- 0.9983
0.168
mean+AF8-var+AD0-36.6232 8.752, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.211932
Kolmogorov-Smirnov statistic: 0.0774 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   68 26.1      0.66
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   56 22.7      2.1
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.3      5.4
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)   43 19.0      8.3

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 68 Z-score: 105.6 bits: 26.1 E(): 0.66
Smith-Waterman score: 68+ADs- 23.077+ACU- identity (51.282+ACU- similar)
in 78 aa overlap (1-72:316-393)

```

```

                                10      20
AAD-12      DEATRALV---HQRSARHSLVYSQSKLGHV
                                :: .. : : ... :. :
gi+AHw-113  NNNYDKWGSYAIGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDV
                290      300      310      320      330      340

```

```

                30      40      50      60      70      80
AAD-12  QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAHAI---PGMDAAESER
                . :. ... :. :. . :. . : :. :. :. :. :. :. :
gi+AHw-113  LENGAIFVASGVDPVLTPEQSAGMIPAEPGESALSLSAGVLSCQPGAPC
                350      360      370      380      390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 init1: 45 opt: 56 Z-score: 96.7 bits: 22.7 E(): 2.1
Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
in 44 aa overlap (2-41:34-77)

```

                                10      20
AAD-12      DEATRALVHQRSARHS----LVYSQSKLGHV
                                .: . : : : : : : : : : : :
gi+AHw-527  HITSNDELQKLLSSTTYVVVDFFADWCPPCKAIAIPVYEQQLSTKHSVPDVLAFAKVNVVDHV
                10      20      30      40      50      60

```

```

                30      40      50      60      70      80
AAD-12  QQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
                : : : : : : : : : : : : : : : :
gi+AHw-527  QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKRVAGA
                70      80      90      100      110      120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 init1: 47 opt: 59 Z-score: 89.3 bits: 23.3 E(): 5.4
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (10-47:198-242)

```

                                10      20      30
AAD-12      DEATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :. :. :. :. :. :. :. :. :. :
gi+AHw-303  LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                170      180      190      200      210      220

```

```

                40      50      60      70      80
AAD-12  YIGYGMDDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESER
                . : : : : : : : : : : : : : :
gi+AHw-303  VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                230      240      250      260      270      280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 init1: 43 opt: 43 Z-score: 85.9 bits: 19.0 E(): 8.3
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (25-45:5-25)

```

                10         20         30         40         50         60
AAD-12 DEATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPS
                .....:..:..:..:
gi+AHw-462                AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
                        10         20         30

                70         80
AAD-12 LLIGRHAHAIPGMDAAESER

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010
Total Scan time: 0.080 Total Display time: 0.000

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

1+AD4APgA+-AAD-12: 150 - 229 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      2      2:+ACo-
      32      0      8: +ACo-
      34      3      21:+AD0- +ACo-
      36      18     44:+AD0APQA9AD0APQA9- +ACo-
      38      56     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      40     102
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACo-
      42     112
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      44     116
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-

```


0.166

mean+AF8-var+AD0-36.6820 8.707, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
 Lambda+AD0- 0.211762
 Kolmogorov-Smirnov statistic: 0.0876 (N+AD0-27) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 67 25.8 0.8
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 56 22.7 2.1
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 23.3 5.2
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 19.0 8.3

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)

initn: 65 initl: 65 opt: 67 Z-score: 104.1 bits: 25.8 E(): 0.8
 Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
 in 67 aa overlap (8-71:327-393)

		10	20	30	
AAD-12		EATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG			
		: . . : : :			
gi+AHw-113	IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FV ASG				
	300 310 320 330 340 350				
	40 50 60 70 80				
AAD-12	MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERF				
	. : . : . : . : . : . : . : . :				
gi+AHw-113	VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC				
	360 370 380 390				

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)

initn: 45 initl: 45 opt: 56 Z-score: 96.8 bits: 22.7 E(): 2.1
 Smith-Waterman score: 56+ADs- 29.545+ACU- identity (63.636+ACU- similar)
 in 44 aa overlap (1-40:34-77)

		10	20	
AAD-12		EATRALVHQRSARHS----LVYSQSKLGHV		
		. : . : . : . : . : . : . :		
gi+AHw-527	HITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQ LSTKHSVPDVLAFKVNVDHV			
	10 20 30 40 50 60			
	30 40 50 60 70 80			
AAD-12	QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF			
	: . . . : . : . :			
gi+AHw-527	QDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAEKLGGLAQKRVAGA			
	70 80 90 100 110 120			

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 89.5 bits: 23.3 E(): 5.2
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (9-46:198-242)

```

                                10      20      30
AAD-12      EATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ...  ...  ...  :  ...
gi+AHw-303  LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
              170      180      190      200      210      220

```

```

              40      50      60      70      80
AAD-12  YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERF
              .....  ::  ..
gi+AHw-303  VLGFGMTDETARKVRGEDDQQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230      240      250      260      270      280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.9 bits: 19.0 E(): 8.3
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (24-44:5-25)

```

              10      20      30      40      50      60
AAD-12  EATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL
              .....  ..  ...  .  ...
gi+AHw-462      AITCGQVSSALSSCLGYLKNNGGAVPPGSSSCGIKNLNSA
                  10      20      30

              70      80
AAD-12  LIGRHAHAIPGMDAAESERF

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 151 - 230 80 aa - 80 aa

[illegible]

```

80      7      4:+AD0AKgA9-
82      5      3:+ACoAPQ-
84      1      3:+ACo-
86      0      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      1      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      1      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     1      0:+AD0-          +ACoAPQ-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.39090.00319+ADs- mu+AD0- 1.8932
0.165
mean+AF8-var+AD0-36.3348 8.662, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.212771
Kolmogorov-Smirnov statistic: 0.0822 (N+AD0-26) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   67 25.9    0.76
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   55 22.4    2.5
gi+AHw-30313867+AHw-gb+AHw-AA038859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.4     5
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38)   43 19.0    8.5

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 initl: 65 opt: 67 Z-score: 104.5 bits: 25.9 E(): 0.76
Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
in 67 aa overlap (7-70:327-393)

                                10      20      30
AAD-12                        ATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
                                :  . . .  . . .  :  . . .  . . .  :
gi+AHw-113 IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEGAAAESMKWNWRTNKGVDLENGAIFVASG
                                300      310      320      330      340      350

```

```

      40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFL
      .: . :: . . : :. :. : . : . :. :
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
      360      370      380      390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 initl: 45 opt: 55 Z-score: 95.2 bits: 22.4 E(): 2.5
Smith-Waterman score: 55+ADs- 30.233+ACU- identity (62.791+ACU- similar)
in 43 aa overlap (1-39:35-77)

```

                                10      20
AAD-12 ATRALVHQRSARHS----LVYSQSKLGHVQ
                                : . . : : : : : : : : : : : :
gi+AHw-527 ITSNDLQKLLSSTTYVVVDFFADWCPPCKAIAPVYEQSLTKHSVPDVLAFKVNVDHVQ
      10      20      30      40      50      60

```

```

      30      40      50      60      70      80
AAD-12 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL
      .: . : . : :
gi+AHw-527 DAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGLA-QKRVAGA
      70      80      90      100      110      120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 initl: 47 opt: 59 Z-score: 89.8 bits: 23.4 E(): 5
Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (8-45:198-242)

```

                                10      20      30
AAD-12 ATRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
      170      180      190      200      210      220

```

```

      40      50      60      70      80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFL
      .: : : : : : : :
gi+AHw-303 VLGFQMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
      230      240      250      260      270      280

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.7 bits: 19.0 E(): 8.5
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (23-43:5-25)

```

      10      20      30      40      50      60
AAD-12 ATRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLL
      : : : : : : : : : : : :
gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
      10      20      30

```

[illegible]

```

50      96
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQA9AD0APQ-          +ACo-
   52    121
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
   54     99
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
A9AD0APQA9ACoAPQA9-
   56    107
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0APQA9AD0APQA9AD0APQA9-
   58     48    62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-          +ACo-
   60     84
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
A9AD0-
   62     44    40:+AD0APQ-+AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
   64     40    32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   66     39    25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
   68     29    20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
   70     20    16:+AD0APQA9AD0APQAqAD0-
   72     14    12:+AD0APQA9ACoAPQ-
   74     14    10:+AD0APQA9ACoAPQ-
   76     21     7:+AD0APQAqAD0APQA9AD0-
   78     11     6:+AD0AKgA9AD0-
   80      8     4:+AD0AKgA9-
   82     10     3:+ACoAPQA9AD0-
   84      4     3:+ACoAPQ-
   86      0     2:+ACo-
   88      0     2:+ACo-                inset +AD0- represents 1 library sequences
   90      1     1:+ACo-
   92      1     1:+ACo-                :+ACo-
   94      1     1:+ACo-                :+ACo-
   96      0     1:+ACo-                :+ACo-
   98      0     0:                  +ACo-
  100      0     0:                  +ACo-
  102      0     0:                  +ACo-
  104      0     0:                  +ACo-
  106      1     0:+AD0-              +ACoAPQ-
  108      0     0:                  +ACo-
  110      0     0:                  +ACo-
  112      0     0:                  +ACo-
  114      0     0:                  +ACo-
  116      0     0:                  +ACo-
  118      0     0:                  +ACo-
+AD4-120      0      0:                  +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.84120.00322+ADs- mu+AD0- 4.5777
0.166
mean+AF8-var+AD0-34.1778 8.106, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0-0.219383
Kolmogorov-Smirnov statistic: 0.0992 (N+AD0-27) at 50

```


FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 67 26.4 0.54

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 54 22.4 2.6

gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
59 23.8 3.7

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 56 22.9 5.1

gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(38) 43 19.0 8.6

gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875)
58 23.5 8.9

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 65 init1: 65 opt: 67 Z-score: 107.2 bits: 26.4 E(): 0.54

Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)

in 67 aa overlap (6-69:327-393)

```

                                10      20      30
AAD-12                      TRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
                                :  . . .  . . .      :  . . .  . . .  :
gi+AHw-113 IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FVASG
          300      310      320      330      340      350

```

```

          40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLE
          . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . .
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
          360      370      380      390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)

initn: 45 init1: 45 opt: 54 Z-score: 94.8 bits: 22.4 E(): 2.6

Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)

in 36 aa overlap (7-38:42-77)

```

                                10      20      30
AAD-12                      TRALVHQRSARHS----LVYSQSKLGHVQQAGSAYI
                                :  . . . . .  : . . . . .  : . . . . .  :
gi+AHw-527 QKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHVQDAAQQYG
          20      30      40      50      60      70

```

```

          40      50      60      70      80
AAD-12 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE
          . . .
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AAAEKLGG LAQKRVAGA
          80      90      100      110      120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 92.2 bits: 23.8 E(): 3.7
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (7-44:198-242)

```

                                10      20      30
AAD-12      TRALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ...  ...  ...  :  ...  .
gi+AHw-303  LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
              170      180      190      200      210      220

```

```

                    40      50      60      70      80
AAD-12  YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLE
          ..... :  ..
gi+AHw-303  VLGFGMTDETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230      240      250      260      270      280

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 89.7 bits: 22.9 E(): 5.1
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (29-80:25-73)

```

                    10      20      30      40      50
AAD-12  TRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLL
                                .:  ...  :  ...  :  .  :  .  .
gi+AHw-249  MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-
              10      20      30      40      50

```

```

                    60      70      80
AAD-12  IGRHAHAIP-GMDAAESERFLE
          ... :  ... ..:
gi+AHw-249  ----PAAVPSGKATTEEQKLIKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFV
              60      70      80      90      100      110

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 initl: 43 opt: 43 Z-score: 85.6 bits: 19.0 E(): 8.6
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (22-42:5-25)

```

                    10      20      30      40      50      60
AAD-12  TRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLI
                                ..... :  ...  .  ...
gi+AHw-462      AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
                  10      20      30

```

```

                    70      80
AAD-12  GRHAHAIPGMDAAESERFLE

```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
 +AFs-Blomia (875 aa)
 initn: 33 initl: 33 opt: 58 Z-score: 85.3 bits: 23.5 E(): 8.9

Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (8-52:4-44)

```

                10         20         30         40         50
AAD-12  TRALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTA-TPLRPLVKVHPETGRPSLL
        ..... :. : : : : : : :
gi+AHw-219  MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSEERE
                10         20         30         40         50

        60         70         80
AAD-12  IGRHAHAIPGMDAAESERFLE

gi+AHw-219  LRQRVEREKSDITVQLMNLTERLEETEGSSSESVTEMNKKRDSELAKLRLKLLLEDVHMESEE
                60         70         80         90        100        110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 153 - 232 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      2      8:+AD0- +ACo-
      34      2     21:+AD0-   +ACo-
      36     36     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38     52     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      40     53    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-

```

```

42      108
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
   44     143
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
   46     151
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
   48     117
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
   50      94
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
   52     110
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
   54     103
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
   56     105
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
   58      51    62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
   60      82
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
   62      47    40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
   64      40    32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   66      38    25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
   68      30    20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
   70      19    16:+AD0APQA9AD0APQAqAD0-
   72      13    12:+AD0APQA9ACoAPQ-
   74      13    10:+AD0APQA9ACoAPQ-
   76      22      7:+AD0APQAqAD0APQA9AD0APQ-
   78      11      6:+AD0AKgA9AD0-
   80       9      4:+AD0AKgA9-
   82      10      3:+ACoAPQA9AD0-
   84       4      3:+ACoAPQ-
   86       0      2:+ACo-
   88       0      2:+ACo-          inset +AD0- represents 1 library sequences
   90       1      1:+ACo-
   92       1      1:+ACo-          :+ACo-
   94       1      1:+ACo-          :+ACo-
   96       0      1:+ACo-          :+ACo-
   98       0      0:                +ACo-
  100       0      0:                +ACo-
  102       0      0:                +ACo-
  104       0      0:                +ACo-
  106       1      0:+AD0-          +ACoAPQ-
  108       0      0:                +ACo-
  110       0      0:                +ACo-
  112       0      0:                +ACo-
```

```

114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.79300.00323+ADs- mu+AD0- 4.9259
0.167
mean+AF8-var+AD0-33.7462 7.960, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.220781
Kolmogorov-Smirnov statistic: 0.0951 (N+AD0-27) at 50

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 67 26.4 0.52
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121) 54 22.4 2.6
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465) 59 23.9 3.6
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339) 56 22.9 5
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
( 38) 43 19.0 8.7
gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (
875) 58 23.5 8.7
gi+AHw-21751+AHw-emb+AHw-CAA31396.1+AHw- high molecular weight glu ( 648)
56 22.9 9.9

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 67 Z-score: 107.5 bits: 26.4 E(): 0.52
Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
in 67 aa overlap (5-68:327-393)

```

                                10      20      30
AAD-12                        RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
                                :  . . .  . .      :  . . .  . . :
gi+AHw-113 IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASG
                                300      310      320      330      340      350

                                40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEG
                                . . . . .  .  : . . . .  : . .  : .
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                                360      370      380      390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 init1: 45 opt: 54 Z-score: 94.9 bits: 22.4 E(): 2.6
Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
in 36 aa overlap (6-37:42-77)

```

                                10          20          30
AAD-12          RALVHQRSARHS----LVYSQSKLGHVQQAGSAYI
                                : : : : : : : : : : : : : : : :
gi+AHw-527 QKLLSSTTYVVVDDFFADWCPPCKAIAPVYEQ LSTKHSVPDVLAFKVNVDHVQDAAQQYG
                                20          30          40          50          60          70

```

```

                                40          50          60          70          80
AAD-12 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
                                .: .
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AA EKLGGLAQKRVAGA
                                80          90          100          110          120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 init1: 47 opt: 59 Z-score: 92.4 bits: 23.9 E(): 3.6
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (6-43:198-242)

```

                                10          20
AAD-12          RALVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                : : : : : : : : : : : : : :
gi+AHw-303 LVQHTASDLNQLDQNP RHF FLAGNIQRSQKQRGERYGLRGQQILADNVFKGFNMEALAD
                                170          180          190          200          210          220

```

```

                                30          40          50          60          70          80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
                                .: : : : : : : : : : : :
gi+AHw-303 VLGF GMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
                                230          240          250          260          270          280

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 init1: 52 opt: 56 Z-score: 89.9 bits: 22.9 E(): 5
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (28-79:25-73)

```

                                10          20          30          40          50
AAD-12 RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLI
                                .: : : : : : : : : : : :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT--
                                10          20          30          40          50

```

```

                                60          70          80
AAD-12 GRHAHAIP-GMDAAESERFLEG
                                .: : : : : : : : : :
gi+AHw-249 ---PAAVPSGKATTEEQK LIEKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVE
                                60          70          80          90          100          110

```

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
 Full+AD0-Non-sp (38 aa)
 initn: 43 init1: 43 opt: 43 Z-score: 85.5 bits: 19.0 E(): 8.7
 Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
 in 21 aa overlap (21-41:5-25)

```

                10         20         30         40         50         60
AAD-12  RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIG
                :.:.:.: :. :.:. :. :.:.
gi+AHw-462      AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
                10         20         30

```

```

                70         80
AAD-12  RHAHAIPGMDAAESERFLEG

```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
+AFs-Blomia (875 aa)
initn: 33 initl: 33 opt: 58 Z-score: 85.5 bits: 23.5 E(): 8.7
Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (7-51:4-44)

```

                10         20         30         40         50
AAD-12  RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA-TPLRPLVKVHPETGRPSLLI
                :.:.:. :.:.:. :. :. :. :. :. :. :. :. :. :. :. :.
gi+AHw-219      MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSEREL
                10         20         30         40         50

```

```

                60         70         80
AAD-12  GRHAHAIPGMDAAESERFLEG

```

```

gi+AHw-219  RQRVEREKSDITVQLMNLTERLEETEGSSESVTENMKKRDSELAKLRKLLLEDVHMESEET
                60         70         80         90         100         110

```

+AD4APg-gi+AHw-21751+AHw-emb+AHw-CAA31396.1+AHw- high molecular weight
gluteni (648 aa)
initn: 54 initl: 54 opt: 56 Z-score: 84.5 bits: 22.9 E(): 9.9
Smith-Waterman score: 56+ADs- 27.778+ACU- identity (63.889+ACU- similar)
in 36 aa overlap (6-41:539-574)

```

                                10         20         30
AAD-12                        RALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGM
                                :.:.:. :. :.:. :. :.:.
gi+AHw-217  QQGYPTSPQQPGQGQQPGQGQQGHCPTSPQQSGQAQQPGQGQQIGQVQQPGQGQQGYYP
                510         520         530         540         550         560

```

```

                40         50         60         70         80
AAD-12  DTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEG
                .. :
gi+AHw-217  TSVQQPGQGQQSGQGQQSGQGHPGQGQQSGQEQQGYDSPYHVSAEQQAASPMVAKAQQP
                570         580         590         600         610         620

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:22 2010 done: Fri Feb 5 12:56:22 2010

Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 154 - 233 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      2      8: +AD0- +ACo-
      34      2     21: +AD0- +ACo-
      36     31     44: +AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      38     56     72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      40     57    101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      42    113
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      44    143
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
      46    138
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      48    110
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      50    117
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      52    113
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
      54     95
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA
A9AD0APQA9ACoAPQ-
      56    101
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA
A9AD0APQA9AD0APQA9AD0-
      58     49     62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-

```



```

60      83
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ
A9AD0-
62      47      40:+AD0APQA9AD0APQ--+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
64      41      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      37      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
68      30      20:+AD0APQA9AD0APQA9ACoAPQA9AD0-
70      19      16:+AD0APQA9AD0APQAqAD0-
72      12      12:+AD0APQA9ACo-
74      19      10:+AD0APQA9ACoAPQA9AD0-
76      18      7:+AD0APQAqAD0APQA9-
78      9       6:+AD0AKgA9-
80      7       4:+AD0AKgA9-
82      9       3:+ACoAPQA9-
84      6       3:+ACoAPQ-
86      0       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     1       0:+AD0-          +ACoAPQ-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.89770.00323+ADs- mu+AD0- 4.4093
0.166
mean+AF8-var+AD0-34.1115 8.104, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.219596
Kolmogorov-Smirnov statistic: 0.0876 (N+AD0-27) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  67 26.3      0.55
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  54 22.3      2.7
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.8      3.8
gi+AHw-21215170+AHw-gb+AHw-AAM43909.1+AHw-AF464911+AF8-1 large subunit (
392)   57 23.2      4.9

```

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.9 5.2
 gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
 (38) 43 19.0 8.6
 gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875)
 58 23.4 9.3
 gi+AHw-83305621+AHw-sp+AHw-Q8NKF4.2+AHw-RL3+AF8-ASPFU RecName: Full+AD0-60
 (392) 54 22.2 9.5

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 initl: 65 opt: 67 Z-score: 107.0 bits: 26.3 E(): 0.55
 Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
 in 67 aa overlap (4-67:327-393)

			10	20	30
AAD-12			ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGY		
			:	:	
gi+AHw-113	IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FVASG				
	300 310 320 330 340 350				

	40	50	60	70	80
AAD-12	MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---	PGMDAAESERFLEGL			
 :	:	:	:
gi+AHw-113	VDPVLTPEQSAGMIPAEFGESALSLTSSAGVLSCQPGAPC				
	360 370 380 390				

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 initl: 45 opt: 54 Z-score: 94.7 bits: 22.3 E(): 2.7
 Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
 in 36 aa overlap (5-36:42-77)

			10	20	30
AAD-12			ALVHQRSARHS----	LVYSQSKLGHVQQAGSAYI	
			: : : : :	:	: : : : :
gi+AHw-527	QKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHVQDAAQQYG				
	20 30 40 50 60 70				

	40	50	60	70	80
AAD-12	GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGL				
	. : .				
gi+AHw-527	ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAGA				
	80 90 100 110 120				

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 92.0 bits: 23.8 E(): 3.8
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (5-42:198-242)

			10	20
AAD-12			ALVHQRSARHSLVYSQSKL-----	GHVQQAGSA
			:	:

AAD-12 ALVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGR

10 20 30 40 50 60
::: : :: . :

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank

```

opt      E()
+ADw- 20    2    0:+AD0-
   22     0    0:           one +AD0- represents 3 library sequences
   24     0    0:
   26     0    0:
   28     0    0:
   30     0    2:+ACo-
   32     2    8:+AD0- +ACo-
   34     4    21:+AD0APQ-   +ACo-
   36    37    44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
   38    53    72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
   40    63
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
   42    106
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9-   +ACo-
   44    149
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9-+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
   46    139
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
   48    105
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
   50    111
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0-   +ACo-
   52    111
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
   54    106
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9-
   56     90
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0APQA9-
   58     59
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
   60     74
50:+AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0AKgA9AD0APOA9AD0APOA9AD0-

```

```

62      49      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64      44      32:+AD0-+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
66      36      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      25      20:+AD0APQA9AD0APQA9ACoAPQA9-
70      19      16:+AD0APQA9AD0APQAqAD0-
72      15      12:+AD0APQA9ACoAPQ-
74      20      10:+AD0APQA9ACoAPQA9AD0-
76      16      7:+AD0APQAqAD0APQA9-
78      10      6:+AD0AKgA9AD0-
80      10      4:+AD0AKgA9AD0-
82       5      3:+ACoAPQ-
84       6      3:+ACoAPQ-
86       0      2:+ACo-
88       1      2:+ACo-          inset +AD0- represents 1 library sequences
90       2      1:+ACo-
92       0      1:+ACo-          :+ACo-
94       1      1:+ACo-          :+ACo-
96       0      1:+ACo-          :+ACo-
98       0      0:              +ACo-
100      0      0:              +ACo-
102      0      0:              +ACo-
104      0      0:              +ACo-
106      1      0:+AD0-          +ACoAPQ-
108      0      0:              +ACo-
110      0      0:              +ACo-
112      0      0:              +ACo-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.83550.00322+ADs- mu+AD0- 4.8730
0.166
mean+AF8-var+AD0-34.3130 8.271, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.218950
Kolmogorov-Smirnov statistic: 0.0876 (N+AD0-28) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  67 26.3      0.57
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  54 22.3      2.8
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.7      3.9
gi+AHw-21215170+AHw-gb+AHw-AAM43909.1+AHw-AF464911+AF8-1 large subunit (
392)   57 23.1      5.1
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.8      5.4
gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName: Full+AD0-No
(  38)  43 18.9      9.2

```

gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875) 58 23.4 9.5
 gi+AHw-83305621+AHw-sp+AHw-Q8NKF4.2+AHw-RL3+AF8-ASPFU RecName: Full+AD0-60 (392) 54 22.2 9.8

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Pollen (396 aa)
 initn: 65 initl: 65 opt: 67 Z-score: 106.7 bits: 26.3 E(): 0.57
 Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
 in 67 aa overlap (3-66:327-393)

```

                                10      20      30
AAD-12                        LVHQRSARHSLVYSQSKLGHVQQAGSAYIGY
                                :  . . .  . . .      :  . . . . . :
gi+AHw-113 IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FVASG
                   300           310           320           330           340           350

```

```

                   40           50           60           70           80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLV
                   . . . . . . . : . . . . . : . . . . . :
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                   360           370           380           390

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-Thior (121 aa)
 initn: 45 initl: 45 opt: 54 Z-score: 94.3 bits: 22.3 E(): 2.8
 Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
 in 36 aa overlap (4-35:42-77)

```

                                10      20
AAD-12                        LVHQRSARHS----LVYSQSKLGHVQQAGSAYI
                                :  . . . . :  . . . . . :  . . . . . :
gi+AHw-527 QKLLSSTTYVVVDFADWCPPCKAIAPVYEQ LSTKHSPDVLAFKVNVDHVQDAAQQYG
                   20           30           40           50           60           70

```

```

                   30           40           50           60           70           80
AAD-12 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
                   . . .
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AA EKLGGLAQKRVAGA
                   80           90           100          110          120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 91.7 bits: 23.7 E(): 3.9
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (4-41:198-242)

```

                                10      20
AAD-12                        LVHQRSARHSLVYSQSKL-----GHVQQAGSA
                                :  . . . . :  . . . . . :  . . . . . :
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
                   170           180           190           200           210           220

                   30           40           50           60           70           80

```

AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV

..... :: ..

gi+AHw-303 VLGFQMDTETARKVRGEDDQQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
230 240 250 260 270 280

+AD4APg-gi+AHw-21215170+AHw-gb+AHw-AAM43909.1+AHw-AF464911+AF8-1 large
subunit rib (392 aa)

initn: 34 initl: 34 opt: 57 Z-score: 89.7 bits: 23.1 E(): 5.1
Smith-Waterman score: 57+ADs- 36.538+ACU- identity (59.615+ACU- similar)
in 52 aa overlap (1-47:17-68)

AAD-12 LVHQRSARH-SLVYSQSKLGHVQQAG-SAYIGY--GMDTTATPL
: : : : : . . : : : : : :
gi+AHw-212 MSHRKYEAPRHGSLAFLPRKRAARHRGKVKSFPKYDPKPKVHLTASMGYKAGMTTVVRDL
10 20 30 40 50 60

AAD-12 -RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
:: : : :
gi+AHw-212 DRPGAKMHKKEIVEAVTIIETPPLVAVGVVGYIETPRGLRSLTTVWAEHLSDEVKRRFYK
70 80 90 100 110 120

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 89.2 bits: 22.8 E(): 5.4
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (26-77:25-73)

AAD-12 LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGR
: : : : : : : : : : : : : : : : : :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT----
10 20 30 40 50

AAD-12 HAHAIP-GMDAAESERFLEGLV
: : : : : : : : : : : : : : : : : :
gi+AHw-249 -PAAVPSGKATTEEQKLEIKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGL
60 70 80 90 100 110

+AD4APg-gi+AHw-462717+AHw-sp+AHw-P33556.1+AHw-NLTP2+AF8-VITSX RecName:
Full+AD0-Non-sp (38 aa)
initn: 43 initl: 43 opt: 43 Z-score: 85.1 bits: 18.9 E(): 9.2
Smith-Waterman score: 43+ADs- 38.095+ACU- identity (71.429+ACU- similar)
in 21 aa overlap (19-39:5-25)

AAD-12 LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRH
: : : : : : : : : : : : : : : : : :
gi+AHw-462 AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
10 20 30

70 80

AAD-12 AHAIPGMDAAESERFLEGLV

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
+AFs-Blomia (875 aa)

initn: 33 initl: 33 opt: 58 Z-score: 84.8 bits: 23.4 E(): 9.5
Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (5-49:4-44)

```

                10         20         30         40         50
AAD-12 LVHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTA-TPLRPLVKVHPETGRPSLLIGR
      ::::.  ::::.  ::  ::  :  ::  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-219 MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSERELRLQ
                10         20         30         40         50
```

```

        60         70         80
AAD-12 HAHAIPGMDAAESERFLEGLV
```

```

gi+AHw-219 RVEREKSDITVQLMNLTERLEETEGSSESVTENKPKRDSELAKLRLLEDVHMESEETAH
        60         70         80         90        100        110
```

+AD4APg-gi+AHw-83305621+AHw-sp+AHw-Q8NKF4.2+AHw-RL3+AF8-ASPFU RecName:
Full+AD0-60S ri (392 aa)
initn: 34 initl: 34 opt: 54 Z-score: 84.6 bits: 22.2 E(): 9.8
Smith-Waterman score: 54+ADs- 36.538+ACU- identity (59.615+ACU- similar)
in 52 aa overlap (1-47:17-68)

```

                10         20         30         40
AAD-12          LVHQRSARH-SLVYSQSKLGHVQQAG-SAYIGY--GMDTTATPL
      : :::::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-833 MSHRKYEAPRHGSLAFLPRKRAARHRGKVKSFPKDDPKKPVHLTASMGYKAGMTTVVRDL
        10         20         30         40         50         60
```

```

        50         60         70         80
AAD-12 -RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLV
      :: ::::
gi+AHw-833 DRPGAKMHKKEIVEAVTIIETPPLVAVGVVGYIETPRGLRSLTTVWAEHLSDEVKRRFYK
        70         80         90        100        110        120
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:23 2010 done: Fri Feb 5 12:56:23 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 156 - 235 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      0      8: +ACo-
      34      4     21: +AD0APQ- +ACo-
      36     44     44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      38     55     72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      40      70
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42     110
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      44     153
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ- +AD0APQA9AD0-
      46     117
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      48     100
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0- +ACo-
      50     129
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
      52      97
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9- +ACo-
      54     114
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
      56      69
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      58      78
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
-
      60      61
50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
      62      52     40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
      64      48     32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
      66      34     25: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      68      38     20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-

```

```

70      13      16:+AD0APQA9AD0APQAq-
72      12      12:+AD0APQA9ACo-
74      27      10:+AD0APQA9ACoAPQA9AD0APQA9-
76      13      7:+AD0APQAqAD0APQ-
78      8       6:+AD0AKgA9-
80      10      4:+AD0AKgA9AD0-
82      5       3:+ACoAPQ-
84      3       3:+ACo-
86      0       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      1       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     1       0:+AD0-          +ACoAPQ-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.47630.00321+ADs- mu+AD0- 6.9927
0.166
mean+AF8-var+AD0-34.8658 8.647, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.217207
Kolmogorov-Smirnov statistic: 0.0850 (N+AD0-27) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   67 26.2      0.61
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   56 22.7      2.6
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)   54 22.1      3.2
gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (
465)   59 23.7        4
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)   56 22.7      5.7
gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (
875)   58 23.4      9.2

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 65 init1: 65 opt: 67 Z-score: 106.3 bits: 26.2 E(): 0.61

```

Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
in 67 aa overlap (2-65:327-393)

```

                                10      20      30
AAD-12                        VHQRSARHSLVYSQSKLGHVQQAGSAYIGYG
                                :  . . . . . :  . . . . . :
gi+AHw-113 IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLNGAIFVASG
                300      310      320      330      340      350

```

```

                40      50      60      70      80
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVD
                . : . : . . : : . : . : . : . :
gi+AHw-113 VDPVLTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC
                360      370      380      390

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 49 init1: 49 opt: 56 Z-score: 95.0 bits: 22.7 E(): 2.6
Smith-Waterman score: 56+ADs- 41.026+ACU- identity (61.538+ACU- similar)
in 39 aa overlap (46-80:79-116)

```

                20      30      40      50      60      70
AAD-12 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                                . . . . . : : : : . . . .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100

```

```

                80
AAD-12 ERFLEGLVD
                . : . : .
gi+AHw-121 EEFRASLVLDYLSHHLNDWNTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 init1: 45 opt: 54 Z-score: 93.3 bits: 22.1 E(): 3.2
Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
in 36 aa overlap (3-34:42-77)

```

                                10      20
AAD-12                        VHQRSARHS----LVYSQSKLGHVQQAGSAYI
                                :  . . . . . :  . . . . . :
gi+AHw-527 QKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVNVDHVQDAAQQYG
                20      30      40      50      60      70

```

```

                30      40      50      60      70      80
AAD-12 GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
                . : .
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGGLAQKR VAGA
                80      90      100      110      120

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
Bertholletia (465 aa)
initn: 47 init1: 47 opt: 59 Z-score: 91.5 bits: 23.7 E(): 4

Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
in 45 aa overlap (3-40:198-242)

```

                                10          20
AAD-12                      VHQRSARHSLVYSQSKL-----GHVQQAGSA
                                ...  ...:  ...  :          :  ...  .
gi+AHw-303 LVQHTASDLNQLDQNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
          170          180          190          200          210          220
```

```

          30          40          50          60          70          80
AAD-12 YIGYGMDT-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
          .....:  ::  ::
gi+AHw-303 VLGFGMTETARKVRGEDDQQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
          230          240          250          260          270          280
```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 88.8 bits: 22.7 E(): 5.7
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (25-76:25-73)

```

          10          20          30          40          50
AAD-12 VHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
                                ..  ...  :  ...:  :  .  .  :  .  ..
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
          10          20          30          40          50
```

```

          60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVD
          ...:  ...:  ....:
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKAAVAAAAVVPPADKYKTFVETFGTATNKAFVEGLA
          60          70          80          90          100          110
```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
+AFs-Blomia (875 aa)
initn: 33 initl: 33 opt: 58 Z-score: 85.0 bits: 23.4 E(): 9.2
Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (4-48:4-44)

```

          10          20          30          40          50
AAD-12 VHQRSARHSLVYSQSKLGHVQQAGSAYIGYGMDTTA-TPLRPLVKVHPETGRPSLLIGRH
          .....:  .....:  ...  :  ...:  :  :  :  :  :  :  :  :  :
gi+AHw-219 MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSELERLRQR
          10          20          30          40          50
```

```

          60          70          80
AAD-12 AHAIPGMDAAESERFLEGLVD
gi+AHw-219 VEREKSDITVQLMNLTERLEETEGSSESVTEMNKKRDSELAKLRLKLEDVHMESEETAHH
          60          70          80          90          100          110
```

80 residues in 1 query sequences

[illegible]

```

54      111      91:+AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqA
D0APQA9AD0APQA9-
   56       80
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9-
   58       74
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
   60       56       50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
   62       54       40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
   64       47       32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
   66       35       25:+AD0APQA9AD0-+AD0APQA9AD0AKgA9AD0APQ-
   68       38       20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
   70       14       16:+AD0APQA9AD0APQAq-
   72       15       12:+AD0APQA9ACoAPQ-
   74       28       10:+AD0APQA9ACoAPQA9AD0APQA9AD0-
   76       13        7:+AD0APQAqAD0APQ-
   78         8        6:+AD0AKgA9-
   80        10        4:+AD0AKgA9AD0-
   82         5        3:+ACoAPQ-
   84         2        3:+ACo-
   86         0        2:+ACo-
   88         1        2:+ACo-          inset +AD0- represents 1 library sequences
   90         1        1:+ACo-
   92         1        1:+ACo-          :+ACo-
   94         0        1:+ACo-          :+ACo-
   96         0        1:+ACo-          :+ACo-
   98         1        0:+AD0-          +ACoAPQ-
  100         0        0:              +ACo-
  102         0        0:              +ACo-
  104         0        0:              +ACo-
  106         1        0:+AD0-          +ACoAPQ-
  108         0        0:              +ACo-
  110         0        0:              +ACo-
  112         0        0:              +ACo-
  114         0        0:              +ACo-
  116         0        0:              +ACo-
  118         0        0:              +ACo-
+AD4-120      0      0:              +ACo-
  331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.59860.00318+ADs- mu+AD0- 6.3379
0.165
mean+AF8-var+AD0-34.9609 8.631, 0's: 2 Z-trim: 3 B-trim: 69 in 1/42
Lambda+AD0- 0.216912
Kolmogorov-Smirnov statistic: 0.0944 (N+AD0-27) at 50

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)    6726.2    0.62

```

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 58 23.3 1.7
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 54 22.1 3.2
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 23.7 4.1
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.7 5.8
 gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875)
 58 23.3 9.7

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 65 init1: 65 opt: 67 Z-score: 106.1 bits: 26.2 E(): 0.62
 Smith-Waterman score: 67+ADs- 22.388+ACU- identity (52.239+ACU- similar)
 in 67 aa overlap (1-64:327-393)

			10	20	30
AAD-12			HQRSARHSLVYSQSKLGHVQQAGSAYIGYG		
			:	:	:
gi+AHw-113	IGGSASPTILSQGNRFCAPDERSKKNVLGRHGEAAAE	SMKWNWRTNKDVL	ENGAI	FVASG	
	300	310	320	330	340 350

	40	50	60	70	80
AAD-12	MDTTATPLRPLVKVHPETGRPSLLIGRHAHAI---	PGMDAAESERFLEGLVDW			

gi+AHw-113	VDPVLTPEQSAGMIPAE	PGESALSLTSSAGVL	SCQPGAPC		
	360	370	380	390	

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 init1: 50 opt: 58 Z-score: 98.4 bits: 23.3 E(): 1.7
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (45-80:79-117)

	20	30	40	50	60	70
AAD-12	KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--	LIGRHA--	HAIPGMDAAES			

gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF					
	50	60	70	80	90	100

	80
AAD-12	ERFLEGLVDW

gi+AHw-121	EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
	110 120 130 140 150

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 init1: 45 opt: 54 Z-score: 93.3 bits: 22.1 E(): 3.2
 Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
 in 36 aa overlap (2-33:42-77)

10 20 30 40 50

```

AAD-12  HQRSARHSLVYSQSKLGHVQQAGSAYIGYMDTTA-TPLRPLVKVHPETGRPSLLIGRH
      ..... :. : : : : : :
gi+AHw-219 MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSEERELRQR
              10          20          30          40          50

              60          70          80
AAD-12  AHAIPGMDAAESERFLEGLVDW

gi+AHw-219 VEREKSDITVQLMNLTERLEETEGSSSESVTEMNKKRDSELAKLRLKLEDVHMESEETAHH
              60          70          80          90         100         110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:23 2010 done: Fri Feb 5 12:56:23 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 158 - 237 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8:  +ACo-
      34      13     21:+AD0APQA9AD0APQ- +ACo-
      36      39     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      38      56     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      40      52     101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42      102
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0-          +ACo-
      44      151
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-

```

0.163¹

mean+AF8-var+AD0-35.1853 8.887, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42
 Lambda+AD0- 0.216219
 Kolmogorov-Smirnov statistic: 0.0919 (N+AD0-27) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 58 23.3 1.7
 gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
 (121) 54 22.1 3.2
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 59 23.7 3.5
 gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-Bertholle (465)
 59 23.7 4.1
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.7 5.7
 gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (875)
 58 23.4 9.4

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 98.3 bits: 23.3 E(): 1.7
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (44-79:79-117)

	20	30	40	50	60
AAD-12	KLGHVQQAGSAYIGYGM	DTTATPLRPLVKVHPETGRPSL	--LIGRHA--	HAIPGMDAAES	
			:: : : ...
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN	RPALKTLIDGLASSHKARGIEKAQF			
	50	60	70	80	90 100

	70	80
AAD-12	ERFLEGLVDWA	
	:: .:::	
gi+AHw-121	EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ	
	110	120 130 140 150

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
 Full+AD0-Thior (121 aa)
 initn: 45 initl: 45 opt: 54 Z-score: 93.2 bits: 22.1 E(): 3.2
 Smith-Waterman score: 54+ADs- 33.333+ACU- identity (66.667+ACU- similar)
 in 36 aa overlap (1-32:42-77)

		10	20
AAD-12		QRSARHS----	LVYSQSKLGHVQQAGSAYI
		: :::::	: :::::
gi+AHw-527	QKLLSSTTYVVVDFFADWCPPCKAIAPVYEQLSTKHSVPDVLAF	AKVNVDPDAAQQYG	
	20	30	40 50 60 70

	30	40	50	60	70	80
AAD-12	GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA					

```

      .: .
gi+AHw-527 ITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA-AAEKLGGLAQKRVAGA
              80          90          100          110          120

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 initl: 55 opt: 59 Z-score: 92.6 bits: 23.7 E(): 3.5
 Smith-Waterman score: 59+ADs- 21.875+ACU- identity (51.562+ACU- similar)
 in 64 aa overlap (3-63:330-393)

```

                                10          20          30
AAD-12                      QRSARHSLVYSQSKLGHVQQAGSAYIGYGMTD
                                .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-113 SASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FVASGVDP
              300          310          320          330          340          350

```

```

                40          50          60          70          80
AAD-12 TATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWA
                .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-113 VLTPEQSAGMIPAEPEGESALSLTSSAGVLSCQPGAPC
              360          370          380          390

```

+AD4APg-gi+AHw-30313867+AHw-gb+AHw-AAO38859.1+AHw- 11S globulin +AFs-
 Bertholletia (465 aa)
 initn: 47 initl: 47 opt: 59 Z-score: 91.4 bits: 23.7 E(): 4.1
 Smith-Waterman score: 59+ADs- 35.556+ACU- identity (60.000+ACU- similar)
 in 45 aa overlap (1-38:198-242)

```

                                10          20
AAD-12                      QRSARHSLVYSQSKL-----GHVQQAGSA
                                .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-303 LVQHTASDLNQLDQNP RHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALAD
              170          180          190          200          210          220

```

```

                30          40          50          60          70          80
AAD-12 YIGYGMTD-TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWA
                .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-303 VLGFGMDTETARKVRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICS
              230          240          250          260          270          280

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 88.7 bits: 22.7 E(): 5.7
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (23-74:25-73)

```

                10          20          30          40          50
AAD-12 QRSARHSLVYSQSKLGHVQQAGSAYIGYGMTTTATPLRPLVKVHPET-GRPSLLIGRH
                .: .: .: .: .: .: .: .: .: .: .:
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10          20          30          40          50

```

```

                60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWA

```

```

      :: :   :: :   :: :
gi+AHw-249 PAAVPSGKATTEEQKLTIEKINAGFKAAVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
      60          70          80          90          100          110

```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
+AFs-Blomia (875 aa)

initn: 33 initl: 33 opt: 58 Z-score: 84.9 bits: 23.4 E(): 9.4
Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (2-46:4-44)

```

      10          20          30          40          50
AAD-12  QRSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA-TPLRPLVKVHPETGRPSLLIGRH
      ::::.  ::::.  ::  ::  :  ::  :  ::  :  ::  :  ::  :
gi+AHw-219 MAARSAKY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSESEELRQR
      10          20          30          40          50

```

```

      60          70          80
AAD-12  AHAIPGMDAAESERFLEGLVDWA

```

```

gi+AHw-219 VEREKSDITVQLMNLTERLEETEGSSESVTENMKKRDSELAKLRKLLLEDVHMESEETAHH
      60          70          80          90          100          110

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:23 2010 done: Fri Feb 5 12:56:23 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 159 - 238 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8:  +ACo-
      34      17     21:+AD0APQA9AD0APQA9ACo-

```

```

36      38      44:+AD0APQA9AD0APQA9AD0APQA9-+AD0APQA9AD0- +ACo-
38      57      72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
40      55      101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
42      97
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9-          +ACo-
44      158
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
46      124      138:+AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0APQA9AD0APQA9AD0APQA9-    +ACo-
48      100
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0-          +ACo-
50      124
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
52      98
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9-   +ACo-
54      117      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
56      83
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
58      73
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
60      55      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      52      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
64      45      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66      45      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-+AD0APQ-
68      40      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
70      12      16:+AD0APQA9AD0- +ACo-
72      13      12:+AD0APQA9ACoAPQ-
74      20      10:+AD0APQA9ACoAPQA9AD0-
76      17      7:+AD0APQAqAD0APQA9-
78      7        6:+AD0AKgA9-
80      10       4:+AD0AKgA9AD0-
82      7        3:+ACoAPQA9-
84      0        3:+ACo-
86      2        2:+ACo-
88      0        2:+ACo-                inset +AD0- represents 1 library sequences
90      1        1:+ACo-
92      1        1:+ACo-                :+ACo-
94      0        1:+ACo-                :+ACo-
96      0        1:+ACo-                :+ACo-
98      1        0:+AD0-                +ACoAPQ-
100     0        0:                    +ACo-
102     0        0:                    +ACo-
104     0        0:                    +ACo-
106     0        0:                    +ACo-

```

```

108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.30330.00317+ADs- mu+AD0- 7.8350
0.165
mean+AF8-var+AD0-34.2788 8.796, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42
Lambda+AD0- 0.219059
Kolmogorov-Smirnov statistic: 0.0925 (N+AD0-26) at 52

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.4      1.6
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  59 23.8      3.1
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.9      5.2
gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
( 121)  50 20.9      7.4
gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen +AFs-B1 (
875)   58 23.6      8.3

```

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 init1: 50 opt: 58 Z-score: 98.8 bits: 23.4 E(): 1.6
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (43-78:79-117)

```

```

          20          30          40          50          60
AAD-12 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
          .:. .:. .: .: .: .:
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50          60          70          80          90         100

          70          80
AAD-12 ERFLEGLVDWAC
          .:. .:.
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
          110         120         130         140         150

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 init1: 55 opt: 59 Z-score: 93.4 bits: 23.8 E(): 3.1
Smith-Waterman score: 59+ADs- 21.875+ACU- identity (51.562+ACU- similar)
in 64 aa overlap (2-62:330-393)

```



```

                                10      20      30
AAD-12      RSARHSLVYSQSKLGHVQQAGSAYIGYGMT
                                .: ... . : . . . .:
gi+AHw-113 SASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKNKDVLENGAIFVASGVDP
          300      310      320      330      340      350

```

```

          40      50      60      70      80
AAD-12 TATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWAC
          . :. . . : . . . : . :
gi+AHw-113 VLTPEQSAGMIPAEFPGESALSLTSSAGVLSCQPGAPC
          360      370      380      390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 89.4 bits: 22.9 E(): 5.2
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (22-73:25-73)

```

          10      20      30      40      50
AAD-12      RSARHSLVYSQSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET-GRPSLLIGRH
                                .: ... : : : : . . : . . :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
          10      20      30      40      50

```

```

          60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWAC
          .: : .: .: .:
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
          60      70      80      90      100      110

```

+AD4APg-gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName:
Full+AD0-Thior (121 aa)
initn: 45 init1: 45 opt: 50 Z-score: 86.8 bits: 20.9 E(): 7.4
Smith-Waterman score: 50+ADs- 32.353+ACU- identity (67.647+ACU- similar)
in 34 aa overlap (2-31:44-77)

```

                                10      20
AAD-12      RSARHS----LVYSQSKLGHVQQAGSAYIGY
                                :...: :... . :...: :
gi+AHw-527 LLSSTTYVVVDFFADWCPPCKAIAPVYEQSLTKHSVPDVLAFKVNVDHVQDAAQQYGIT
          20      30      40      50      60      70

```

```

          30      40      50      60      70      80
AAD-12 GMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC
          .: :
gi+AHw-527 AMPTFMFFKEGKQVAVNGQAVIKGADPRTLGA AA EKLGGLAQKRVAGA
          80      90      100      110      120

```

+AD4APg-gi+AHw-21954740+AHw-gb+AHw-AAM83103.1+AHw- paramyosin allergen
+AFs-Blomia (875 aa)
initn: 33 init1: 33 opt: 58 Z-score: 85.9 bits: 23.6 E(): 8.3
Smith-Waterman score: 58+ADs- 34.783+ACU- identity (60.870+ACU- similar)
in 46 aa overlap (1-45:4-44)

```

      10      20      30      40      50
AAD-12  RSARHSLVYSQSKLGHVQQAGSAYIGYGMDDTA-TPLRPLVKVHPETGRPSLLIGRH
      ..... ::  .. : :: : : : : ..  :
gi+AHw-219 MAARSACY--MYQSSRAGH---GGDISIEYGTDLGALTRLEDKIRLLSEDLSELERELRQR
      10      20      30      40      50

      60      70      80
AAD-12  AHAIPGMDAAESERFLEGLVDWAC

gi+AHw-219 VEREKSDITVQLMNLTERLEETEGSSSVTEMNKKRDSELAKLRKLLLEDVHMESEETAHH
      60      70      80      90      100     110

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:23 2010 done: Fri Feb 5 12:56:23 2010
Total Scan time: 0.090 Total Display time: 0.000

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 160 - 239 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

inset +AD0- represents 1 library sequences

331323 residues in 1471 sequences

Expectation+AF8-n fit: $\rho(\ln(x))+AD0-4.24530.00313+ADs- \mu+AD0-8.0930$
0.163

mean+AF8-var+AD0-33.7205 8.747, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42

Lambda+AD0- 0.220865

Kolmogorov-Smirnov statistic: 0.0931 (N+AD0-27) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 58 23.5 1.5

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 59 23.9 2.9

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 56 22.9 4.9

gi+AHw-52783462+AHw-sp+AHw-Q8TFM8.1+AHw-THIO+AF8-FUSCU RecName: Full+AD0-T
(121) 50 20.9 7.1

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

initn: 50 init1: 50 opt: 58 Z-score: 99.3 bits: 23.5 E(): 1.5
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (42-77:79-117)

	20	30	40	50	60
AAD-12	KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES				
			 :: : :	
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF				
	50 60 70 80 90 100				

	70	80
AAD-12	ERFLEGLVDWACQ	
	.. : : : .	
gi+AHw-121	EEFRASLVLDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ	
	110 120 130 140 150	

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 55 init1: 55 opt: 59 Z-score: 93.9 bits: 23.9 E(): 2.9
Smith-Waterman score: 59+ADs- 21.875+ACU- identity (51.562+ACU- similar)
in 64 aa overlap (1-61:330-393)

		10	20	30
AAD-12		SARHSLVYSQSKLGHVQQAGSAYIGYGMDT		
		.. : : . : . : . : .		
gi+AHw-113	SASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDVLNGAIFVASGVDP			
	300 310 320 330 340 350			

	40	50	60	70	80
AAD-12	TATPLRPLVKVHPETGRPSLLIGRHAHAI--PGMDAAESERFLEGLVDWACQ				
	. : : . : : : . : : : .				

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

opt      E()
+ADw- 20      2      0:+AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      0      0:
30      0      2:+ACo-
32      1      8:+AD0- +ACo-
34      15     21:+AD0APQA9AD0APQ- +ACo-
36      37     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
38      49     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
40      63
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42      108
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
44      144     136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9A
D0-
46      130
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
48      106
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
50      125
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
52      95      106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
54      122
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQ-
56      77
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58      66
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60      52      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
62      53      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
64      46      32:+AD0-+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
66      49      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
68      41      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
70      14      16:+AD0APQA9AD0APQAq-

```

```

72      14      12:+AD0APQA9ACoAPQ-
74      13      10:+AD0APQA9ACoAPQ-
76      20      7:+AD0APQAqAD0APQA9AD0-
78      10      6:+AD0AKgA9AD0-
80      8       4:+AD0AKgA9-
82      7       3:+ACoAPQA9-
84      1       3:+ACo-
86      0       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.27780.00312+ADs- mu+AD0- 8.0118
0.162
mean+AF8-var+AD0-33.4410 8.797, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42
Lambda+AD0- 0.221786
Kolmogorov-Smirnov statistic: 0.0890 (N+AD0-27) at 52

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.5      1.5
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  58 23.6      3.7
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.9      5

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 initl: 50 opt: 58 Z-score: 99.3 bits: 23.5 E(): 1.5
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (41-76:79-117)

                20          30          40          50          60
AAD-12 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                .... : : : : : : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF

```

```

50          60          70          80          90          100
      70      80
AAD-12 ERFLEGLVDWACQA
      ::  ::::
gi+AHw-121 EEFRASLVLDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
  initn: 55 initl: 55 opt: 58 Z-score: 92.2 bits: 23.6 E(): 3.7
Smith-Waterman score: 58+ADs- 22.222+ACU- identity (50.794+ACU- similar)
in 63 aa overlap (1-60:331-393)

      10      20      30
AAD-12      ARHSLVYSQSKLGHVQQAGSAYIGYGMDDT
      :  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
gi+AHw-113 ASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDVLNGAIFVASGVDPV
      310      320      330      340      350      360

      40      50      60      70      80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQA
      ::  .  .  :  ::  ::  .  :  ::  ::
gi+AHw-113 LTPEQSAGMIPAEPEGESALSLTSSAGVLSCQPGAPC
      370      380      390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
  initn: 52 initl: 52 opt: 56 Z-score: 89.9 bits: 22.9 E(): 5
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (20-71:25-73)

      10      20      30      40      50
AAD-12      ARHSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
      ::  ::  :  ::  :  ::  :  ::  :  ::  :  ::
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
      10      20      30      40      50

      60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQA
      ::  :  ::  ::::
gi+AHw-249 PAAVPSGKATTEEQKLIEKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
      60      70      80      90      100      110
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-


```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 162 - 241 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      1      8: +AD0- +ACo-
      34     15     21: +AD0APQA9AD0APQ- +ACo-
      36     39     44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      38     45     72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      40     67
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      42     102
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0- +ACo-
      44     145
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
      46     122
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      48     106
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      50     128
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
      52     99
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9- +ACo-
      54     125
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9-
      56     72
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      58     73
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
```

```

60      55      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      52      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
64      45      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66      47      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0-
68      38      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
70      14      16:+AD0APQA9AD0APQAq-
72      15      12:+AD0APQA9ACoAPQ-
74      21      10:+AD0APQA9ACoAPQA9AD0-
76      14      7:+AD0APQAqAD0APQ-
78      10      6:+AD0AKgA9AD0-
80      9       4:+AD0AKgA9-
82      5       3:+ACoAPQ-
84      1       3:+ACo-
86      1       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.42650.00311+ADs- mu+AD0- 7.3117
0.162
mean+AF8-var+AD0-33.3830 8.825, 0's: 2 Z-trim: 2 B-trim: 69 in 1/42
Lambda+AD0- 0.221979
Kolmogorov-Smirnov statistic: 0.0919 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.5      1.5
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 23.2      4.8
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.9      5.1
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  55 22.6      8.2

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

```

initn: 50 initl: 50 opt: 58 Z-score: 99.3 bits: 23.5 E(): 1.5
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (40-75:79-117)

```

      10      20      30      40      50      60
AAD-12 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
              .... : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90     100

      70      80
AAD-12 ERFLEGLVDWACQAP
      :: : : :
gi+AHw-121 EEFRASLVDYLSHHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110     120     130     140     150
```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 initl: 55 opt: 57 Z-score: 90.2 bits: 23.2 E(): 4.8
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (14-59:345-393)

```

              10      20      30      40
AAD-12              RHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
                      : . : . . . : : . : : . : :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
      320     330     340     350     360     370

      50      60      70      80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAP
      : . : . : : : :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
      380     390
```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 89.6 bits: 22.9 E(): 5.1
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (19-70:25-73)

```

              10      20      30      40      50
AAD-12              RHSLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
                      . : : : : : : : : : : :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
              10      20      30      40      50

      60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAP
      : : : : : : :
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
      60      70      80      90     100     110
```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

initn: 55 init1: 55 opt: 55 Z-score: 85.9 bits: 22.6 E(): 8.2
 Smith-Waterman score: 55+ADs- 42.857+ACU- identity (61.905+ACU- similar)
 in 21 aa overlap (60-80:246-266)

```

      30      40      50      60      70      80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAP
      .....:..:..:..:..:
gi+AHw-370 APDIKTAKAELDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 163 - 242 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      0      2:+ACo-
      32      1      8:+AD0- +ACo-
      34      15     21:+AD0APQA9AD0APQ- +ACo-
      36      36     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      46     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      40      67
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      42     116
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-

```

inset +AD0- represents 1 library sequences

Expectation+AF8-n fit: rho(ln(x))+AD0- 4.66650.00303+ADs- mu+AD0- 6.2752
0.158

mean+AF8-var+AD0-35.3205 9.283, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43

Lambda+AD0- 0.215805

Kolmogorov-Smirnov statistic: 0.0803 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 58 23.2 1.8
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 57 22.9 6
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 56 22.6 6.4
gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160) 52 21.3 7.1

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

initn: 50 init1: 50 opt: 58 Z-score: 97.6 bits: 23.2 E(): 1.8
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (39-74:79-117)

10	20	30	40	50	60
AAD-12 KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES					
.....::: : : :... ..					
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF					
50	60	70	80	90	100

70	80			
AAD-12 ERFLEGLVDWACQAPR				
::: .:::				
gi+AHw-121 EEFRASLVLDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ				
110	120	130	140	150

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 55 init1: 55 opt: 57 Z-score: 88.4 bits: 22.9 E(): 6
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (13-58:345-393)

10	20	30	40		
AAD-12 HSLVYSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET					
: . : . . . : : : . : :					
gi+AHw-113 PDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEP					
320	330	340	350	360	370

50	60	70	80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPR			
: . : . : : : :			
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC			

380

390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 87.9 bits: 22.6 E(): 6.4
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (18-69:25-73)

```

                10      20      30      40      50
AAD-12      HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
                .:  :.  :  :.  :  :  :  :  :  :  :  :
gi+AHw-249  MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50

                60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPR
                .:  :  :  :.  :  :.  :  :.  :  :.  :
gi+AHw-249  PAAVPSGKATTEEQKLIKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
 +AFs-Oryza s (160 aa)
 initn: 36 initl: 36 opt: 52 Z-score: 87.1 bits: 21.3 E(): 7.1
 Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
 in 73 aa overlap (8-80:89-154)

```

                10      20      30
AAD-12      HSLVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
                :  :.  :.  :  :  :  :  :  :  :  :
gi+AHw-139  HGAPGGAVDEQLRQDCCRQLAAVDDSWCRCSALNHM--VGGIYRELGATDVG---HPMAE
                60      70      80      90      100     110

                40      50      60      70      80
AAD-12  VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPR
                :  :  :  :.  :  :.  :  :.  :  :.  :
gi+AHw-139  VFPGCRRGDL--ERAAASLPAFCNVDPNGTGGVCYWLGYTPRTPRTGH
                120     130     140     150     160

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-l2: 164 - 243 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

opt      E()
+ADw- 20      2      0: +AD0-
22      0      0:      one +AD0- represents 3 library sequences
24      0      0:
26      0      0:
28      1      0: +AD0-
30      0      2: +ACo-
32      2      8: +AD0- +ACo-
34      15     21: +AD0APQA9AD0APQ- +ACo-
36      35     44: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
38      45     72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
40      70
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42      119
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
44      135
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
46      125
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
48      108
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
50      136
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
52      113
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
54      122
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQ-
56      73
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58      71      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0AKgA9AD0APQ-
60      55      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
62      41      40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      53      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
66      35      25: +AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      30      20: +AD0APQA9AD0APQA9ACoAPQA9AD0-
70      19      16: +AD0APQA9AD0APQAqAD0-
72      9       12: +AD0APQA9ACo-

```



```

74      21      10:+AD0APQA9ACoAPQA9AD0-
76      12       7:+AD0APQAqAD0-
78       7       6:+AD0AKgA9-
80       8       4:+AD0AKgA9-
82       4       3:+ACoAPQ-
84       1       3:+ACo-
86       0       2:+ACo-
88       3       2:+ACo-          inset +AD0- represents 1 library sequences
90       0       1:+ACo-
92       0       1:+ACo-          :+ACo-
94       0       1:+ACo-          :+ACo-
96       0       1:+ACo-          :+ACo-
98       1       0:+AD0-          +ACoAPQ-
100      0       0:              +ACo-
102      0       0:              +ACo-
104      0       0:              +ACo-
106      0       0:              +ACo-
108      0       0:              +ACo-
110      0       0:              +ACo-
112      0       0:              +ACo-
114      0       0:              +ACo-
116      0       0:              +ACo-
118      0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.63200.00301+ADs- mu+AD0- 6.4630
0.157
mean+AF8-var+AD0-34.5747 9.121, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.218120
Kolmogorov-Smirnov statistic: 0.0830 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.3      1.7
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 23.0      5.7
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.7      6
gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (
160)  52 21.4      6.8
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  55 22.3      9.7

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 init1: 50 opt: 58 Z-score: 98.1 bits: 23.3 E(): 1.7
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (38-73:79-117)

```

10 20 30 40 50 60

```

AAD-12  KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
          .... : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50      60      70      80      90      100

```

```

          70      80
AAD-12  ERFLEGLVDWACQAPRV
          : : : :
gi+AHw-121 EEFRASLVDYLSHHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
          110     120     130     140     150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 init1: 55 opt: 57 Z-score: 88.8 bits: 23.0 E(): 5.7
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (12-57:345-393)

```

          10      20      30      40
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
          : . . . . : : . : : . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEP
          320     330     340     350     360     370

```

```

          50      60      70      80
AAD-12  GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRV
          : . : . : . : :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
          380     390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 88.4 bits: 22.7 E(): 6
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (17-68:25-73)

```

          10      20      30      40      50
AAD-12  SLVYSQSKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
          . : : . : : : : : :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
          10      20      30      40      50

```

```

          60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRV
          : : : : : :
gi+AHw-249 PAAVPSGKATTEEQKLIEKINAGFKA AVAAA VPPADKYKTFVETFGTATNKAFVEGLA
          60      70      80      90      100     110

```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
+AFs-Oryza s (160 aa)
initn: 36 init1: 36 opt: 52 Z-score: 87.5 bits: 21.4 E(): 6.8
Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (7-79:89-154)

```

AAD-12                      SLVYSQSKLGHVQQAGSAYIGYMDTTATPLRPLVK
                               : :. . . . . : : . . . . .
gi+AHw-139 HGAPGGAVDEQLRQDCCRQLAAVDDSWCRCSALNHM--VGGIYRELGATDVG---HPMAE
          60          70          80          90          100          110

```

```

          40          50          60          70          80
AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV
          : :      : :      : :      : :      : :      : :
gi+AHw-139 VFPGCRRGDL--ERAAASLP AFCNV DIPNGTGGVVCYWLGYTPRTPRTGH
          120          130          140          150          160

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 55 initl: 55 opt: 55 Z-score: 84.6 bits: 22.3 E(): 9.7
Smith-Waterman score: 55+ADs- 42.857+ACU- identity (61.905+ACU- similar)
in 21 aa overlap (58-78:246-266)

```

          30          40          50          60          70          80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRV
                               : :. . . . . : : . . . . .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
          220          230          240          250          260          270

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
          280          290          300          310          320          330

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 165 - 244 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	

```

28      1      0:+AD0-
30      0      2:+ACo-
32      2      8:+AD0- +ACo-
34     15     21:+AD0APQA9AD0APQ- +ACo-
36     35     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
38     45     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
40     70
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42    116
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
44    137
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
46    126
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
48    104
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
50    137    121:+AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
52    110
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0-
54    129
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0-
56     74
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58     71
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
60     50     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
62     43     40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64     57     32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
66     31     25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68     32     20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
70     20     16:+AD0APQA9AD0APQAqAD0-
72      6     12:+AD0APQ- +ACo-
74     25     10:+AD0APQA9ACoAPQA9AD0APQA9-
76      9      7:+AD0APQAq-
78      6      6:+AD0AKg-
80      9      4:+AD0AKgA9-
82      4      3:+ACoAPQ-
84      1      3:+ACo-
86      0      2:+ACo-
88      3      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      0      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-

```

```

 98      1      0:+AD0-      +ACoAPQ-
100      0      0:      +ACo-
102      0      0:      +ACo-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      0      0:      +ACo-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.59340.00302+ADs- mu+AD0- 6.6270
0.158
mean+AF8-var+AD0-34.3439 9.071, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.218852
Kolmogorov-Smirnov statistic: 0.0858 (N+AD0-28) at 48

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.3      1.7
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 23.0      5.5
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.7      5.9
gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (
160)  52 21.4      6.6
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  55 22.4      9.5

```

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 init1: 50 opt: 58 Z-score: 98.3 bits: 23.3 E(): 1.7
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (37-72:79-117)

```

```

      10      20      30      40      50      60
AAD-12 KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      ..... :: : : ... ..
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90     100

      70      80
AAD-12 ERFLEGLVDWACQAPRVH
      ... ..
gi+AHw-121 EEFRASLVVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110     120     130     140     150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:

Full+AD0-Pollen (396 aa)

initn: 55 initl: 55 opt: 57 Z-score: 89.1 bits: 23.0 E(): 5.5

Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)

in 49 aa overlap (11-56:345-393)

```

                                10      20      30      40
AAD-12      LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
                                : . . . . . : : : . :
gi+AHw-113  PDERSKKNVLGRHGEAAAESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEP
                320      330      340      350      360      370
```

```

                    50      60      70      80
AAD-12  GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVH
                : . . : : : : :
gi+AHw-113  GESALSLTSSAGVLSCQPGAPC
                380      390
```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:

Full+AD0-Major (339 aa)

initn: 52 initl: 52 opt: 56 Z-score: 88.6 bits: 22.7 E(): 5.9

Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)

in 54 aa overlap (16-67:25-73)

```

                                10      20      30      40      50
AAD-12      LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
                                : : : : : : : : : :
gi+AHw-249  MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50
```

```

                    60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVH
                : : : : : : :
gi+AHw-249  PAAVPSGKATTEEQKLEKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
                60      70      80      90      100      110
```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein

+AFs-Oryza s (160 aa)

initn: 36 initl: 36 opt: 52 Z-score: 87.6 bits: 21.4 E(): 6.6

Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)

in 73 aa overlap (6-78:89-154)

```

                                10      20      30
AAD-12      LVYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
                                : : : . . : : . . : : :
gi+AHw-139  HGAPGGAVDEQLRQDCCRQLAAVDDSWCRCALNHM--VGGIYRELGATDVG---HPMAE
                60      70      80      90      100      110
```

```

                    40      50      60      70      80
AAD-12  VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
                : : : : : : : : : :
gi+AHw-139  VFPGCRRGDL--ERAAASLPAFCNVDPNGTGGVCYWLGYTPRTPRTGH
                120      130      140      150      160
```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 55 init1: 55 opt: 55 Z-score: 84.9 bits: 22.4 E(): 9.5
 Smith-Waterman score: 55+ADs- 42.857+ACU- identity (61.905+ACU- similar)
 in 21 aa overlap (57-77:246-266)

```

      30      40      50      60      70      80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
      :::: :: . ::: : . :
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:24 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 166 - 245 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      0      2:+ACo-
      32      2      8:+AD0- +ACo-
      34      15     21:+AD0APQA9AD0APQ- +ACo-
      36      35     44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      44     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
      40      70
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-

```

[illegible]


```

116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.61490.00297+ADs- mu+AD0- 6.4884
0.155
mean+AF8-var+AD0-33.8874 9.002, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.220321
Kolmogorov-Smirnov statistic: 0.0844 (N+AD0-28) at 48

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  58 23.4      1.6
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)  57 23.1      5.3
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)  56 22.8      5.6
gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (
160)  52 21.5      6.4
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  55 22.4      9.2

```

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 initl: 50 opt: 58 Z-score: 98.7 bits: 23.4 E(): 1.6
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (36-71:79-117)

```

```

      10      20      30      40      50      60
AAD-12 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      .... : : : : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      70      80
AAD-12 ERFLEGLVDWACQAPRVHA
      .. : : : :
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 initl: 55 opt: 57 Z-score: 89.4 bits: 23.1 E(): 5.3
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (10-55:345-393)

```

```

      10      20      30
AAD-12 VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
      : . : . . . : : . : : . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP

```

```

          320          330          340          350          360          370
      40          50          60          70          80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHA
      .. .. : .. :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
          380          390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 88.9 bits: 22.8 E(): 5.6
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (15-66:25-73)

```

          10          20          30          40
AAD-12          VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
          .. ... : ... : . . : . . :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
          10          20          30          40          50

```

```

          50          60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHA
          ... : ... :
gi+AHw-249 PAAVPSGKATTEEQKLTIEKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
 +AFs-Oryza s (160 aa)
 initn: 36 initl: 36 opt: 52 Z-score: 87.9 bits: 21.5 E(): 6.4
 Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
 in 73 aa overlap (5-77:89-154)

```

          10          20          30
AAD-12          VYSQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
          : ... . : : . . :
gi+AHw-139 HGAPGGAVDEQLRQDCCRQLAAVDDSWCRCSALNHM--VGGIYRELGATDVG---HPMAE
          60          70          80          90          100          110

```

```

          40          50          60          70          80
AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHA
          : : : : : : : : : :
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVDIPNGTGGVCYWLGYTPRTPTRGH
          120          130          140          150          160

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 55 initl: 55 opt: 55 Z-score: 85.1 bits: 22.4 E(): 9.2
 Smith-Waterman score: 55+ADs- 42.857+ACU- identity (61.905+ACU- similar)
 in 21 aa overlap (56-76:246-266)

```

          30          40          50          60          70          80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHA
          ... : : . : : :
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT

```

[illegible]

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo

(151) 58 23.2 1.8

gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po

(396) 57 22.9 6.1

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M

(339) 56 22.6 6.4

gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (

160) 52 21.4 7

gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)

56 22.6 8.6

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:

Full+AD0-Globin (151 aa)

initn: 50 init1: 50 opt: 58 Z-score: 97.7 bits: 23.2 E(): 1.8

Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)

in 40 aa overlap (35-70:79-117)

```

          10          20          30          40          50          60
AAD-12  KLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
          .... : : : : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50          60          70          80          90         100

```

```

          70          80
AAD-12  ERFLEGLVDWACQAPRVHAH
          .. : : : :
gi+AHw-121 EEFRASLVDYLSHHLDWNMTMKSTWDLALNNMFFYILHALEVAQ
          110         120         130         140         150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:

Full+AD0-Pollen (396 aa)

initn: 55 init1: 55 opt: 57 Z-score: 88.3 bits: 22.9 E(): 6.1

Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)

in 49 aa overlap (9-54:345-393)

```

          10          20          30
AAD-12  YSQSKLGHVQQAGSAYIGYGMDDTATPLRPLVKVHPET
          : . : . . . : : . : : . :
gi+AHw-113 PDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
          320         330         340         350         360         370

```

```

          40          50          60          70          80
AAD-12  GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAH
          : . : . : : : :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
          380         390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:

Full+AD0-Major (339 aa)

initn: 52 init1: 52 opt: 56 Z-score: 87.9 bits: 22.6 E(): 6.4

Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (14-65:25-73)

```

                10      20      30      40
AAD-12          YSQSKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPET-GRPSLLIGRH
                ..  ...  :  ...  :  .  .  :  .  .
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50

                50      60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAH
                ... :  ... ..:
gi+AHw-249 PAAVPSGKATTEEQKLTIEKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein

+AFs-Oryza s (160 aa)

initn: 36 initl: 36 opt: 52 Z-score: 87.2 bits: 21.4 E(): 7
Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (4-76:89-154)

```

                10      20      30
AAD-12          YSQSKLGHVQQAGSAYIGYMDTTATPLRPLVK
                :  ...  ... :  :  ..  ....
gi+AHw-139 HGAPGGAVDEQLRQDCCRQLAAVDDSWCRC SALNHM--VGGIYRELGATDVG---HPMAE
                60      70      80      90      100     110

                40      50      60      70      80
AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAH
                :  :  :  :  :  ... ..  ..  :  :  ...
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVDPNGTGGVCYWLGYTPRTPRTGH
                120     130     140     150     160

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)

initn: 37 initl: 37 opt: 56 Z-score: 85.6 bits: 22.6 E(): 8.6
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (26-80:46-108)

```

                10      20      30      40
AAD-12          YSQSKLGHVQQAGSAYIGYMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                :  ...  ... :  ... :  :  .
gi+AHw-253 IEEPEMIAPTTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20      30      40      50      60      70

                50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAH
                ... .  ... ..  :  :  ... ..
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                80      90      100     110     120     130

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHNMVSGHPHPTHLEHSS
                140     150     160     170     180     190

```

[illegible]

```

54      117
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
   56      82
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
A9AD0-
   58      67
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
   60      49      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
   62      50      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
   64      51      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
   66      28      25:+AD0APQA9AD0APQA9AD0APQAqAD0-
   68      37      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0-
   70      20      16:+AD0APQA9AD0APQAqAD0-
   72      10      12:+AD0APQA9ACo-
   74      22      10:+AD0APQA9ACoAPQA9AD0APQ-
   76          9       7:+AD0APQAq-
   78          9       6:+AD0AKgA9-
   80          7       4:+AD0AKgA9-
   82          2       3:+ACo-
   84          4       3:+ACoAPQ-
   86          1       2:+ACo-
   88          2       2:+ACo-           inset +AD0- represents 1 library sequences
   90          0       1:+ACo-
   92          0       1:+ACo-           :+ACo-
   94          0       1:+ACo-           :+ACo-
   96          0       1:+ACo-           :+ACo-
   98          1       0:+AD0-         +ACoAPQ-
100          0       0:               +ACo-
102          0       0:               +ACo-
104          0       0:               +ACo-
106          0       0:               +ACo-
108          0       0:               +ACo-
110          0       0:               +ACo-
112          0       0:               +ACo-
114          0       0:               +ACo-
116          0       0:               +ACo-
118          0       0:               +ACo-
+AD4-120      0       0:               +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.77600.00301+ADs- mu+AD0- 5.5288
0.157
mean+AF8-var+AD0-36.0086 9.628, 0's: 2 Z-trim: 2 B-trim: 0 in 0/43
Lambda+AD0- 0.213733
Kolmogorov-Smirnov statistic: 0.0844 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                               opt bits E(1471)
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)    5823.2        1.9
```


gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
(396) 57 22.8 6.2
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
(339) 56 22.5 6.5
gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160)
52 21.3 7.1
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
56 22.5 8.7

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 50 initl: 50 opt: 58 Z-score: 97.5 bits: 23.2 E(): 1.9
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (34-69:79-117)

```

      10      20      30      40      50
AAD-12 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      .....::: : : :...:
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90     100

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQ
      ::: .....
gi+AHw-121 EEFRASLVDYLSHHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110     120     130     140     150
```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 initl: 55 opt: 57 Z-score: 88.2 bits: 22.8 E(): 6.2
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (8-53:345-393)

```

      10      20      30
AAD-12 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
      : . : . . . : : . : : . :
gi+AHw-113 PDERSKKNVLGRHGEAAAESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEP
      320     330     340     350     360     370

      40      50      60      70      80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQ
      :. :. : :.. :. :.
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
      380     390
```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 87.7 bits: 22.5 E(): 6.5
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (13-64:25-73)

```

      10      20      30      40
AAD-12 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
      .. :.. : :.. : . . : : . .
```

gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
 10 20 30 40 50

 50 60 70 80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQ
 ::: : ::: :::::

gi+AHw-249 PAAVPSGKATTEEQKLIIEKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKA FVEGLA
 60 70 80 90 100 110

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
+AFs-Oryza s (160 aa)
 initn: 36 initl: 36 opt: 52 Z-score: 87.0 bits: 21.3 E(): 7.1
Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (3-75:89-154)

 10 20 30
AAD-12 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPLVK
 : :::: .::: : : .. :....
gi+AHw-139 HGAPGGAVDEQLRQDCCRQLAAVDDSWCRCSALNHM--VGGIYRELGATDVG---HPMAE
 60 70 80 90 100 110

 40 50 60 70 80
AAD-12 VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQ
 : : : : : : :.... .. : : : : :
gi+AHw-139 VFPGCRRGDL--ERAAASLPAFCNVDPNGTGGVVCYWLGYTPRTPRTGH
 120 130 140 150 160

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 85.5 bits: 22.5 E(): 8.7
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (25-79:46-108)

 10 20 30 40
AAD-12 SQSKLGHVQQAGSAYIGYGMDDTTATPLRPL---VKVHPETGRPSLL--IGRH--
 : :::: : : : : : : : : : :
gi+AHw-253 IEEPEMIAPTTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
 20 30 40 50 60 70

 50 60 70 80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQ
 ::: . :::: :. :. : : :
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRRHRAHSAQSSA
 80 90 100 110 120 130

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHNMVSGHPHPTHLEHSS
 140 150 160 170 180 190

80 residues in 1 query sequences
331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:24 2010 done: Fri Feb 5 12:56:25 2010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 169 - 248 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

	opt	E()
+ADw-	20	2 0:+AD0-
22	0	0:
24	0	0:
26	0	0:
28	0	0:
30	1	2:+ACo-
32	3	8:+AD0- +ACo-
34	17	21:+AD0APQA9AD0APQA9ACo-
36	37	44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
38	44	72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
40	59	101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-		
42	120	
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-		
44	127	
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-		
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-		
46	148	
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-		
48	104	
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-		
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-		
50	135	
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-		
52	113	106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-		
54	127	
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0-		
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-		
56	71	
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-		
+ACo-		

```

58      73
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0-
60      61
50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
62      42      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      47      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66      34      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      23      20:+AD0APQA9AD0APQA9ACoAPQ-
70      11      16:+AD0APQA9AD0- +ACo-
72      17      12:+AD0APQA9ACoAPQA9-
74      18      10:+AD0APQA9ACoAPQA9-
76      10      7:+AD0APQAqAD0-
78      10      6:+AD0AKgA9AD0-
80      2      4:+AD0AKg-
82      4      3:+ACoAPQ-
84      1      3:+ACo-
86      3      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      1      1:+ACo-
92      3      1:+ACo-          :+ACoAPQA9-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120 0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.68030.00306+ADs- mu+AD0- 6.1866
0.160
mean+AF8-var+AD0-36.903910.119, 0's: 2 Z-trim: 2 B-trim: 5 in 1/42
Lambda+AD0- 0.211124
Kolmogorov-Smirnov statistic: 0.0796 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 66 25.5 1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 58 23.0 2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.4 2.4
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838) 64 24.9 3.2

```

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.4 3.3
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.4 3.3
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 59 23.3 4.9
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 57 22.7 6.7
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.1
 gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160)
 52 21.2 7.8
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.4

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 101.6 bits: 25.5 E(): 1.1
 Smith-Waterman score: 66+ADs- 35.714+ACU- identity (53.571+ACU- similar)
 in 28 aa overlap (53-80:246-273)

	30	40	50	60	70	80
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW					
			 :: . .:: :	. :	..
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270

gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
	280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 init1: 50 opt: 58 Z-score: 96.6 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (33-68:79-117)

	10	20	30	40	50
AAD-12	KLGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES				
			 :: : :	
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF				
	50 60 70 80 90 100				

	60	70	80
AAD-12	ERFLEGLVDWACQAPRVHAHQW		
	.. :....		
gi+AHw-121	EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ		
	110 120 130 140 150		

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (64-80:68-86)

```

      40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQW
      : . . . . : : . . . . :
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100          110

```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aestivum+AF0- (838 aa)
 initn: 43 initl: 43 opt: 64 Z-score: 93.3 bits: 24.9 E(): 3.2
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (5-39:140-171)

```

                        10          20          30
AAD-12                      QSKLGHVQQAGSAYIGYGMTTATPLRPLVKVHP
                        : . : . . . . : : . . . . : :
gi+AHw-736 RYYPSTSPQQVSYYPGQASPQRPGQGQQPGQGQQSGQGQQGY---YPTSPQQPGQWQQP
      110          120          130          140          150          160

```

```

      40          50          60          70          80
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
      : : :
gi+AHw-736 EQGQPGYYPTSPQQPGQLQQPAQGQQPGQGQQGRQPGQGQPGYYPTSSQLQPGQLQQPAQ
      170          180          190          200          210          220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (64-80:68-86)

```

      40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQW
      : . . . . : : . . . . :
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40          50          60          70          80          90

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (64-80:68-86)

```

      40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQW
      : . . . . : : . . . . :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 59 initl: 59 opt: 59 Z-score: 90.0 bits: 23.3 E(): 4.9
 Smith-Waterman score: 59+ADs- 32.143+ACU- identity (53.571+ACU- similar)
 in 28 aa overlap (53-80:247-274)

30 40 50 60 70 80
 AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQW
 :::: :: . .: : . :.
 gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
 220 230 240 250 260 270

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
 280 290 300 310 320 330

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 87.6 bits: 22.7 E(): 6.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (7-52:345-393)

10 20 30
 AAD-12 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET
 : . :. :: . :: . :.
 gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
 320 330 340 350 360 370

40 50 60 70 80
 AAD-12 GRPSLLIGRHAHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQW
 :. :. . : .. :.
 gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
 380 390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 87.1 bits: 22.4 E(): 7.1
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (12-63:25-73)

10 20 30 40
 AAD-12 QSKLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPET-GRPSLLIGRH
 .: :. : :. : . . : . :.
 gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
 10 20 30 40 50

50 60 70 80
 AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQW
 ::. : .: :. :.
 gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
 60 70 80 90 100 110

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448


```

opt      E()
+ADw-   20    2       0:+AD0-
     22      0        0:           one +AD0- represents 3 library sequences
     24      0        0:
     26      0        0:
     28      0        0:
     30      1        2:+ACo-
     32      2        8:+AD0- +ACo-
     34     17       21:+AD0APQA9AD0APQA9ACo-
     36     37       44:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
     38     45       72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-          +ACo-
     40     62
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
     42     113
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
     44     133
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
     46     148
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
     48     102
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
         +ACo-
     50     134
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
     52     112
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
     54     131
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
     56     73
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
     58     70
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
     60     58       50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
     62     44       40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
     64     46       32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
     66     33       25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
     68     23       20:+AD0APQA9AD0APQA9ACoAPQ-
     70     12       16:+AD0APQA9AD0- +ACo-

```

```

72      17      12:+AD0APQA9ACoAPQA9-
74      20      10:+AD0APQA9ACoAPQA9AD0-
76      9       7:+AD0APQAq-
78      10      6:+AD0AKgA9AD0-
80      3       4:+AD0AKg-
82      3       3:+ACo-
84      1       3:+ACo-
86      3       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      1       1:+ACo-
92      3       1:+ACo-          :+ACoAPQA9-
94      1       1:+ACo-          :+ACo-
96      1       1:+ACo-          :+ACo-
98      0       0:              +ACo-
100     0       0:              +ACo-
102     1       0:+AD0-        +ACoAPQ-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.62860.00309+ADs- mu+AD0- 6.4242
0.162
mean+AF8-var+AD0-37.169310.164, 0's: 2 Z-trim: 2 B-trim: 5 in 1/42
Lambda+AD0- 0.210369
Kolmogorov-Smirnov statistic: 0.0796 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   66 25.5      1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   58 23.0      2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)    56 22.4      2.5
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)    64 24.9      3.2
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4      3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4      3.4
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   59 23.3      4.9
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   57 22.7      6.7

```

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.1
 gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160)
 52 21.2 7.9
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.4

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 101.5 bits: 25.5 E(): 1.1
 Smith-Waterman score: 66+ADs- 35.714+ACU- identity (53.571+ACU- similar)
 in 28 aa overlap (52-79:246-273)

	30	40	50	60	70	80
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA					
				::: :: . ::: : . :		::
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNPSDKSKWIT					
	220	230	240	250	260	270

gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 96.5 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (32-67:79-117)

	10	20	30	40	50
AAD-12	KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES				
			 ::: :: : : ... ::	
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF				
	50	60	70	80	90

	60	70	80
AAD-12	ERFLEGLVDWACQAPRVHAHQWA		
	::	
gi+AHw-121	EEFRASLVLDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ		
	110	120	130

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 95.3 bits: 22.4 E(): 2.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (63-79:68-86)

	40	50	60	70	80
AAD-12	PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWA				
			: :: ... :::	
gi+AHw-219	YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF				
	40	50	60	70	80

gi+AHw-219	SFSDRSGLLLKQKVSDE	
	100	110

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aestivum+AF0- (838 aa)

initn: 43 initl: 43 opt: 64 Z-score: 93.3 bits: 24.9 E(): 3.2
Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
in 35 aa overlap (4-38:140-171)

```

                                10      20      30
AAD-12                        SKLGHVQQAGSAYIGYGMDTTATPLRPLVKVHP
                                :. :.:.:. :. :. :. :.
gi+AHw-736 RYYPSTSPQQVSYYPGQASPQRPGQGQPGQGQSGQGQGY---YPTSPQQPGQWQQP
          110      120      130      140      150      160

```

```

          40      50      60      70      80
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA
          : :.
gi+AHw-736 EQGQPGYIPTSPQQPGQLQQPAQGQPGQGQGRQPGQGPGYIPTSSQLQPGQLQQPAQ
          170      180      190      200      210      220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (63-79:68-86)

```

          40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWA
          : :.:. :. :. :.
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMNF
          40      50      60      70      80      90

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (63-79:68-86)

```

          40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWA
          : :.:. :. :. :.
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMDF
          40      50      60      70      80      90

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100      110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)

initn: 59 initl: 59 opt: 59 Z-score: 90.0 bits: 23.3 E(): 4.9
Smith-Waterman score: 59+ADs- 32.143+ACU- identity (53.571+ACU- similar)
in 28 aa overlap (52-79:247-274)

30 40 50 60 70 80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWA
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
220 230 240 250 260 270

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 initl: 55 opt: 57 Z-score: 87.5 bits: 22.7 E(): 6.7
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (6-51:345-393)

10 20 30
AAD-12 SKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPET
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEP
320 330 340 350 360 370

40 50 60 70 80
AAD-12 GRPSLLIGRHAHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWA
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
380 390

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 87.1 bits: 22.4 E(): 7.1
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (11-62:25-73)

10 20 30 40
AAD-12 SKLGHVQQAGSAYIGYMDTTATPLRPLVKVHPET-GRPSLLIGRH
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
10 20 30 40 50

50 60 70 80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWA
gi+AHw-249 PAAVPSGKATTEEQKLIEKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
60 70 80 90 100 110

+AD4APg-gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein
+AFs-Oryza s (160 aa)
initn: 36 initl: 36 opt: 52 Z-score: 86.2 bits: 21.2 E(): 7.9
Smith-Waterman score: 52+ADs- 24.658+ACU- identity (50.685+ACU- similar)
in 73 aa overlap (1-73:89-154)

10 20 30
AAD-12 SKLGHVQQAGSAYIGYMDTTATPLRPLVK

```
1+AD4APgA+-AAD-12: 171 - 250 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

94      1      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:          +ACo-
106     0      0:          +ACo-
108     0      0:          +ACo-
110     0      0:          +ACo-
112     0      0:          +ACo-
114     0      0:          +ACo-
116     0      0:          +ACo-
118     0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.61290.00309+ADs- mu+AD0- 6.4472
0.162
mean+AF8-var+AD0-37.329710.188, 0's: 2 Z-trim: 2 B-trim: 5 in 1/42
Lambda+AD0- 0.209917
Kolmogorov-Smirnov statistic: 0.0803 (N+AD0-28) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   66 25.5      1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   58 23.0      2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)    56 22.4      2.5
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)    64 24.9      3.2
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4      3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4      3.4
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   59 23.3      4.8
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   57 22.7      6.7
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)   56 22.4      7.1
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4      9.3

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 66 init1: 66 opt: 66 Z-score: 101.5 bits: 25.5 E(): 1.1
Smith-Waterman score: 66+ADs- 35.714+ACU- identity (53.571+ACU- similar)
in 28 aa overlap (51-78:246-273)

```

30 40 50 60 70 80

AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA

 gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
 220 230 240 250 260 270

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
 280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 96.5 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (31-66:79-117)

10 20 30 40 50
 AAD-12 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES

 gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
 50 60 70 80 90 100

60 70 80
 AAD-12 ERFLEGLVDWACQAPRVHAHQWAA
 ...
 gi+AHw-121 EEFRASLVDYLSHHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
 110 120 130 140 150

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 95.3 bits: 22.4 E(): 2.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (62-78:68-86)

40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAA
 :
 gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum
 aestivum+AF0- (838 aa)
 initn: 43 initl: 43 opt: 64 Z-score: 93.4 bits: 24.9 E(): 3.2
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (3-37:140-171)

10 20 30
 AAD-12 KLGHVQQAGSAYIGYGMDDTTATPLRPLVKVHP

 gi+AHw-736 RYYPSTVSPQQVSYYPGQASPQRPGQGQPGQGQSGQGQGY---YPTSPQQPGQWQQP
 110 120 130 140 150 160
 40 50 60 70 80

AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA

: :::

gi+AHw-736 EQGQPGYYPTSPQQPGQLQQPAQGGQPGQGQGRQPGQGPGYYPTSSQLQPGQLQQPAQ
170 180 190 200 210 220

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (62-78:68-86)

40 50 60 70 80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAA

: ::::: :: ... :::

gi+AHw-456 YVWKISEFYGRKPEGTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
40 50 60 70 80 90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (62-78:68-86)

40 50 60 70 80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAA

: ::::: :: ... :::

gi+AHw-184 YVWKISEFYGRKPEGTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

gi+AHw-184 SFDSRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)

initn: 59 init1: 59 opt: 59 Z-score: 90.1 bits: 23.3 E(): 4.8
Smith-Waterman score: 59+ADs- 32.143+ACU- identity (53.571+ACU- similar)
in 28 aa overlap (51-78:247-274)

30 40 50 60 70 80
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA

: ::::: :: . .: : . .: .:

gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
220 230 240 250 260 270

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)

initn: 55 init1: 55 opt: 57 Z-score: 87.6 bits: 22.7 E(): 6.7

Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (5-50:345-393)

```

                                10      20      30
AAD-12                        KLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET
                                : . . . . : : . . . :
gi+AHw-113 PDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAIFVASGVDPVLTPEQSAGMIPAEP
                   320      330      340      350      360      370

```

```

                   40      50      60      70      80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                   : . . . . : . . . :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
                   380      390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 87.1 bits: 22.4 E(): 7.1
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (10-61:25-73)

```

                                10      20      30      40
AAD-12                        KLGHVQQAGSAYIGYGMTTATPLRPLVKVHPET-GRPSLLIGRH
                                . : . . . : : : . . . : . :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                   10      20      30      40      50

```

```

                   50      60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAA
                   : : : . . : . . . :
gi+AHw-249 PAAVPSGKATTEEQKLEKINAGFKAAVAAAAVVPPADKYKTFVETFGTATNKAFVEGLA
                   60      70      80      90      100      110

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 init1: 37 opt: 56 Z-score: 85.0 bits: 22.4 E(): 9.3
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (22-76:46-108)

```

                                10      20      30      40
AAD-12                        KLGHVQQAGSAYIGYGMTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                : : : : . . . : . . . : : . :
gi+AHw-253 IEEPEMIAPTTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                   20      30      40      50      60      70

```

```

                   50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                   : : . . . : . : : : : :
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                   80      90      100      110      120      130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
                   140      150      160      170      180      190

```

[illegible]

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 27.6 0.26
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 25.5 1.1
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 58 23.0 2.1
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 22.4 2.4
 gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (838)
 64 24.9 3.2
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.4 3.3
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.4 3.3
 gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
 (396) 57 22.7 6.7
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.1
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.4

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 113.0 bits: 27.6 E(): 0.26
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (50-80:246-276)

20	30	40	50	60	70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
::: :: . .:: : . : .: .					
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGVQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
220	230	240	250	260	270
80					
AAD-12 G					
:					
gi+AHw-370 GPQLAEELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
280	290	300	310	320	330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 101.5 bits: 25.5 E(): 1.1
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (50-80:247-277)

20	30	40	50	60	70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
::: :: . .: : . : .: .					
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS					
220	230	240	250	260	270
80					
AAD-12 G					
:					

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
 280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 50 initl: 50 opt: 58 Z-score: 96.6 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (30-65:79-117)

10 20 30 40 50
 AAD-12 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
 : : ... :.
 gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
 50 60 70 80 90 100

60 70 80
 AAD-12 ERFLEGLVDWACQAPRVHAHQWAAG
 :. :....
 gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
 110 120 130 140 150

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (61-77:68-86)

40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAG
 : :. :. :.
 gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum
 aestivum+AF0- (838 aa)
 initn: 43 initl: 43 opt: 64 Z-score: 93.3 bits: 24.9 E(): 3.2
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (2-36:140-171)

10 20 30
 AAD-12 LGHVQQAGSAYIGYGMDTTATPLRPLVKVHP
 .. :..... :. :. :.
 gi+AHw-736 RYYPSTSPQQVSYYPGQASPPRPGQGQPGQGQSGQGQGY---YPTSPQQPGQWQQP
 110 120 130 140 150 160

40 50 60 70 80
 AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG
 : :.
 gi+AHw-736 EQGQPGYYPTSPQQPGQLQQPAQGQPGQGQGRQPGQGQPGYYPTSSQLQPGQLQQPAQ
 170 180 190 200 210 220

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (61-77:68-86)

```

                40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAG
                : . . . . : : . . . . :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
                40          50          60          70          80          90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100         110         120         130         140         150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (61-77:68-86)

```

                40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAG
                : . . . . : : . . . . :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40          50          60          70          80          90

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                100         110         120         130         140         150

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
 Full+AD0-Pollen (396 aa)
 initn: 55 initl: 55 opt: 57 Z-score: 87.6 bits: 22.7 E(): 6.7
 Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
 in 49 aa overlap (4-49:345-393)

```

                                10          20          30
AAD-12                                LGHVQQAGSAYIGYGMTTATPLRPLVKVHPET
                                : . . . . : : . . . . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEP
                320         330         340         350         360         370

```

```

                40          50          60          70          80
AAD-12 GRPSLLIGRHAHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAAG
                : . . . . : : . . . . :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
                380         390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
 Full+AD0-Major (339 aa)
 initn: 52 initl: 52 opt: 56 Z-score: 87.1 bits: 22.4 E(): 7.1
 Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
 in 54 aa overlap (9-60:25-73)


```

                10      20      30      40
AAD-12          LGHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
                .:  :::  :  :::  :  .  .  :  .  .
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50

```

```

                50      60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAG
                :::  :  :::  .:::
gi+AHw-249 PAAVPSGKATTEEQKLEKINAGFKA AVAAA VVPADKYKTFVETFGTATNKAFVEGLA
                60      70      80      90      100     110

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 initl: 37 opt: 56 Z-score: 84.9 bits: 22.4 E(): 9.4
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (21-75:46-108)

```

                10      20      30      40
AAD-12          LGHVQQAGSAYIGYGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                :::::  ....:  .:::  :  .:
gi+AHw-253 IEEPEMIAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20      30      40      50      60      70

```

```

                50      60      70      80
AAD-12  -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAG
                .:  .  .:::  .:  .:  .:  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDLDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                80      90      100     110     120     130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNHLNANQFNFEVPGHMNVSGHPHLEHSS
                140     150     160     170     180     190

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010
Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 173 - 252 80 aa - 80 aa

[illegible]

```

82      4      3:+ACoAPQ-
84      1      3:+ACo-
86      2      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      3      1:+ACo-          :+ACoAPQA9-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0:+AD0-          +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.76120.00306+ADs- mu+AD0- 5.7931
0.160
mean+AF8-var+AD0-37.371210.173, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.209800
Kolmogorov-Smirnov statistic: 0.0766 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 27.5      0.27
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 25.4      1.2
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   58 23.0      2.2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)    56 22.4      2.5
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)    64 24.8      3.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4      3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4      3.4
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)   52 21.1      5.6
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   57 22.7      7
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)   56 22.4      7.4
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4      9.8

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 initl: 73 opt: 73 Z-score: 112.5 bits: 27.5 E(): 0.27
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (49-79:246-276)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . :: : . : ::
gi+AHw-370 APDIKTAKALDLIVSAIEAAGYTGVQDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
      220      230      240      250      260      270

```

```

      80
AAD-12 GD
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 101.1 bits: 25.4 E(): 1.2
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (49-79:247-277)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . :: : . : ::
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPNESDPSKWLS
      220      230      240      250      260      270

```

```

      80
AAD-12 GD
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDWVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 58 Z-score: 96.3 bits: 23.0 E(): 2.2
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (29-64:79-117)

```

      10      20      30      40      50
AAD-12 GHVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      :::: :::: :: : : ::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGD
      :: ::::
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 95.2 bits: 22.4 E(): 2.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (60-76:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGD
      : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum
 aestivum+AF0- (838 aa)
 initn: 43 initl: 43 opt: 64 Z-score: 92.8 bits: 24.8 E(): 3.4
 Smith-Waterman score: 64+ADs- 34.286+ACU- identity (60.000+ACU- similar)
 in 35 aa overlap (1-35:140-171)

```

                                10      20      30
AAD-12                        GHVQQAGSAYIGYGMDDTTATPLRPLVKVHP
                                : : : : : : : : : : : : : : : : : :
gi+AHw-736 RYYPSVTSPQQVSYYPGQASPPRPGQGQPGQGQSGQGQGGY---YPTSPQQPGQWQQP
      110      120      130      140      150      160

                                40      50      60      70      80
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
      : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-736 EQGQPGYYPTSPQQPGQLQQPAQGQPGQGQGRQPGQGQPGYYPTSSQLQPGQLQQPAQ
      170      180      190      200      210      220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.7 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (60-76:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGD
      : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.7 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (60-76:68-86)

```

      30      40      50      60      70      80
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGD
              : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100     110     120     130     140     150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)
initn: 47 initl: 47 opt: 52 Z-score: 89.0 bits: 21.1 E(): 5.6
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (14-80:19-84)

```

      10      20      30      40      50
AAD-12      GHVQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
              : : : : : . : : : : : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDVK--KD
      10      20      30      40      50

```

```

      60      70      80
AAD-12  RFLE-GLVDWACQAPRVHAHQWAAGD
      . . . : : . . . : : : :
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
      60      70      80      90      100     110

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 initl: 55 opt: 57 Z-score: 87.2 bits: 22.7 E(): 7
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (3-48:345-393)

```

      10      20      30
AAD-12      GHVQQAGSAYIGYGMDTTATPLRPLVKVHPET
              : . : . . . : : . : : . : :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPVLTPEQSAGMIPAEP
      320     330     340     350     360     370

```

```

      40      50      60      70      80
AAD-12  GRPSLLIGRHAHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
      : . : . : : : : : :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
      380     390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 86.8 bits: 22.4 E(): 7.4
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (8-59:25-73)

```

      10      20      30      40
AAD-12      GHVQQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH

```

```

      .:  ...  :  :::  :  .  :  :  .  .
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
              10          20          30          40          50

```

```

              50          60          70          80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGD

```

```

      .:  :  ...  ....:
gi+AHw-249 PAAVPSGKATTEEQKLEKINAGFKA AVAAA VVPPADKYKTFVETFGTATNKAFVEGLA
              60          70          80          90          100          110

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 initl: 37 opt: 56 Z-score: 84.5 bits: 22.4 E(): 9.8
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (20-74:46-108)

```

              10          20          30          40
AAD-12      GHVQQAGSAYIGYGMTTATPLRPL---VKVHPETGRPSLL--IGRH--
              :::::  ....:  ....:  :  .:  .
gi+AHw-253 IEEPEMIAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
              20          30          40          50          60          70

```

```

              50          60          70          80
AAD-12  -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGD
      .:  .  ...  ..  .:  ...  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDLDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
              80          90          100          110          120          130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPTHLEHSS
              140          150          160          170          180          190

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 174 - 253 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

[illegible]


```

86      1      2: +ACo-
88      1      2: +ACo-          inset +AD0- represents 1 library sequences
90      1      1: +ACo-
92      0      1: +ACo-          : +ACo-
94      2      1: +ACo-          : +ACoAPQ-
96      2      1: +ACo-          : +ACoAPQ-
98      0      0:              +ACo-
100     0      0:              +ACo-
102     1      0: +AD0-        +ACoAPQ-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     1      0: +AD0-        +ACoAPQ-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.85830.00311+ADs- mu+AD0- 5.3847
0.162
mean+AF8-var+AD0-35.7748 9.793, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.214430
Kolmogorov-Smirnov statistic: 0.0739 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 27.7      0.24
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 25.5      1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   58 23.1      1.9
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.5      2.2
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.5      3.1
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.5      3.1
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)   52 21.3      5
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396)   57 22.8      6.6
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)   56 22.5      6.9
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4      9.3
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838)   59 23.3      9.3

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:

Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 113.6 bits: 27.7 E(): 0.24

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)

in 31 aa overlap (48-78:246-276)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .:: : . : .::
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

```

```

      80
AAD-12 GDV
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:

Full+AD0-Enolase (440 aa)

initn: 66 init1: 66 opt: 66 Z-score: 101.9 bits: 25.5 E(): 1.1

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)

in 31 aa overlap (48-78:247-277)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .: : . : .::
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      80
AAD-12 GDV
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:

Full+AD0-Globin (151 aa)

initn: 51 init1: 51 opt: 58 Z-score: 97.2 bits: 23.1 E(): 1.9

Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)

in 40 aa overlap (28-63:79-117)

```

      10      20      30      40      50
AAD-12 HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      .....:: : : :...::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDV
      :: .....
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 96.1 bits: 22.5 E(): 2.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (59-75:68-86)

```
      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDV
              : . . . . : : . . . . :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 93.6 bits: 22.5 E(): 3.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (59-75:68-86)

```
      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDV
              : . . . . : : . . . . :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 93.6 bits: 22.5 E(): 3.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (59-75:68-86)

```
      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDV
              : . . . . : : . . . . :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)
initn: 47 initl: 47 opt: 52 Z-score: 89.8 bits: 21.3 E(): 5
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (13-79:19-84)

```
      10      20      30      40      50
AAD-12      HVQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
              : : : : : . : : : : .
```

AAD-12 HVQQAGSAYIGYGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
 ::: ::: ::: : :
 ::: ::: ::: :

```
gi+AHw-253 IEEPEMIAPTPPGQFPHQPISSPNRTSRNTPLRPESTEIETHHHANHPALPVLGMQLP
           20           30           40           50           60           70
```

```
           50           60           70           80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
      ... . :. . :. :. :. :. :.
```

```
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
           80           90          100          110          120          130
```

```
gi+AHw-253 GLPPTGFASHLPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
           140          150          160          170          180          190
```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum
aestivum+AF0- (838 aa)

initn: 43 initl: 43 opt: 59 Z-score: 85.0 bits: 23.3 E(): 9.3
Smith-Waterman score: 59+ADs- 34.375+ACU- identity (59.375+ACU- similar)
in 32 aa overlap (3-34:143-171)

```
           10           20           30
AAD-12 HVQQAGSAYIGYGMDTTATPLRPLVKVHPETG
      ..... :. :. :. :. :. :.
gi+AHw-736 PSVTSPQQVSYYPGQASFPQRPGQGQQPGQGQQSGQGQQGY---YPTSPQQPGQWQQPEQG
           120          130          140          150          160
```

```
           40           50           60           70           80
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDV
      .:
gi+AHw-736 QPGYYPTSPQQPGQLQQPAQGQQPGQGQQGRQPGQGQPGYYPTSSQLQPGQLQQPAQGQQ
           170          180          190          200          210          220
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010

Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 175 - 254 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()

[illegible]

```

90      0      1:+ACo-
92      2      1:+ACo-      :+ACoAPQ-
94      1      1:+ACo-      :+ACo-
96      1      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     0      0:      +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     1      0:+AD0-      +ACoAPQ-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.72780.00337+ADs- mu+AD0- 6.0498
0.176
mean+AF8-var+AD0-36.3164 9.871, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.212825
Kolmogorov-Smirnov statistic: 0.0674 (N+AD0-29) at 48

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.7 0.24
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.5 1.1
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 58 23.1 2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.4 2.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4 3.2
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4 3.2
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110) 52 21.2 5.3
gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName: Full+AD0-Po
( 396) 57 22.7 6.6
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339) 56 22.4 7
gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum aesti (
838) 59 23.4 9.2
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4 9.3

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 113.4 bits: 27.7 E(): 0.24

```

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (47-77:246-276)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      .....:..:..:..:..:..:..
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

```

```

      80
AAD-12 GDVV
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 101.7 bits: 25.5 E(): 1.1
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (47-77:247-277)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      .....:..:..:..:..:..:..
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGLYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      80
AAD-12 GDVV
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 58 Z-score: 96.8 bits: 23.1 E(): 2
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (27-62:79-117)

```

      10      20      30      40      50
AAD-12 VQQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      .....:..:..:..:..:..:..
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVV
      :..:.....
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 95.7 bits: 22.4 E(): 2.4

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (58-74:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 93.2 bits: 22.4 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (58-74:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVV
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

gi+AHw-456 SFGSDRSGLLLKQKVSDDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 93.2 bits: 22.4 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (58-74:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVV
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-184 SFDSDRSGLLLKQKVSDDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)

initn: 47 initl: 47 opt: 52 Z-score: 89.4 bits: 21.2 E(): 5.3
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (12-78:19-84)

```

      10      20      30      40      50
AAD-12 VQQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
      10      20      30      40      50

```

```

        60          70          80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVV
      ... :      :      :      :
gi+AHw-135 LLLNVGSGGGAAPLPEALLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-113475+AHw-sp+AHw-P27759.1+AHw-MPA11+AF8-AMBAR RecName:
Full+AD0-Pollen (396 aa)
initn: 55 init1: 55 opt: 57 Z-score: 87.6 bits: 22.7 E(): 6.6
Smith-Waterman score: 57+ADs- 24.490+ACU- identity (53.061+ACU- similar)
in 49 aa overlap (1-46:345-393)

```

                                10          20          30
AAD-12                                VQQAGSAYIGYGMDDTATPLRPLVKVHPET
                                : . . . . . : : . . . . :
gi+AHw-113 PDERSKKNVLGRHGEEAAESMKWNWRTNKDVLNGAIFVASGVDPVLTPEQSAGMIPAEP
        320          330          340          350          360          370

```

```

        40          50          60          70          80
AAD-12 GRPSLLIGRHAHAI---PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
      .. . : .. :
gi+AHw-113 GESALSLTSSAGVLSCQPGAPC
        380          390

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 87.2 bits: 22.4 E(): 7
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (6-57:25-73)

```

                                10          20          30          40
AAD-12                                VQQAGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
                                .. : : : : : . . : : . :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
        10          20          30          40          50

```

```

        50          60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
      : : : : :
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA VPPADKYKTFVETFGTATNKAFVEGLA
        60          70          80          90          100          110

```

+AD4APg-gi+AHw-736319+AHw-emb+AHw-CAA27052.1+AHw- glutenin +AFs-Triticum
aestivum+AF0- (838 aa)
initn: 43 init1: 43 opt: 59 Z-score: 85.1 bits: 23.4 E(): 9.2
Smith-Waterman score: 59+ADs- 34.375+ACU- identity (59.375+ACU- similar)
in 32 aa overlap (2-33:143-171)

```

                                10          20          30
AAD-12                                VQQAGSAYIGYGMDDTATPLRPLVKVHPETG
                                : : : : : : : : : : :
gi+AHw-736 PSVTSPQQVSYYPGQASPGQPGQGGQGGQSGQGGQGY---YPTSPQQPGQWQQPEQG
        120          130          140          150          160

```

```

                40          50          60          70          80
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
      .:
gi+AHw-736 QPGYYPTSPQQPGQLQQPAQGGQQPGQGQGRQPGQGQPGYYPTSSQLQPGQLQQPAQGGQ
      170          180          190          200          210          220

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 initl: 37 opt: 56 Z-score: 85.0 bits: 22.4 E(): 9.3
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (18-72:46-108)

```

                10          20          30          40
AAD-12          VQQAGSAYIGYGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
      :::::      ...: .....: : .:.
gi+AHw-253 IEEPEMIAPTTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
      20          30          40          50          60          70

```

```

                50          60          70          80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVV
      ...: . :...: .: .: .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRRHAHSAQSSA
      80          90          100          110          120          130

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPTHLEHSS
      140          150          160          170          180          190

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:25 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 176 - 255 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:

```

```

26      0      0:
28      0      0:
30      1      2:+ACo-
32      2      8:+AD0- +ACo-
34     13     21:+AD0APQA9AD0APQ- +ACo-
36     27     44:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
38     49     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
40     61
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42    101
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0- +ACo-
44    137
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0-+AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
46    175
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA
9AD0APQA9AD0APQ-
48    105
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQ- +ACo-
50    144
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
52    130    106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
54    117
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
56     69
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58     62
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAq-
60     43     50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62     37     40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64     48     32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66     31     25: +AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68     23     20: +AD0APQA9AD0APQA9ACoAPQ-
70     15     16: +AD0APQA9AD0APQAq-
72     24     12: +AD0APQA9ACoAPQA9AD0APQ-
74     11     10: +AD0APQA9ACo-
76     15       7: +AD0APQAqAD0APQ-
78     13       6: +AD0AKgA9AD0APQ-
80      1       4: +AD0AKg-
82      5       3: +ACoAPQ-
84      2       3: +ACo-
86      1       2: +ACo-
88      1       2: +ACo- inset +AD0- represents 1 library sequences
90      0       1: +ACo-
92      2       1: +ACo- :+ACoAPQ-
94      1       1: +ACo- :+ACo-

```

```

96      1      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     1      0:+AD0-      +ACoAPQ-
102     0      0:      +ACo-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     1      0:+AD0-      +ACoAPQ-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.91590.00346+ADs- mu+AD0- 4.9447
0.180
mean+AF8-var+AD0-37.304310.079, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.209988
Kolmogorov-Smirnov statistic: 0.0795 (N+AD0-29) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.5 0.27
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.4 1.2
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 58 23.0 2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.4 2.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4 3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4 3.4
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110) 52 21.2 5.4
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339) 56 22.4 7.5
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.3 10

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 112.5 bits: 27.5 E(): 0.27
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (46-76:246-276)

20 30 40 50 60 70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
:::: :: . .:: : . : .: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGlyDLDFKNPNSDKSKWIT

```

```

220      230      240      250      260      270
      80
AAD-12 GDVVV
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
  initn: 66 init1: 66 opt: 66 Z-score: 101.0 bits: 25.4 E(): 1.2
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (46-76:247-277)

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

      80
AAD-12 GDVVV
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
  initn: 51 init1: 51 opt: 58 Z-score: 96.5 bits: 23.0 E(): 2.1
Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
in 40 aa overlap (26-61:79-117)

      10      20      30      40      50
AAD-12 QQAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVV
      : : : :
gi+AHw-121 EEFRASLVLDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
  initn: 40 init1: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (57-73:68-86)

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAAGDVVV
      : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF

```

40 50 60 70 80 90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (57-73:68-86)

30 40 50 60 70 80

AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVV
: : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
40 50 60 70 80 90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (57-73:68-86)

30 40 50 60 70 80

AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVV
: : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)
initn: 47 init1: 47 opt: 52 Z-score: 89.2 bits: 21.2 E(): 5.4
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (11-77:19-84)

10 20 30 40 50

AAD-12 QQAGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
: : : : : . : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFKALEGKDV--KD
10 20 30 40 50

60 70 80

AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVV
: : : : : : : : : :
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
60 70 80 90 100 110

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:

Full+AD0-Major (339 aa)

initn: 52 initl: 52 opt: 56 Z-score: 86.7 bits: 22.4 E(): 7.5

Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)

in 54 aa overlap (5-56:25-73)

```

                                10      20      30
AAD-12                      QQAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
                                .:  .:.  :  :::  :  .  :  :  .:
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                                10      20      30      40      50

```

```

        40      50      60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
        .:.  :  .:.  .:.  .:.
gi+AHw-249 PAAVPSGKATTEEQKLTIEKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
        60      70      80      90     100     110

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix

protein +AFs-F (450 aa)

initn: 37 initl: 37 opt: 56 Z-score: 84.4 bits: 22.3 E(): 10

Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)

in 63 aa overlap (17-71:46-108)

```

                                10      20      30
AAD-12                      QQAGSAYIGYGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                .:  .:.  :  .:  .:  .:  .:  .:
gi+AHw-253 IEEPEMIAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                                20      30      40      50      60      70

```

```

        40      50      60      70      80
AAD-12  -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVV
        .:.  .  .:.  .:  .:  .:  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
        80      90     100     110     120     130

```

```

gi+AHw-253 GLPPTGFASHLPASSGPVSLGWNMYHVPPNHLNANQFNFEVPGHMNVSGHPTHLEHSS
        140     150     160     170     180     190

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:25 2010 done: Fri Feb 5 12:56:26 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

[illegible]

```

84      1      3:+ACo-
86      2      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0:+AD0-          +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.92120.00341+ADs- mu+AD0- 4.8674
0.178
mean+AF8-var+AD0-37.454010.121, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.209568
Kolmogorov-Smirnov statistic: 0.0827 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 27.5      0.28
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 25.4      1.2
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   58 23.0      2.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.4      2.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4      3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4      3.4
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)   52 21.2      5.4
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339)   56 22.4      7.5
gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (
228)   54 21.8      7.5
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.3      10

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

```

initn: 73 initl: 73 opt: 73 Z-score: 112.4 bits: 27.5 E(): 0.28
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (45-75:246-276)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . :: : . : :: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

```

```

      80
AAD-12 GDVVVW
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 100.9 bits: 25.4 E(): 1.2
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (45-75:247-277)

```

      20      30      40      50      60      70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . :: : . : :: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGLYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      80
AAD-12 GDVVVW
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 58 Z-score: 96.5 bits: 23.0 E(): 2.1
 Smith-Waterman score: 58+ADs- 40.000+ACU- identity (62.500+ACU- similar)
 in 40 aa overlap (25-60:79-117)

```

      10      20      30      40      50
AAD-12 QAGSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      :::: :::: :: : : ::::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVW
      :: .:::.
gi+AHw-121 EEFRASLVDYLSHHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)

initn: 40 initl: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (56-72:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVW
      : : : : : : : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (56-72:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVW
      : : : : : : : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (56-72:68-86)

```

      30      40      50      60      70      80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVW
      : : : : : : : : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 initl: 47 opt: 52 Z-score: 89.2 bits: 21.2 E(): 5.4
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (10-76:19-84)

```

      10      20      30      40      50
AAD-12 QAGSAYIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
      : : : : : : : : : : : : : : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFKALEGKDV--KD
      10      20      30      40      50

```

```

                60          70          80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVW
      ... :      :      :      :
gi+AHw-135 LLLNVGSGGGAAPLPEALLRWRAADAAPAAEEKKEEEEKESDEDMGFGLFD
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 86.7 bits: 22.4 E(): 7.5
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (4-55:25-73)

```

                        10          20          30
AAD-12                      QAGSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
                        .. ... : ... : . . : . . :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                        10          20          30          40          50

```

```

                40          50          60          70          80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW
      ... :      :      :
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKAAVAAA VVPADKYKTFVETFGTATNKAFVEGLA
                60          70          80          90          100          110

```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
Penicillium citrin (228 aa)
initn: 54 initl: 54 opt: 54 Z-score: 86.6 bits: 21.8 E(): 7.5
Smith-Waterman score: 54+ADs- 20.253+ACU- identity (51.899+ACU- similar)
in 79 aa overlap (2-80:74-152)

```

                        10          20          30
AAD-12                      QAGSAYIGYGMDTTATPLRPLVKVHPETGRP
                        ..... : ... : : :
gi+AHw-383 SPDAEKYPHVARWYKHIASESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEE
                50          60          70          80          90          100

```

```

                40          50          60          70          80
AAD-12 SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVW
      ... :      :      :      :
gi+AHw-383 DLFASDSEDEDP AVVAERNKNLEEYKKKKAAKGPKPAKSLVTLEVKPWDDDET NLEELEA
                110          120          130          140          150          160

```

```

gi+AHw-383 NVRAIEMDGLVWGASKFVAVGFGIKKLQINLVVEDEK VSTDELQAQIEEDEDHVQSTDVA
                170          180          190          200          210          220

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 initl: 37 opt: 56 Z-score: 84.4 bits: 22.3 E(): 10
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (16-70:46-108)

```

                        10          20          30
AAD-12                      QAGSAYIGYGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--

```

[illegible]

inset +AD0- represents 1 library sequences

331323 residues in 1471 sequences
 Expectation+AF8-n fit: $\rho(\ln(x))+AD0-4.86640.00332+ADs- \mu+AD0-5.1505$
 0.174

mean+AF8-var+AD0-36.8902 9.934, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43

Lambda+AD0- 0.211163

Kolmogorov-Smirnov statistic: 0.0814 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
 ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)
 gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 27.6 0.26
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 64 24.9 0.57
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 25.4 1.1
 gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (228)
 62 24.3 1.3
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 22.5 2.4
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.4 3.2
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.4 3.2
 gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
 (110) 52 21.2 5.2
 gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName: Full+AD0-
 (731) 60 23.6 6.8
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.1
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 113.0 bits: 27.6 E(): 0.26
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (44-74:246-276)

	20	30	40	50	60	70
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
	::: :: . : : . : .					
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270
	80					
AAD-12	GDVVVD					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 64 Z-score: 106.7 bits: 24.9 E(): 0.57
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (24-80:79-133)

```

                10      20      30      40
AAD-12      AGSAYIGYGMDDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                .... : : : :
gi+AHw-121  DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100
```

```

                50      60      70      80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
                : : : : : : : :
gi+AHw-121  EEFRASLV DYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 101.4 bits: 25.4 E(): 1.1
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (44-74:247-277)

```

                20      30      40      50      60      70
AAD-12  ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                : : : : : : : :
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270
```

```

                80
AAD-12  GDVVVWD
                :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDWVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330
```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
Penicillium citrin (228 aa)
initn: 62 initl: 62 opt: 62 Z-score: 100.1 bits: 24.3 E(): 1.3
Smith-Waterman score: 62+ADs- 21.250+ACU- identity (52.500+ACU- similar)
in 80 aa overlap (1-80:74-153)

```

                10      20      30
AAD-12      AGSAYIGYGMDDTTATPLRPLVKVHPETGRP
                ..... : : :
gi+AHw-383  SPDAEKYPHVARWYKHIASESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEE
                50      60      70      80      90      100
```

```

                40      50      60      70      80
AAD-12  SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
                : : : : : : : :
gi+AHw-383  DLFASDSEDEDPVVAAERNKNLEEYKKKKAAGPKPAKSLVTLEVKPWDDETNLEELEA
                110      120      130      140      150      160
```

gi+AHw-383 NVRAIEMDGLVWGASKFVAVGFGIKKLQINLVVEDEKVVSTDELQAQIEEDEDHVQSTDVA
 170 180 190 200 210 220

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)

initn: 40 initl: 40 opt: 56 Z-score: 95.7 bits: 22.5 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (55-71:68-86)

30 40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWD
 : : : . . . : :
 gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 93.2 bits: 22.4 E(): 3.2
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (55-71:68-86)

30 40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWD
 : : : . . . : :
 gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
 40 50 60 70 80 90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 93.2 bits: 22.4 E(): 3.2
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (55-71:68-86)

30 40 50 60 70 80
 AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWD
 : : : . . . : :
 gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 initl: 47 opt: 52 Z-score: 89.5 bits: 21.2 E(): 5.2
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (9-75:19-84)

```

                10      20      30      40      50
AAD-12      AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
                :: ::  ::  ::::  .  ::::  ::  ::
gi+AHw-135  MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
                10      20      30      40      50

```

```

                60      70      80
AAD-12  RFLE-GLVDWACQAPRVHAHQWAAAGDVVVWD
                ... :  :  ...  :: ::
gi+AHw-135  LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName:
Full+AD0-Cucu (731 aa)
initn: 35 init1: 35 opt: 60 Z-score: 87.5 bits: 23.6 E(): 6.8
Smith-Waterman score: 60+ADs- 29.412+ACU- identity (52.941+ACU- similar)
in 85 aa overlap (4-80:548-631)

```

                10      20      30
AAD-12      AGSAYIGYGMDDTATPLRPLVKVHPETGRPSLL
                : :  .. ::::  . . : . :
gi+AHw-711  FNIISGTSMSCPHITGIATYVKTYNPTWSPAAIKSALMTTASPMNARFNPQAEFAYGSGH
                520      530      540      550      560      570

```

```

                40      50      60      70      80
AAD-12  IGRHAHAIPGM--DAAESE--RFLEGLVDWACQAPRVHAHQWAA---GDV-VVWD
                ..  . ::  :: ::  :::: :  . :: :  . ....  ... ::
gi+AHw-711  VNPLKAVRPGLVYDANESDYVKFLCGQ-GYNTQAVRRITGDYSACTSGNTGRVWDLNYP
                580      590      600      610      620      630

```

```

gi+AHw-711  FGLSVSPSQTFNQYFNRTLTSVAPQASTYRAMISAPQGLTISVNPVLSFNGLGDRKSFT
                640      650      660      670      680      690

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 init1: 52 opt: 56 Z-score: 87.0 bits: 22.4 E(): 7.1
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (3-54:25-73)

```

                10      20      30
AAD-12      AGSAYIGYGMDDTATPLRPLVKVHPET-GRPSLLIGRH
                .:  ::  : ::  : . . : . :
gi+AHw-249  MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50

```

```

                40      50      60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWD
                :: :  :: ::::
gi+AHw-249  PAAVPSGKATTEEQKLIEKINAGFKA AVAAA VPPADKYKTFVETFGTATNKAFVEGLA
                60      70      80      90      100      110

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 init1: 37 opt: 56 Z-score: 84.8 bits: 22.4 E(): 9.6

Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (15-69:46-108)

```

                        10      20      30
AAD-12                AGSAYIGYGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                        :::::  ....:  ....:  :  ::
gi+AHw-253 IEEPEMIAPTPPGQFFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20      30      40      50      60      70

                40      50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWD
                ...:  .  ....:  ..  .:  ...:  .:
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                80      90      100      110      120      130

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPTHLEHSS
                140      150      160      170      180      190

```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:26 2010 done: Fri Feb 5 12:56:26 2010

Total Scan time: 0.090 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 179 - 258 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      1      2:+ACo-
      32      3      8:+AD0- +ACo-
      34      11     21:+AD0APQA9AD0- +ACo-
      36      24     44:+AD0APQA9AD0APQA9AD0APQ- +ACo-
      38      53     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-

```

```

40      57      101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
42      109
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
44      126      136:+AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
46      173
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA
9AD0APQA9AD0-
48      131
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
50      132
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
52      133
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
54      113
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
56      60      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
58      69
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      38      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
62      31      40:+AD0APQ-+AD0APQA9AD0APQA9AD0APQA9-      +ACo-
64      52      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
66      32      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68      22      20:+AD0APQA9AD0APQA9ACoAPQ-
70      19      16:+AD0APQA9AD0APQAqAD0-
72      24      12:+AD0APQA9ACoAPQA9AD0APQ-
74      10      10:+AD0APQA9ACo-
76      18      7:+AD0APQAqAD0APQA9-
78      11      6:+AD0AKgA9AD0-
80      3      4:+AD0AKg-
82      3      3:+ACo-
84      1      3:+ACo-
86      2      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      2      1:+ACo-          :+ACoAPQ-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     1      0:+AD0-          +ACoAPQ-
108     0      0:              +ACo-
110     0      0:              +ACo-

```

```

112      1      0: +AD0-          +ACoAPQ-
114      0      0:          +ACo-
116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.97720.00329+ADs- mu+AD0- 4.6011
0.172
mean+AF8-var+AD0-37.2608 9.980, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.210111
Kolmogorov-Smirnov statistic: 0.0834 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.5 0.27
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 24.8 0.6
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.4 1.2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 22.4 2.4
gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (
228) 59 23.3 2.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4 3.3
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4 3.3
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110) 52 21.2 5.3
gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName: Full+AD0-
( 731) 60 23.5 7.2
gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
( 339) 56 22.4 7.5

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

initn: 73 initl: 73 opt: 73 Z-score: 112.4 bits: 27.5 E(): 0.27
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (43-73:246-276)

```

                20          30          40          50          60          70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                ....:..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220          230          240          250          260          270

                80
AAD-12 GDVVVWDN
                :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK

```

280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 64 Z-score: 106.4 bits: 24.8 E(): 0.6
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (23-79:79-133)

```

                10      20      30      40
AAD-12      GSAYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                ....  ::  :  :  ...  .
gi+AHw-121  DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
            50      60      70      80      90      100

            50      60      70      80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDN
            ::  .....  :  ::  ...
gi+AHw-121  EEFRASLV DYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
            110      120      130      140      150
```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 101.0 bits: 25.4 E(): 1.2
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (43-73:247-277)

```

                20      30      40      50      60      70
AAD-12  ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                ....  ::  .  :  :  .  .  .
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
            220      230      240      250      260      270

            80
AAD-12  GDVVVWDN
            :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
            280      290      300      310      320      330
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 95.5 bits: 22.4 E(): 2.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (54-70:68-86)

```

                30      40      50      60      70      80
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDN
                :  ....  ::  ...  ...
gi+AHw-219  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
            40      50      60      70      80      90

gi+AHw-219  SFDSDRSGLLLKQKVSDE
            100      110
```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-

Penicillium citrin (228 aa)

initn: 59 initl: 59 opt: 59 Z-score: 94.8 bits: 23.3 E(): 2.6

Smith-Waterman score: 59+ADs- 20.513+ACU- identity (51.282+ACU- similar)

in 78 aa overlap (3-80:77-154)

```

                                10      20      30
AAD-12                        GSAYIGYGMDDTTATPLRPLVKVHPETGRPSLL
                                :. .:. . . . : : : . . .
gi+AHw-383 AEKYPHVARWYKHIASYESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEEEDLF
                   50          60          70          80          90          100

```

```

                   40          50          60          70          80
AAD-12 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDN
                   .      :. . : . . . : : : . . . : :
gi+AHw-383 ASDSEDEDPAVVAERNKNLEEYKKKKAAGKPKAAKSLVTLEVKPWDDDETNLLEELEANVR
                   110         120         130         140         150         160

```

```

gi+AHw-383 AIEMDGLVWGASKFVAVGFGIKKLQINLVVEDEKVVSTDELQAQIEEDEDHVQSTDVAAMQ
                   170         180         190         200         210         220

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)

in 19 aa overlap (54-70:68-86)

```

                   30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDN
                                : . . . . : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMNF
                   40          50          60          70          80          90

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                   100         110         120         130         140         150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 93.0 bits: 22.4 E(): 3.3

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)

in 19 aa overlap (54-70:68-86)

```

                   30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDN
                                : . . . . : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMDF
                   40          50          60          70          80          90

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                   100         110         120         130         140         150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:

Full+AD0-60S ac (110 aa)

initn: 47 initl: 47 opt: 52 Z-score: 89.3 bits: 21.2 E(): 5.3

Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (8-74:19-84)

```

                10      20      30      40
AAD-12          GSAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
                :: ::  ::  ::::  .  ::::  ::  ::
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
                10      20      30      40      50
```

```

        50      60      70      80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAAGDVVVWDN
        ... :  :  ::  :: ::
gi+AHw-135 LLLNVGSGGGAAPLPEALLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
        60      70      80      90      100     110
```

+AD4APg-gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName:
Full+AD0-Cucu (731 aa)
initn: 35 initl: 35 opt: 60 Z-score: 87.0 bits: 23.5 E(): 7.2
Smith-Waterman score: 60+ADs- 29.412+ACU- identity (52.941+ACU- similar)
in 85 aa overlap (3-79:548-631)

```

                10      20      30
AAD-12          GSAYIGYGMDTTATPLRPLVKVHPETGRPSLL
                : :  .. ::::  . .  :  :
gi+AHw-711 FNIISGTSMSCPHITGIATYVKTYNPTWSPAAIKSALMTTASPMNARFNPQAEFAYGSGH
        520      530      540      550      560      570
```

```

        40      50      60      70      80
AAD-12 IGRHAHAIPGM--DAAESE--RFLEGLVDWACQAPRVHAHQWAA---GDV-VVWDN
        ..  .  ::  :: ::  :: :  .  :: :  .  ::::  ...  ::
gi+AHw-711 VNPLKAVRPGLVYDANESDYVKFLCGQ-GYNTQAVRRITGDYSACTSGNTGRVWDLNYPs
        580      590      600      610      620      630
```

```

gi+AHw-711 FGLSVSPSQTFNQYFNRTLTSVAPQASTYRAMISAPQGLTISVNPVLSFNGLGDRKSFT
        640      650      660      670      680      690
```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)
initn: 52 initl: 52 opt: 56 Z-score: 86.7 bits: 22.4 E(): 7.5
Smith-Waterman score: 56+ADs- 29.630+ACU- identity (53.704+ACU- similar)
in 54 aa overlap (2-53:25-73)

```

                10      20      30
AAD-12          GSAYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
                ::  ::  :  :::  :  .  :  :  .  .
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                10      20      30      40      50
```

```

        40      50      60      70      80
AAD-12 AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDN
        ::: :  ::  ::::
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAA AVVPPADKYKTFVETFGTATNKAFVEGLA
        60      70      80      90      100     110
```

Total Scan time: 0.090 Total Display time: 0.000

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 27.6 0.26
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 64 24.9 0.56
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 25.4 1.1
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 22.5 2.3
 gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (228)
 59 23.4 2.5
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.5 3.2
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.5 3.2
 gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
 (110) 52 21.3 5.1
 gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName: Full+AD0-
 (731) 60 23.6 7
 gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M
 (339) 56 22.4 7.2
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.4 9.7

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 113.0 bits: 27.6 E(): 0.26
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (42-72:246-276)

	20	30	40	50	60	70
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
				...	:	:
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTQVVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270
	80					
AAD-12	GDVVVDNR					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 106.9 bits: 24.9 E(): 0.56
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (22-78:79-133)

	10	20	30	40
AAD-12	SAYIGYGMDDTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES			
		...	:	:
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF			
	50	60	70	80
	50	60	70	80

AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR

```

      ::  ::::  :  ::  ::
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110              120              130              140              150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 101.4 bits: 25.4 E(): 1.1
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (42-72:247-277)

```

      20          30          40          50          60          70
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .: : . .: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGYDLDFKNPESDPSKWLS
      220          230          240          250          260          270

```

```

      80
AAD-12 GDVVVWDNR
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 95.9 bits: 22.5 E(): 2.3
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (53-69:68-86)

```

      30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : :::: :: ... ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100          110

```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
Penicillium citrin (228 aa)
initn: 59 initl: 59 opt: 59 Z-score: 95.2 bits: 23.4 E(): 2.5
Smith-Waterman score: 59+ADs- 20.513+ACU- identity (51.282+ACU- similar)
in 78 aa overlap (2-79:77-154)

```

      10          20          30
AAD-12 SAYIGYGMDTTATPLRPLVKVHPETGRPSLL
      .. :::: . . . : : : . .
gi+AHw-383 AEKYPHVARWYKHIASYESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEEEDLF
      50          60          70          80          90          100

```

```

      40          50          60          70          80
AAD-12 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR
      .   :.. : ... . :   : :::: ... .. : ::
gi+AHw-383 ASDSEDEDPVVAERNKNLEEYKKKKAAKGPKPAAKSLVTLEVKPWDDETNLLEELEANVR

```

```

110          120          130          140          150          160
gi+AHw-383 AIEMDGLVWGASKFVAVGFGIKKLQINLVVEDEKVVSTDELQAQIEEDEDHVQSTDVAAMQ
170          180          190          200          210          220

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 93.4 bits: 22.5 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (53-69:68-86)

          30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 93.4 bits: 22.5 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (53-69:68-86)

          30          40          50          60          70          80
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)
  initn: 47 initl: 47 opt: 52 Z-score: 89.7 bits: 21.3 E(): 5.1
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (7-73:19-84)

          10          20          30          40
AAD-12          SAYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
          : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFKALEGKDV--KD
          10          20          30          40          50

          50          60          70          80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-135 LLLNVGSGGGAAPLPEALLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
          60          70          80          90          100          110
```

40 50 60 70 80
 AAD-12 -AHAIPGMDAAEERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR
 ::: ::: ::: ::: ::: ::: ::: ::: ::: :::

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPTHLEHSS
140 150 160 170 180 190

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 181 - 260 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

Kolmogorov-Smirnov statistic: 0.0909 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are:

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En

(439) 73 27.3 0.31

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo

(151) 64 24.7 0.67

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno

(440) 66 25.2 1.3

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (

115) 56 22.3 2.6

gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (

228) 59 23.1 2.9

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)

56 22.3 3.7

gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)

56 22.3 3.7

gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60

(110) 52 21.1 5.8

gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName: Full+AD0-

(731) 60 23.4 7.9

gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve

(206) 53 21.4 9

gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName: Full+AD0-M

(339) 55 21.9 10

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:

Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 111.5 bits: 27.3 E(): 0.31

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)

in 31 aa overlap (41-71:246-276)

	20	30	40	50	60	70
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
				::: :: . ::: : . : :: .		
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTQVQDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270

	80
AAD-12	GDVVVDNRC
	:
gi+AHw-370	GPQLAELEYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
	280
	290
	300
	310
	320
	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:

Full+AD0-Globin (151 aa)

initn: 51 init1: 51 opt: 64 Z-score: 105.5 bits: 24.7 E(): 0.67

Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)

in 61 aa overlap (21-77:79-133)

	10	20	30	40
AAD-12	AYIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES			

```

          .... :: : : ... ..
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50          60          70          80          90          100

```

```

          50          60          70          80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRC
          :: ..... : : :

```

```

gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
          110          120          130          140          150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 100.1 bits: 25.2 E(): 1.3
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (41-71:247-277)

```

          20          30          40          50          60          70
AAD-12  ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          :::: : : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
          220          230          240          250          260          270

```

```

          80
AAD-12  GDVVVWDNRC
          :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 94.8 bits: 22.3 E(): 2.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (52-68:68-86)

```

          30          40          50          60          70
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : ..... :: ... ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          80
AAD-12  C

```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
          100          110

```

+AD4-+AD4-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
Penicillium citrin (228 aa)
initn: 59 init1: 59 opt: 59 Z-score: 94.1 bits: 23.1 E(): 2.9
Smith-Waterman score: 59+ADs- 20.513+ACU- identity (51.282+ACU- similar)
in 78 aa overlap (1-78:77-154)

```

          10          20          30
AAD-12  AYIGYGMDTTATPLRPLVKVHPETGRPSLL

```

```

      initn:  47 initl:  47 opt:   52 Z-score: 88.7 bits: 21.1 E():  5.8
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (6-72:19-84)

```

```

          10      20      30      40
AAD-12      AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
              :: ::  :: ::::  .      :::: : : . .
gi+AHw-135  MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
              10      20      30      40      50

```

```

          50      60      70      80
AAD-12  RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRC
          ... :      :      :: ::
gi+AHw-135  LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
          60      70      80      90      100      110

```

+AD4APg-gi+AHw-71153243+AHw-sp+AHw-Q39547.1+AHw-CUCM1+AF8-CUCME RecName:
Full+AD0-Cucu (731 aa)
initn: 35 initl: 35 opt: 60 Z-score: 86.3 bits: 23.4 E(): 7.9
Smith-Waterman score: 60+ADs- 29.412+ACU- identity (52.941+ACU- similar)
in 85 aa overlap (1-77:548-631)

```

          10      20      30
AAD-12      AYIGYGMDTTATPLRPLVKVHPETGRPSLL
              : : . . :::: . . : . :
gi+AHw-711  FNIISGTSMSCPHITGIATYVKTYNPTWSPAAIKSALMTTASPMNARFNPQAEFAYGSGH
          520      530      540      550      560      570

```

```

          40      50      60      70      80
AAD-12  IGRHAHAIPGM--DAAESE--RFLEGLVDWACQAPRVHAHQWAA---GDV-VVWDNRC
          .. . :::: :: :::: :::: : . :: : . .... :.. ::
gi+AHw-711  VNPLKAVRPGLVYDANESDYVKFLCGQ-GYNTQAVRRITGDYSACTSGNTGRVWDLNYPs
          580      590      600      610      620      630

```

```

gi+AHw-711  FGLSVSPSQTFNQYFNRTLTSVAPQASTYRAMISAPQGLTISVNPVLSFNGLGDRKSFT
          640      650      660      670      680      690

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
Full+AD0-Venom (206 aa)
initn: 34 initl: 34 opt: 53 Z-score: 85.2 bits: 21.4 E(): 9
Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (26-80:54-104)

```

          10      20      30      40      50
AAD-12      AYIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
              : .. : .... :: . : : . ::::
gi+AHw-250  PSKNCAGKVIKSVGPTEEEKKLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
          30      40      50      60      70      80

```

```

          60      70      80
AAD-12  WACQAPRVHAHQWAAGDVVVWDNRC
          : . . . : :: . . ::
gi+AHw-250  WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTKLIQLWENEV
          90      100      110      120      130

```

+AD4APg-gi+AHw-2498582+AHw-sp+AHw-Q40237.1+AHw-MPA5B+AF8-LOLPR RecName:
Full+AD0-Major (339 aa)

initn: 51 init1: 51 opt: 55 Z-score: 84.4 bits: 21.9 E(): 10
 Smith-Waterman score: 55+ADs- 30.189+ACU- identity (52.830+ACU- similar)
 in 53 aa overlap (1-51:26-73)

```

                                10      20      30
AAD-12                        AYIGYGMDTTATPLRPLVKVHPET-GRPSLLIGRH
                                :  ::  :  ::  :  .  .  :  .  :
gi+AHw-249 MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPAT-----
                                10      20      30      40      50

                                40      50      60      70      80
AAD-12  AHAIP-GMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRC
                                ::  :  ::  ::  :
gi+AHw-249 PAAVPSGKATTEEQKLIKINAGFKA AVAAAVVPPADKYKTFVETFGTATNKAFVEGLA
                                60      70      80      90     100     110

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:26 2010 done: Fri Feb 5 12:56:26 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 182 - 261 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      1      0:+AD0-
      30      0      2:+ACo-
      32      3      8:+AD0- +ACo-
      34     15     21:+AD0APQA9AD0APQ- +ACo-
      36     19     44:+AD0APQA9AD0APQA9AD0- +ACo-
      38     49     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      40     54    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-

```

[illegible]

```

116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.01210.00313+ADs- mu+AD0- 4.5390
0.164
mean+AF8-var+AD0-37.1168 9.823, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.210518
Kolmogorov-Smirnov statistic: 0.0834 (N+AD0-29) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.5  0.28
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.8  0.6
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.3  1.2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 22.4  2.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4  3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4  3.4
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)  52 21.2  5.4
gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-Penicillium ci (
228)  54 21.7  7.6
gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
( 206)  53 21.4  8.5

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 112.3 bits: 27.5 E(): 0.28
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (40-70:246-276)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . :: : . : . :
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
      220      230      240      250      260      270

      70      80
AAD-12 GDVVVWDNRCL
      :
gi+AHw-370 GPQLAELEYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)

initn: 51 initl: 51 opt: 64 Z-score: 106.3 bits: 24.8 E(): 0.6
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (20-76:79-133)

```

                10      20      30      40
AAD-12      YIGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                .... : : ...
gi+AHw-121  DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100

```

```

                50      60      70      80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCL
                :: ..... : : :
gi+AHw-121  EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 100.8 bits: 25.3 E(): 1.2
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (40-70:247-277)

```

                10      20      30      40      50      60
AAD-12  ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                .... : : : :
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

                70      80
AAD-12  GDVVVWDNRCL
                :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (51-67:68-86)

```

                30      40      50      60      70
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : ..... : : :
gi+AHw-219  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40      50      60      70      80      90

```

```

                80
AAD-12  CL
                :
gi+AHw-219  SFDSDRSGLLLKQKVSDE
                100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (51-67:68-86)

```

          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

80
 AAD-12 CL

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (51-67:68-86)

```

          30          40          50          60          70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

80
 AAD-12 CL

```

gi+AHw-184 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 initl: 47 opt: 52 Z-score: 89.2 bits: 21.2 E(): 5.4
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (5-71:19-84)

```

          10          20          30          40
AAD-12          YIGYGMTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
          : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFKALEGKDV--KD
          10          20          30          40          50

```

```

          50          60          70          80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCL
          : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWAADAAPAAEEKKEEEKEESDEDMGFGLFD
          60          70          80          90          100          110

```

+AD4APg-gi+AHw-38326693+AHw-gb+AHw-AAR17475.1+AHw- unknown +AFs-
 Penicillium citrin (228 aa)

initn: 51 initl: 51 opt: 54 Z-score: 86.5 bits: 21.7 E(): 7.6
 Smith-Waterman score: 54+ADs- 19.481+ACU- identity (50.649+ACU- similar)
 in 77 aa overlap (1-77:78-154)

```

                                10      20      30
AAD-12                        YIGYGMDTTATPLRPLVKVHPETGRPSLLI
                                . . . . . : : : . . .
gi+AHw-383 EKYPHVARWYKHIA SYESEFPTLP GDASKAFTAYGPEGSEASANPKDKPAEEEEEEEDLFA
                   50      60      70      80      90     100

                   40      50      60      70      80
AAD-12 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCL
                   . . . . . : : : . . . . . : : : . . .
gi+AHw-383 SDSEDEDP AVVAERNKNLE EYKKKKAAGPKPAKSLVTLEV KPWDD ETNLEELEANVRA
                   110     120     130     140     150     160

gi+AHw-383 IEMDGLVWGASKFVAVGFGIKKLQINLVVEDEK VSTDELQAQIEEDEDHVQSTDVAAMQK
                   170     180     190     200     210     220

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
 Full+AD0-Venom (206 aa)
 initn: 34 initl: 34 opt: 53 Z-score: 85.7 bits: 21.4 E(): 8.5
 Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
 in 55 aa overlap (25-79:54-104)

```

                                10      20      30      40      50
AAD-12                        YIGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
                                : . . : . . . : : . : . : . . . :
gi+AHw-250 PSKNCAGKVIKSVGPTEEEKKLIVEEHNRF RQKVAQGLETRGNPGPQPAASN--MNNLV-
                   30      40      50      60      70      80

                   60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVWDNRCL
                   : . . : . . : : . . . :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFP SVTKLIQLWENEV
                   90      100     110     120     130

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:26 2010 done: Fri Feb 5 12:56:26 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:
 W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 183 - 262 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

76      15      7:+AD0APQAqAD0APQ-
78      10      6:+AD0AKgA9AD0-
80       3      4:+AD0AKg-
82       7      3:+ACoAPQA9-
84       1      3:+ACo-
86       1      2:+ACo-
88       1      2:+ACo-          inset +AD0- represents 1 library sequences
90       0      1:+ACo-
92       2      1:+ACo-          :+ACoAPQ-
94       1      1:+ACo-          :+ACo-
96       0      1:+ACo-          :+ACo-
98       0      0:              +ACo-
100      1      0:+AD0-          +ACoAPQ-
102      0      0:              +ACo-
104      0      0:              +ACo-
106      1      0:+AD0-          +ACoAPQ-
108      0      0:              +ACo-
110      0      0:              +ACo-
112      1      0:+AD0-          +ACoAPQ-
114      0      0:              +ACo-
116      0      0:              +ACo-
118      0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.04940.0031+ADs- mu+AD0- 4.3569
0.163
mean+AF8-var+AD0-37.1029 9.772, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.210557
Kolmogorov-Smirnov statistic: 0.0843 (N+AD0-29) at 40

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 27.5      0.28
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   64 24.8      0.6
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 25.3      1.2
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)    56 22.4      2.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.4      3.4
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.4      3.4
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)   52 21.2      5.4
gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
( 206)   53 21.4      8.5

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

```

initn: 73 initl: 73 opt: 73 Z-score: 112.3 bits: 27.5 E(): 0.28
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (39-69:246-276)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . :: : . : ::
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLL
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 64 Z-score: 106.3 bits: 24.8 E(): 0.6
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (19-75:79-133)

```

      10      20      30      40
AAD-12 IGYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      :::: :::: :: : : ::::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      50      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLL
      :: :::: : :: ::
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 100.7 bits: 25.3 E(): 1.2
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (39-69:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . :: : . : ::
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLL
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)

initn: 40 initl: 40 opt: 56 Z-score: 95.4 bits: 22.4 E(): 2.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (50-66:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
      : : : : : : : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
 AAD-12 CLL

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (50-66:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
      : : : : : : : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

80
 AAD-12 CLL

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.9 bits: 22.4 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (50-66:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
      : : : : : : : : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
 AAD-12 CLL

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 89.3 bits: 21.2 E(): 5.4
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (4-70:19-84)

```

                        10      20      30      40
AAD-12      IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
                        :: :: :: :::: . :::: : : ..
gi+AHw-135  MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12  RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCLL
                    : : : : : : : :
gi+AHw-135  LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
                    60      70      80      90      100      110

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
 Full+AD0-Venom (206 aa)
 initn: 34 init1: 34 opt: 53 Z-score: 85.7 bits: 21.4 E(): 8.5
 Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
 in 55 aa overlap (24-78:54-104)

```

                        10      20      30      40      50
AAD-12      IGYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
                        : . : : : : : : : : :
gi+AHw-250  PSKNCAGKVIKSVGPTEEEKKLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
                        30      40      50      60      70      80

                    60      70      80
AAD-12  WACQAPRVHAHQWAAGDVVVWDNRCLL
                    : . . : : : : : :
gi+AHw-250  WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTKLIQLWENEV
                    90      100      110      120      130

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:26 2010 done: Fri Feb 5 12:56:26 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library


```

opt      E()
+ADw- 20    2      0:+AD0-
22       0      0:           one +AD0- represents 3 library sequences
24       0      0:
26       0      0:
28       1      0:+AD0-
30       0      2:+ACo-
32       3      8:+AD0- +ACo-
34      17     21:+AD0APQA9AD0APQA9ACo-
36      22     44:+AD0APQA9AD0APQA9AD0APQ-          +ACo-
38      31     72:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-          +ACo-
40      60    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
42     118    123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0AKg-
44     129
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-   +ACo-
46     165
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA
9AD0-
48     155
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
50     129
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
52     121
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
54      98
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0APQA9ACoAPQA9-
56      55     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
58      77
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
-
60      36     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9-   +ACo-
62      45     40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
64      44     32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66      42     25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
68      34     20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
70      18     16:+AD0APQA9AD0APQAq-
72      18     12:+AD0APQA9ACoAPQA9-
74       8     10:+AD0APQA9ACo-
76      14      7:+AD0APQAqAD0APQ-
78       8      6:+AD0AKgA9-
80       4      4:+AD0AKq-

```

```

82      7      3:+ACoAPQA9-
84      2      3:+ACo-
86      1      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      1      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      1      1:+ACo-          :+ACo-
96      1      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     1      0:+AD0-          +ACoAPQ-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0:+AD0-          +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 5.08150.00309+ADs- mu+AD0- 4.2168
0.162
mean+AF8-var+AD0-36.1527 9.323, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.213306
Kolmogorov-Smirnov statistic: 0.0854 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 27.6    0.26
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   64 24.9    0.55
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 25.4    1.1
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.5     2.3
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.5     3.2
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.5     3.2
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)   52 21.3     5
gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
( 206)   53 21.5     8.1
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.4     9.9

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 113.0 bits: 27.6 E(): 0.26

```

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (38-68:246-276)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      .... : . : . : . : . : . : . :
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLLH
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 64 Z-score: 107.0 bits: 24.9 E(): 0.55
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (18-74:79-133)

```

      10      20      30      40
AAD-12 GYGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      .... : : : : : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      50      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLH
      .. : : : : : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 101.3 bits: 25.4 E(): 1.1
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (38-68:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      .... : . : : . : . : . :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLLH
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 96.0 bits: 22.5 E(): 2.3

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (49-65:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
AAD-12 CLLH

gi+AHw-219 SFDSDRSGLLLKQKVSDE
100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.4 bits: 22.5 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (49-65:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

80
AAD-12 CLLH

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.4 bits: 22.5 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (49-65:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
AAD-12 CLLH

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 89.7 bits: 21.3 E(): 5

Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (3-69:19-84)

```

                        10      20      30      40
AAD-12                GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
                        :: ::  ::  ::::  .  ::::  ::  ::
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFAKALEGKDV--KD
                        10      20      30      40      50

```

```

                    50      60      70      80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH
                    .:: :  :  ::  :: ::
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
                    60      70      80      90      100     110

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
Full+AD0-Venom (206 aa)
initn: 34 initl: 34 opt: 53 Z-score: 86.1 bits: 21.5 E(): 8.1
Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (23-77:54-104)

```

                        10      20      30      40      50
AAD-12                GYGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
                        :  .  :  .... ::  .  :  .  ....:
gi+AHw-250 PSKNCAGKVIKSVGPTEEEEKKLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
                        30      40      50      60      70      80

```

```

                    60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVVWDNRCLLH
                    :  .  .. ::  ::  .. ::
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTCLIQLWENEV
                    90      100     110     120     130

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 initl: 37 opt: 56 Z-score: 84.5 bits: 22.4 E(): 9.9
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (9-63:46-108)

```

                        10      20      30
AAD-12                GYGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                        ::::  .... ::::  :  ::
gi+AHw-253 IIEPEMIAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                        20      30      40      50      60      70

```

```

                    40      50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLH
                    .:: . ::::  ::  ::  ::::  ::
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
                    80      90      100     110     120     130

```

```

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHNMVSGHPHLEHSS
                    140     150     160     170     180     190

```

[illegible]

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 27.9 0.21
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 64 25.1 0.49
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 25.7 0.96
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 22.6 2.1
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 22.6 2.9
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 22.6 2.9
 gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
 (110) 52 21.4 4.8
 gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
 (206) 53 21.6 7.4
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.5 8.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 114.6 bits: 27.9 E(): 0.21
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (37-67:246-276)

10	20	30	40	50	60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
			...	:	:
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTQGVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
220	230	240	250	260	270

70	80
AAD-12 GDVVVWDNRCLLHR	
:	
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK	
280	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 107.9 bits: 25.1 E(): 0.49
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (17-73:79-133)

10	20	30	40
AAD-12 YGMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES			
	
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF			
50	60	70	100

50	60	70	80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHR			
...	:	...
gi+AHw-121 EEFRASLV DYLS----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ			
110	120	130	150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 102.7 bits: 25.7 E(): 0.96
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (37-67:247-277)

	10	20	30	40	50	60
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
				:	:	:
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS					
	220	230	240	250	260	270

	70	80
AAD-12	GDVVVDNRCLLHR	
	:	
gi+AHw-232	GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT	
	280	330

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 96.5 bits: 22.6 E(): 2.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (48-64:68-86)

	20	30	40	50	60	70
AAD-12	PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR					
				:	:	:
gi+AHw-219	YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF					
	40	50	60	70	80	90

	80
AAD-12	CLLHR
	:
gi+AHw-219	SFSDRSGLLLKQKVSDE
	100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 94.0 bits: 22.6 E(): 2.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (48-64:68-86)

	20	30	40	50	60	70
AAD-12	PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR					
				:	:	:
gi+AHw-456	YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF					
	40	50	60	70	80	90

	80
AAD-12	CLLHR
	:
gi+AHw-456	SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
	100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 94.0 bits: 22.6 E(): 2.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (48-64:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      80
AAD-12 CLLHR

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
Full+AD0-60S ac (110 aa)
initn: 47 initl: 47 opt: 52 Z-score: 90.1 bits: 21.4 E(): 4.8
Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
in 68 aa overlap (2-68:19-84)

```

      10      20      30      40
AAD-12 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE
      : : : : . : : : : : : :
gi+AHw-135 MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTLFKALEGKDV--KD
      10      20      30      40      50

      50      60      70      80
AAD-12 RFLE-GLVDWACQAPRVHAHQWAAGDVVVDNRCLLHR
      . . . : : : . . : : :
gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEEKKEEEKEESDEDMGFGLFD
      60      70      80      90      100      110

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
Full+AD0-Venom (206 aa)
initn: 34 initl: 34 opt: 53 Z-score: 86.7 bits: 21.6 E(): 7.4
Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (22-76:54-104)

```

      10      20      30      40      50
AAD-12 YGMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
      : . : : : : : : : : :
gi+AHw-250 PSKNCAGKVIKSVGPTEEEKKLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
      30      40      50      60      70      80

      60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVVDNRCLLHR
      : . . . : : : . . : :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTCLIQLWENEV
      90      100      110      120      130

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
 protein +AFs-F (450 aa)
 initn: 37 initl: 37 opt: 56 Z-score: 85.5 bits: 22.5 E(): 8.6
 Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
 in 63 aa overlap (8-62:46-108)

```

                                10          20          30
AAD-12          YGMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
                                :::::  ....:  :  .
gi+AHw-253  IEEPEMIAPTPPGQFPHQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
                20          30          40          50          60          70

                40          50          60          70          80
AAD-12  -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
                ..:  .  :::.  .:  .:  .:  .:
gi+AHw-253  VPGTVPESSRAQSRASLNLDLDLHAPSHPSHLSHGAPHEQEHAHEIQRRHRAHSAQSSA
                80          90          100          110          120          130

gi+AHw-253  GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
                140          150          160          170          180          190

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 186 - 265 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      3      8:+AD0- +ACo-
      34     19     21:+AD0APQA9AD0APQA9ACo-

```

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36      22      44: +AD0APQA9AD0APQA9AD0APQ-          +ACo-
38      33      72: +AD0APQA9AD0APQA9AD0APQA9AD0APQ-          +ACo-
40      78
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
Q-          +ACo-
42      116
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
44      117
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-          +ACo-
46      172
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9A
D0APQA9AD0APQA9AD0-
48      145
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
50      127
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
52      122
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
54      79      91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-          +ACo-
56      57      76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
58      94
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ
A9AD0APQA9AD0APQ-
60      53      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
62      39      40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
64      47      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
66      30      25: +AD0APQA9AD0APQA9AD0APQAqAD0-
68      33      20: +AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
70      16      16: +AD0APQA9AD0APQAq-
72      16      12: +AD0APQA9ACoAPQA9-
74      7      10: +AD0APQA9ACo-
76      11      7: +AD0APQAqAD0-
78      9      6: +AD0AKgA9-
80      8      4: +AD0AKgA9-
82      4      3: +ACoAPQ-
84      3      3: +ACo-
86      2      2: +ACo-
88      0      2: +ACo-          inset +AD0- represents 1 library sequences
90      1      1: +ACo-
92      0      1: +ACo-          : +ACo-
94      2      1: +ACo-          : +ACoAPQ-
96      1      1: +ACo-          : +ACo-
98      0      0:          +ACo-
100     0      0:          +ACo-
102     1      0: +AD0-          +ACoAPQ-
104     0      0:          +ACo-

```

```

106      0      0:      +ACo-
108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      1      0:+AD0-      +ACoAPQ-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.83680.00305+ADs- mu+AD0- 5.4607
0.161
mean+AF8-var+AD0-34.8181 9.243, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.217356
Kolmogorov-Smirnov statistic: 0.0807 (N+AD0-28) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 27.9   0.21
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   64 25.1   0.48
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 25.7   0.96
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.7   2.1
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.6   2.8
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.6   2.8
gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName: Full+AD0-60
( 110)   52 21.4   4.7
gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
( 206)   53 21.7   7.3
gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei ( 450)
56 22.6   8.6

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 114.6 bits: 27.9 E(): 0.21
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (36-66:246-276)

```

```

          10          20          30          40          50          60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          :::: :: . ::: : . : .::
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSWIT
          220          230          240          250          260          270

          70          80
AAD-12 GDVVVWDNRCLLHRA
:
```

gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPRIKK
280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 64 Z-score: 108.1 bits: 25.1 E(): 0.48
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (16-72:79-133)

AAD-12 10 20 30 40
GMDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
..... :: : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
50 60 70 80 90 100

AAD-12 50 60 70 80
ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
:: : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 102.7 bits: 25.7 E(): 0.96
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (36-66:247-277)

AAD-12 10 20 30 40 50 60
ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
:::: :: . . : : . : .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
220 230 240 250 260 270

AAD-12 70 80
GDVVVWDNRCLLHRA
:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 96.8 bits: 22.7 E(): 2.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (47-63:68-86)

AAD-12 20 30 40 50 60 70
PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: :: ... : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

80
AAD-12 CLLHRA

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 94.2 bits: 22.6 E(): 2.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (47-63:68-86)

	20	30	40	50	60	70
AAD-12	PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR					
				::	:: ... :::
gi+AHw-456	YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF					
	40	50	60	70	80	90

80
 AAD-12 CLLHRA

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 94.2 bits: 22.6 E(): 2.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (47-63:68-86)

	20	30	40	50	60	70
AAD-12	PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR					
				::	:: ... :::
gi+AHw-184	YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF					
	40	50	60	70	80	90

80
 AAD-12 CLLHRA

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1350779+AHw-sp+AHw-P49148.1+AHw-RLA1+AF8-ALTAL RecName:
 Full+AD0-60S ac (110 aa)

initn: 47 init1: 47 opt: 52 Z-score: 90.3 bits: 21.4 E(): 4.7
 Smith-Waterman score: 52+ADs- 26.471+ACU- identity (50.000+ACU- similar)
 in 68 aa overlap (1-67:19-84)

		10	20	30	40
AAD-12		GMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESE			
		::: ::	::
gi+AHw-135	MSTSELATSYAALILADDGVDITADKLQSLIKAAKIEEVEPIWTTTLFAKALEGKDV--KD				
	10	20	30	40	50

	50	60	70	80
AAD-12	RFLE-GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA			
	...	:	:	...
	:	:	...	::: :::

gi+AHw-135 LLLNVGSGGGAAPLPEALLLRWRAADAAPAAEEKKEEEEKEESDEDMGFGLFD
60 70 80 90 100 110

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
Full+AD0-Venom (206 aa)
initn: 34 initl: 34 opt: 53 Z-score: 86.9 bits: 21.7 E(): 7.3
Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (21-75:54-104)

AAD-12 10 20 30 40 50
GMDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
: . : . . . : : . : : . . . :
gi+AHw-250 PSKNCAGKVIKSVGPTEEEKKLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
30 40 50 60 70 80

AAD-12 60 70 80
WACQAPRVHAHQWAAGDVVVWDNRCLLHRA
: . . : : : . . . :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTCLIQLWENEV
90 100 110 120 130

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 initl: 37 opt: 56 Z-score: 85.6 bits: 22.6 E(): 8.6
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (7-61:46-108)

AAD-12 10 20
GMDTTATPLRPL---VKVHPETGRPSLL--IGRH--
: : : : : : : : : : : : :
gi+AHw-253 IEEPEMIAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
20 30 40 50 60 70

AAD-12 30 40 50 60 70 80
-AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
: : . : : : : : : : : : : :
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRHRAHSAQSSA
80 90 100 110 120 130

gi+AHw-253 GLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHMNVSGHPHLEHSS
140 150 160 170 180 190

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank

[illegible]

```

66      33      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQ-
68      45      20:+AD0APQA9AD0APQA9ACoAPQA9AD0APQA9AD0APQA9-
70      15      16:+AD0APQA9AD0APQAq-
72      11      12:+AD0-+AD0APQAq-
74      18      10:+AD0APQA9ACoAPQA9-
76      8        7:+AD0APQAq-
78      9        6:+AD0AKgA9-
80      4        4:+AD0AKg-
82      4        3:+ACoAPQ-
84      4        3:+ACoAPQ-
86      1        2:+ACo-
88      4        2:+ACoAPQ-          inset +AD0- represents 1 library
sequences
90      0        1:+ACo-
92      0        1:+ACo-          :+ACo-
94      2        1:+ACo-          :+ACoAPQ-
96      1        1:+ACo-          :+ACo-
98      0        0:              +ACo-
100     0        0:              +ACo-
102     0        0:              +ACo-
104     1        0:+AD0-          +ACoAPQ-
106     0        0:              +ACo-
108     1        0:+AD0-          +ACoAPQ-
110     0        0:              +ACo-
112     0        0:              +ACo-
114     0        0:              +ACo-
116     1        0:+AD0-          +ACoAPQ-
118     0        0:              +ACo-
+AD4-120 0        0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.88450.00306+ADs- mu+AD0- 5.1693
0.162
mean+AF8-var+AD0-33.7186 9.451, 0's: 2 Z-trim: 4 B-trim: 44 in 1/42
Lambda+AD0- 0.220871
Kolmogorov-Smirnov statistic: 0.0807 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 28.1    0.18
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 25.3    0.42
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.8    0.86
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.8    1.8
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.8    2.6
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.8    2.6

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 22.1 5.4
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 22.1 5.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 22.1 5.5
 gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve
 (206) 53 21.8 6.7
 gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix protei (450)
 56 22.7 8
 gi+AHw-51093377+AHw-gb+AHw-AAT95010.1+AHw- allergen Pol d 5 precu (227)
 52 21.5 9.3
 gi+AHw-170708+AHw-gb+AHw-AAA34274.1+AHw- gamma-gliadin B precursor (291)
 53 21.8 9.7
 gi+AHw-1398915+AHw-dbj+AHw-BAA07711.1+AHw- allergenic protein +AFs-Ory (160)
 50 20.9 9.9

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 115.6 bits: 28.1 E(): 0.18
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (35-65:246-276)

	10	20	30	40	50	60
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
				...	:	:
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTQGVDIAMDVASSEFYKDGlyDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270

	70	80
AAD-12	GDVVVDNRCLLHRAE	
	:	
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK	
	280	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 109.1 bits: 25.3 E(): 0.42
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (15-71:79-133)

	10	20	30	40
AAD-12	MDTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES			
		...	:	:
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF			
	50	60	70	100

	50	60	70	80
AAD-12	ERFLEGLVDWACQAPRVHAHQWAAAGDVVVVDNRCLLHRAE			
	...	:	:	:
gi+AHw-121	EEFRASLVDYLS----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ			
	110	120	130	150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:

Full+AD0-Enolase (440 aa)

initn: 66 initl: 66 opt: 66 Z-score: 103.6 bits: 25.8 E(): 0.86

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)

in 31 aa overlap (35-65:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      : : : : : : : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270
```

```

      70      80
AAD-12 GDVVVWDNRCLLHRAE
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)

initn: 40 initl: 40 opt: 56 Z-score: 97.6 bits: 22.8 E(): 1.8

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)

in 19 aa overlap (46-62:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90
```

```

      80
AAD-12 CLLHRAE
gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 95.0 bits: 22.8 E(): 2.6

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)

in 19 aa overlap (46-62:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90
```

```

      80
AAD-12 CLLHRAE
gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 95.0 bits: 22.8 E(): 2.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (46-62:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : ..... :: ... ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

80
AAD-12 CLLHRAE

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 89.2 bits: 22.1 E(): 5.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (66-80:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAE
      : ..... ::
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRDHGGC
      100      110      120      130      140      150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 89.1 bits: 22.1 E(): 5.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (66-80:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAE
      : ..... ::
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRDHGGC
      100      110      120      130      140      150

```

```

gi+AHw-124 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 89.1 bits: 22.1 E(): 5.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (66-80:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAE
      : ..... :...
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRRHDGGC
      100      110      120      130      140      150

```

```

gi+AHw-209 RKELAAVSVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
Full+AD0-Venom (206 aa)
initn: 34 init1: 34 opt: 53 Z-score: 87.6 bits: 21.8 E(): 6.7
Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (20-74:54-104)

```

      10      20      30      40
AAD-12 MDTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
      : .. : .... :: . : . ....:
gi+AHw-250 PSKNCAGKVIKSVGPTEEEKKLIVEEHNRFQKVAQGLETRGNPGPQPAASN--MNNLV-
      30      40      50      60      70      80

```

```

      50      60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
      : . . . :.. . . :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPSVTCLIQLWENEV
      90      100      110      120      130

```

+AD4APg-gi+AHw-25361513+AHw-gb+AHw-AAN73248.1+AHw- helix-loop-helix
protein +AFs-F (450 aa)
initn: 37 init1: 37 opt: 56 Z-score: 86.1 bits: 22.7 E(): 8
Smith-Waterman score: 56+ADs- 26.984+ACU- identity (55.556+ACU- similar)
in 63 aa overlap (6-60:46-108)

```

      10      20
AAD-12 MDTTATPLRPL---VKVHPETGRPSLL--IGRH--
      : : : : : : : : : : : :
gi+AHw-253 IEEPemiAPTPPGQFPHQQPISSPNRTSRNTPLRPESTEIETHHHANHPPALPVLGMQLP
      20      30      40      50      60      70

```

```

      30      40      50      60      70      80
AAD-12 -AHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
      : : . : : . : . : : : :
gi+AHw-253 VPGTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQEHAHEIQRRHAHSAQSSA
      80      90      100      110      120      130

```

```

gi+AHw-253 GLPPTGFASHLPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPGHNMNVSGHPHLEHSS
      140      150      160      170      180      190

```

+AD4APg-gi+AHw-51093377+AHw-gb+AHw-AAT95010.1+AHw- allergen Pol d 5
precursor (227 aa)
initn: 34 init1: 34 opt: 52 Z-score: 85.0 bits: 21.5 E(): 9.3
Smith-Waterman score: 52+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (20-74:75-125)

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 188 - 267 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]


```

56      65
76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
58      67
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQ-
60      42      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9-+AD0APQ-      +ACo-
62      58      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      41      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      44      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
68      21      20:+AD0APQA9AD0APQA9ACo-
70      13      16:+AD0APQA9AD0APQAq-
72      15      12:+AD0APQA9ACoAPQ-
74      26      10:+AD0APQA9ACoAPQA9AD0APQA9-
76      14      7:+AD0APQAqAD0APQ-
78      5      6:+AD0AKg-
80      6      4:+AD0AKg-
82      4      3:+ACoAPQ-
84      3      3:+ACo-
86      3      2:+ACo-
88      0      2:+ACo-      inset +AD0- represents 1 library sequences
90      1      1:+ACo-
92      2      1:+ACo-      :+ACoAPQ-
94      1      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      0      0:      +ACo-
100     1      0:+AD0-      +ACoAPQ-
102     0      0:      +ACo-
104     1      0:+AD0-      +ACoAPQ-
106     0      0:      +ACo-
108     0      0:      +ACo-
110     0      0:      +ACo-
112     1      0:+AD0-      +ACoAPQ-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.60980.00317+ADs- mu+AD0- 6.7431
0.168
mean+AF8-var+AD0-38.252110.902, 0's: 2 Z-trim: 4 B-trim: 15 in 1/42
Lambda+AD0- 0.207370
Kolmogorov-Smirnov statistic: 0.0814 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:      opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.4 0.3
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 24.6 0.7
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.3 1.3

```

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 22.2 2.8
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 22.2 3.8
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 22.2 3.8
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.8 4.9
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.6 7.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.6 7.6
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.6 7.6
 gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName: Full+AD0-Ve (206) 53 21.3 9.2

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 111.8 bits: 27.4 E(): 0.3
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (34-64:246-276)

10 20 30 40 50 60
 AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
 :::: :: . :: : . : ::
 gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTQGVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
 220 230 240 250 260 270

70 80
 AAD-12 GDVVVWDNRCLLHRAEP
 :
 gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
 280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 105.2 bits: 24.6 E(): 0.7
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (14-70:79-133)

10 20 30
 AAD-12 DTTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
 :: : : ... ::
 gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
 50 60 70 80 90 100

40 50 60 70 80
 AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEP
 :: : : :
 gi+AHw-121 EEFRASLV DYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
 110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:

Full+AD0-Enolase (440 aa)

initn: 66 initl: 66 opt: 66 Z-score: 100.4 bits: 25.3 E(): 1.3

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)

in 31 aa overlap (34-64:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270
```

```

      70      80
AAD-12 GDVVVWDNRCLLHRAEP
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)

initn: 40 initl: 40 opt: 56 Z-score: 94.3 bits: 22.2 E(): 2.8

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)

in 19 aa overlap (45-61:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90
```

```

      80
AAD-12 CLLHRAEP
gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.0 bits: 22.2 E(): 3.8

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)

in 19 aa overlap (45-61:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90
```

```

      80
AAD-12 CLLHRAEP
gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.0 bits: 22.2 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (45-61:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      80
AAD-12 CLLHRAEP

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 initl: 43 opt: 61 Z-score: 89.9 bits: 23.8 E(): 4.9
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (16-80:424-492)

```

      10      20      30      40
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
      : : . . : . . . : . . . : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCLEFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
      400      410      420      430      440      450

```

```

      50      60      70      80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEP
      : . . : : . . : . : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
      460      470      480      490      500      510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 86.6 bits: 21.6 E(): 7.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (65-79:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEP
      : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 86.6 bits: 21.6 E(): 7.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (65-79:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEP
      : ..... :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

gi+AHw-209 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 86.6 bits: 21.6 E(): 7.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (65-79:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEP
      : ..... :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

gi+AHw-124 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-25091511+AHw-sp+AHw-P83377.1+AHw-VA5+AF8-POLGA RecName:
Full+AD0-Venom (206 aa)
initn: 34 initl: 34 opt: 53 Z-score: 85.1 bits: 21.3 E(): 9.2
Smith-Waterman score: 53+ADs- 23.636+ACU- identity (60.000+ACU- similar)
in 55 aa overlap (19-73:54-104)

```

      10      20      30      40
AAD-12 DTTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVD
      : .. : .... :: . : . : .. :
gi+AHw-250 PSKNCAGKVIKSVGPTEEEKKLIVEEHNFRQKVAQGLETRGNPGPQPAASN--MNNLV-
      30      40      50      60      70      80

      50      60      70      80
AAD-12 WACQAPRVHAHQWAAGDVVVWDNRCLLHRAEP
      : . . . : . : . : . :
gi+AHw-250 WNDEQAKI-AQVWASQCQILVHDKCRNTEKYQVGQNIAYAGSSNHFPVTKLIQLWENEV
      90      100      110      120      130

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 189 - 268 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

56      65      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQ-   +ACo-
58      65
62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60      44      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
62      59      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
64      49      32:+AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
66      41      25:+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
68      16      20:+AD0APQA9AD0APQA9ACo-
70      11      16:+AD0APQA9AD0- +ACo-
72      15      12:+AD0APQA9ACoAPQ-
74      14      10:+AD0APQA9ACoAPQ-
76      20      7:+AD0APQAqAD0APQA9AD0-
78      11      6:+AD0AKgA9AD0-
80      5       4:+AD0AKg-
82      5       3:+ACoAPQ-
84      3       3:+ACo-
86      1       2:+ACo-
88      1       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      1       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     1       0:+AD0-          +ACoAPQ-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     1       0:+AD0-          +ACoAPQ-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120     0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.68580.00312+ADs- mu+AD0- 6.3795
0.166
mean+AF8-var+AD0-40.198211.205, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.202288
Kolmogorov-Smirnov statistic: 0.0916 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.1    0.37
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.3    0.83
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.0    1.5

```

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 22.0 3.2
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 22.0 4.4
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 22.0 4.4
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.6 5.7
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.5 8.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.5 8.6
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.5 8.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 110.1 bits: 27.1 E(): 0.37
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (33-63:246-276)

	10	20	30	40	50	60
AAD-12	ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
				...	:	:
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270

	70	80
AAD-12	GDVVVDNRCLLHRAEPW	
	:	
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK	
	280	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 103.8 bits: 24.3 E(): 0.83
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (13-69:79-133)

	10	20	30
AAD-12	TTATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES		

gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF		
	50	60	100

	40	50	60	70	80
AAD-12	ERFLEGLVDWACQAPRVHAHQWAAAGDVVVVDNRCLLHRAEPW				
	:
gi+AHw-121	EEFRASLVDYLS----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ				
	110	120	130	140	150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 99.1 bits: 25.0 E(): 1.5

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (33-63:247-277)

```

          10          20          30          40          50          60
AAD-12  ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          : : : : : : : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
          220          230          240          250          260          270

```

```

          70          80
AAD-12  GDVVVWDNRCLLHRAEPW
          :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDQKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)

initn: 40 init1: 40 opt: 56 Z-score: 93.2 bits: 22.0 E(): 3.2
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (44-60:68-86)

```

          20          30          40          50          60          70
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          80
AAD-12  CLLHRAEPW
          :
gi+AHw-219 SFDSDRSGLLLKQKVSDE
          100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.9 bits: 22.0 E(): 4.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (44-60:68-86)

```

          20          30          40          50          60          70
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
          : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

```

          80
AAD-12  CLLHRAEPW
          :
gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.9 bits: 22.0 E(): 4.4

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (44-60:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
      : . . . . : : . . . . :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      80
AAD-12 CLLHRAEPW

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 init1: 43 opt: 61 Z-score: 88.8 bits: 23.6 E(): 5.7
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (15-79:424-492)

```

      10      20      30      40
AAD-12 TTATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
      : : . . . . : . . . . :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCLEFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
      400      410      420      430      440      450

```

```

      50      60      70      80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPW
      : . . : . . . : . : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
      460      470      480      490      500      510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.7 bits: 21.5 E(): 8.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (64-78:122-138)

```

      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLL--HRAEPW
      : : . . . . : : . . . . :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 85.6 bits: 21.5 E(): 8.6

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (64-78:122-138)

```

          40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPW
          : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

gi+AHw-209 RKELAAVSVDCSEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.6 bits: 21.5 E(): 8.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (64-78:122-138)

```

          40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPW
          : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

gi+AHw-124 RKELAAVSVDCSEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010
Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 190 - 269 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:
      24      0      0:

```

one +AD0- represents 3 library sequences

[illegible]

```

 96      0      1:+ACo-      :+ACo-
 98      1      0:+AD0-      +ACoAPQ-
100      0      0:          +ACo-
102      0      0:          +ACo-
104      1      0:+AD0-      +ACoAPQ-
106      0      0:          +ACo-
108      0      0:          +ACo-
110      1      0:+AD0-      +ACoAPQ-
112      0      0:          +ACo-
114      0      0:          +ACo-
116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.68230.00311+ADs- mu+AD0- 6.4235
0.166
mean+AF8-var+AD0-39.864211.089, 0's: 2 Z-trim: 4 B-trim: 0 in 0/43
Lambda+AD0- 0.203134
Kolmogorov-Smirnov statistic: 0.0922 (N+AD0-29) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 27.1    0.36
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   64 24.4    0.81
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 25.0    1.5
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)    56 22.0    3.2
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.0    4.3
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.0    4.3
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)   61 23.6    5.6
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)   54 21.5    8.4
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210)   54 21.5    8.5
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210)   54 21.5    8.5
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)    50 20.2    8.6

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 110.3 bits: 27.1 E(): 0.36
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (32-62:246-276)

```

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .:: : . : .: .
gi+AHw-370 APDIKTAKAALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLLHRAEPWD
      :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 64 Z-score: 104.0 bits: 24.4 E(): 0.81
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (12-68:79-133)

```

      10      20      30
AAD-12 TATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
      :::: :::: :: : : : .. ::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
      50      60      70      80      90      100

```

```

      40      50      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWD
      :: .::: : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 99.2 bits: 25.0 E(): 1.5
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (32-62:247-277)

```

      10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
      :::: :: . .: : . : .: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGGKYDLDFKNPESDPSKWLS
      220      230      240      250      260      270

```

```

      70      80
AAD-12 GDVVVWDNRCLLHRAEPWD
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 93.3 bits: 22.0 E(): 3.2
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (43-59:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      80
AAD-12 CLLHRAEPWD

```

```

gi+AHw-219 SFDSDRSGLLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 91.0 bits: 22.0 E(): 4.3
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (43-59:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

```

      80
AAD-12 CLLHRAEPWD

```

```

gi+AHw-456 SFGSDRSGLLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 91.0 bits: 22.0 E(): 4.3
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (43-59:68-86)

```

      20      30      40      50      60      70
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      80
AAD-12 CLLHRAEPWD

```

```

gi+AHw-184 SFDSDRSGLLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 init1: 43 opt: 61 Z-score: 88.9 bits: 23.6 E(): 5.6
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (14-78:424-492)

10 20 30 40
 AAD-12 TATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
 : : . : . : . : . :
 gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFELGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
 400 410 420 430 440 450

50 60 70 80
 AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWD
 : . . : : . . : : : : : :
 gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
 460 470 480 490 500 510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQQLKTVMG
 520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
 +AFs-Gallus gal (208 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.8 bits: 21.5 E(): 8.4
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (63-77:122-138)

40 50 60 70 80
 AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLL--HRAEPWD
 : : : : : : : :
 gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
 100 110 120 130 140 150

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
 160 170 180 190 200

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
 gallus+AF0- (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.7 bits: 21.5 E(): 8.5
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (63-77:122-138)

40 50 60 70 80
 AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLL--HRAEPWD
 : : : : : : : :
 gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
 100 110 120 130 140 150

gi+AHw-209 RKELAAVSDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
 160 170 180 190 200 210

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
 Full+AD0-Ovomuco (210 aa)
 initn: 49 init1: 49 opt: 54 Z-score: 85.7 bits: 21.5 E(): 8.5
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (63-77:122-138)

40 50 60 70 80
 AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLL--HRAEPWD
 : : : : : : : :

gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
 100 110 120 130 140 150

gi+AHw-124 RKELAAVSVDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
 160 170 180 190 200 210

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 40 initl: 40 opt: 50 Z-score: 85.6 bits: 20.2 E(): 8.6
 Smith-Waterman score: 50+ADs- 31.429+ACU- identity (45.714+ACU- similar)
 in 35 aa overlap (46-80:29-59)

20 30 40 50 60 70
 AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
 : ::: : .. : .. :: : .
 gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
 10 20 30 40 50

80
 AAD-12 AEPWD
 ::
 gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
 60 70 80 90

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010
 Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 191 - 270 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 3 library sequences
24	0	0:	
26	0	0:	
28	0	0:	
30	0	2:+ACo-	

```

32      0      8:  +ACo-
34     12     21: +AD0APQA9AD0-  +ACo-
36     22     44: +AD0APQA9AD0APQA9AD0- +AD0-      +ACo-
38     41     72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
40     72
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42     98
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9-      +ACo-
44    124
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-      +ACo-
46    175    138: +AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
48    168
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA
9AD0APQ-
50    127
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
52    122
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
54     82
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ
A9AD0-  +ACo-
56     73
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58     64
62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0-
60    42    50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-  +ACo-
62    55    40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
64    44    32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
66    39    25: +AD0- +AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
68    22    20: +AD0APQA9AD0APQA9ACoAPQ-
70    11    16: +AD0APQA9AD0-  +ACo-
72    11    12: +AD0APQA9ACo-
74    15    10: +AD0APQA9ACoAPQ-
76    17     7: +AD0APQAqAD0APQA9-
78    11     6: +AD0AKgA9AD0-
80     7     4: +AD0AKgA9-
82     3     3: +ACo-
84     5     3: +ACoAPQ-
86     0     2: +ACo-
88     1     2: +ACo-      inset +AD0- represents 1 library sequences
90     2     1: +ACo-
92     1     1: +ACo-      :+ACo-
94     0     1: +ACo-      :+ACo-
96     0     1: +ACo-      :+ACo-
98     1     0: +AD0-      +ACoAPQ-

```

```

100      0      0:      +ACo-
102      1      0:+AD0-      +ACoAPQ-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.64370.00312+ADs- mu+AD0- 6.6954
0.166
mean+AF8-var+AD0-41.382311.924, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.199373
Kolmogorov-Smirnov statistic: 0.0936 (N+AD0-27) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 26.9 0.42
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 24.2 0.94
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 24.9 1.7
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 21.8 3.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9 4.8
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9 4.8
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608) 61 23.5 6.2
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208) 54 21.3 9.3
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210) 54 21.3 9.4
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210) 54 21.3 9.4
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 50 20.1 9.6

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 109.1 bits: 26.9 E(): 0.42
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (31-61:246-276)

```

```

10      20      30      40      50      60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA

```

gi+AHw-370 APDIKTAEALDLIVSAIEAAGYTQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
220 230 240 250 260 270

70 80
AAD-12 GDVVVWDNRCLLHRAEPWDF
:

gi+AHw-370 GPQLAEELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 64 Z-score: 102.9 bits: 24.2 E(): 0.94
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (11-67:79-133)

10 20 30
AAD-12 ATPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
.... : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
50 60 70 80 90 100

40 50 60 70 80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDF
: : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 98.3 bits: 24.9 E(): 1.7
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (31-61:247-277)

10 20 30 40 50 60
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
: : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGYDLDFKNPESDPSKWLS
220 230 240 250 260 270

70 80
AAD-12 GDVVVWDNRCLLHRAEPWDF
:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.4 bits: 21.8 E(): 3.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (42-58:68-86)

20 30 40 50 60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR

```

                                : . . . . : :: ... ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
              40          50          60          70          80          90

```

```

              70          80
AAD-12 CLLHRAEPWDF

```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
              100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (42-58:68-86)

```

              20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : . . . . : :: ... ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
              40          50          60          70          80          90

```

```

              70          80
AAD-12 CLLHRAEPWDF

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
              100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (42-58:68-86)

```

              20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : . . . . : :: ... ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
              40          50          60          70          80          90

```

```

              70          80
AAD-12 CLLHRAEPWDF

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
              100          110          120          130          140          150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.1 bits: 23.5 E(): 6.2
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (13-77:424-492)

```

              10          20          30
AAD-12 ATPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF

```

```

                                : : . :. :... .: ... .: :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLG EYGFQNALLVRYTKKVPQVSTPTLVEVSRS
              400          410          420          430          440          450

```

```

              40          50          60          70          80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDF
              : . . : :... . : . : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKTKCTESLVNRRPCFS
              460          470          480          490          500          510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
              520          530          540          550          560          570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.3
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (62-76:122-138)

```

              40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDF
                                : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVITYDNECLLCAHKVEQGASVDKRHDGGC
              100          110          120          130          140          150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160          170          180          190          200

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (62-76:122-138)

```

              40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDF
                                : : : : : : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVITYDNECLLCAHKVEQGASVDKRHDGGC
              100          110          120          130          140          150

```

```

gi+AHw-209 RKELAAVSDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160          170          180          190          200          210

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (62-76:122-138)

```

              40          50          60          70          80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDF
                                : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVITYDNECLLCAHKVEQGASVDKRHDGGC
              100          110          120          130          140          150

```

```
gi+AHw-124 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160          170          180          190          200          210
```

```
+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
```

```
Full+AD0-Chiti (91 aa)
```

```
initn: 40 initl: 40 opt: 50 Z-score: 84.8 bits: 20.1 E(): 9.6
```

```
Smith-Waterman score: 50+ADs- 31.429+ACU- identity (45.714+ACU- similar)
in 35 aa overlap (45-79:29-59)
```

```

      20      30      40      50      60      70
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
              :   :::   : .. : ..   :: : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYPNQNN---WDLRAVSAY
              10      20      30      40      50
```

```

      80
AAD-12 AEPWDF
      ::
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
              60      70      80      90
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:27 2010 done: Fri Feb 5 12:56:27 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 192 - 271 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8:  +ACo-
      34      8      21:+AD0APQA9-  +ACo-
```

```

36      25      44: +AD0APQA9AD0APQA9AD0APQA9-      +ACo-
38      39      72: +AD0APQA9AD0APQA9AD0- +AD0APQA9AD0APQA9-      +ACo-
40      70
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
42      94
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ-      +ACo-
44      133
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
46      177
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9ACoAPQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
48      172
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA
9AD0APQA9AD0-
50      126
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
52      122
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQ-
54      87
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0- +ACo-
56      73
76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg
-
58      57      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
60      54      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
62      51      40: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
64      39      32: +AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0-
66      34      25: +AD0APQA9AD0APQA9AD0APQAqAD0APQA9-
68      16      20: +AD0APQA9AD0APQA9ACo-
70      7      16: +AD0APQA9- +ACo-
72      12      12: +AD0APQA9ACo-
74      11      10: +AD0APQA9ACo-
76      19      7: +AD0APQAqAD0APQA9AD0-
78      22      6: +AD0AKgA9AD0APQA9AD0APQ-
80      7      4: +AD0AKgA9-
82      3      3: +ACo-
84      4      3: +ACoAPQ-
86      0      2: +ACo-
88      2      2: +ACo-      inset +AD0- represents 1 library sequences
90      2      1: +ACo-
92      0      1: +ACo-      : +ACo-
94      0      1: +ACo-      : +ACo-
96      0      1: +ACo-      : +ACo-
98      1      0: +AD0-      +ACoAPQ-
100     0      0:      +ACo-

```



```

102      1      0: +AD0-          +ACoAPQ-
104      0      0:          +ACo-
106      0      0:          +ACo-
108      1      0: +AD0-          +ACoAPQ-
110      0      0:          +ACo-
112      0      0:          +ACo-
114      0      0:          +ACo-
116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.50980.00322+ADs- mu+AD0- 7.4479
0.172
mean+AF8-var+AD0-42.743112.786, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.196174
Kolmogorov-Smirnov statistic: 0.0936 (N+AD0-27) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.7 0.47
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.0 1.1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.7 1.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.7 4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.7 5.3
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.7 5.3
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.4 6.6

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 108.3 bits: 26.7 E(): 0.47
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (30-60:246-276)

```

          10          20          30          40          50
AAD-12  TPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          :::: :: . ::: : . : . : .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTQGVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
          220          230          240          250          260          270

          60          70          80
AAD-12  GDVVVWDNRCLLHRAEPWDFK
          :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 64 Z-score: 101.9 bits: 24.0 E(): 1.1
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (10-66:79-133)

```

                                10          20          30
AAD-12          TPLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                        ....  ::  :  :  ...  ::
gi+AHw-121  DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
              50          60          70          80          90          100

```

```

              40          50          60          70          80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHRAEPWDFK
          ::  .....  :  :  .....  ::
gi+AHw-121  EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
            110          120          130          140          150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 97.6 bits: 24.7 E(): 1.8
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (30-60:247-277)

```

              10          20          30          40          50
AAD-12  TPLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                        ....  ::  .  :  :  .  :  .  :  .  :  .  :  .
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
            220          230          240          250          260          270

```

```

              60          70          80
AAD-12  GDVVVDNRCLLHRAEPWDFK
          :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDWVHFFERVGDKIQIVGDDLTVTNPTRIKT
            280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 91.5 bits: 21.7 E(): 4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (41-57:68-86)

```

              20          30          40          50          60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
                        :  ....  ::  ...  ::
gi+AHw-219  YVWKISEFYGRKPEGTTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
            40          50          60          70          80          90

```

```

              70          80
AAD-12  CLLHRAEPWDFK

gi+AHw-219  SFDSDRSGLLLKQKVSDE
            100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 89.4 bits: 21.7 E(): 5.3
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (41-57:68-86)

```

                20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
                : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
           40          50          60          70          80          90

           70          80
AAD-12 CLLHRAEPWDFK

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
           100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 89.4 bits: 21.7 E(): 5.3
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (41-57:68-86)

```

                20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
                : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
           40          50          60          70          80          90

           70          80
AAD-12 CLLHRAEPWDFK

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
           100          110          120          130          140          150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)

initn: 43 initl: 43 opt: 61 Z-score: 87.7 bits: 23.4 E(): 6.6
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (12-76:424-492)

```

                        10          20          30
AAD-12                        TPLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                        : : . : . . . : : . : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
           400          410          420          430          440          450

           40          50          60          70          80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWDFK
           : . . : : . . . : : . : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
           460          470          480          490          500          510

```

```
gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQLKTVMG
           520           530           540           550           560           570
```

```
80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
Total Scan time: 0.090 Total Display time: 0.000
```

```
Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 193 - 272 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 3 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      0      8: +ACo-
      34     10     21: +AD0APQA9AD0- +ACo-
      36     26     44: +AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38     40     72: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      40     65
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      42     95
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ- +ACo-
      44     138
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      46     175
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9A
D0APQA9AD0-
      48     168
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are:

opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En

(439) 73 26.7 0.47

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo

(151) 64 24.0 1.1

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno

(440) 66 24.7 1.9

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (

115) 56 21.7 4

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)

56 21.7 5.3

gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)

56 21.7 5.3

gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se

(608) 61 23.4 6.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:

Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 108.2 bits: 26.7 E(): 0.47

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)

in 31 aa overlap (29-59:246-276)

```

                10         20         30         40         50
AAD-12  PLRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                ::: :: . ::: : . : . :
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTQVQDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220         230         240         250         260         270

                60         70         80
AAD-12  GDVVVDNRCLLHRAEPWDFKL
:
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280         290         300         310         320         330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:

Full+AD0-Globin (151 aa)

initn: 51 init1: 51 opt: 64 Z-score: 101.9 bits: 24.0 E(): 1.1

Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)

in 61 aa overlap (9-65:79-133)

```

                10         20         30
AAD-12  PLRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                .... ::: :: : : ... ::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50         60         70         80         90         100

                40         50         60         70         80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAAGDVVVVDNRCLLHRAEPWDFKL
                :: .::: . : : :
gi+AHw-121 EEFRASLV DYLS----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110         120         130         140         150

```

70 80
AAD-12 CLLHRAEPWDFKL

gi+AHw-456 SFGSDRSGLLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS

100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 89.3 bits: 21.7 E(): 5.3
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (40-56:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVWDNR
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKL

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)
 initn: 43 initl: 43 opt: 61 Z-score: 87.6 bits: 23.4 E(): 6.6
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (11-75:424-492)

```

      10      20      30
AAD-12          PLRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
      : : . : . : . : . : . :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCLEFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
      400      410      420      430      440      450

      40      50      60      70      80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVWDNR-CLLHRAEPWDFKL
      : . . : : . . : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
      460      470      480      490      500      510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
      520      530      540      550      560      570

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
 Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

[illegible]

```

72      12      12:+AD0APQA9ACo-
74      10      10:+AD0APQA9ACo-
76      18      7:+AD0APQAqAD0APQA9-
78      23      6:+AD0AKgA9AD0APQA9AD0APQ-
80      9       4:+AD0AKgA9-
82      2       3:+ACo-
84      3       3:+ACo-
86      0       2:+ACo-
88      3       2:+ACo-          inset +AD0- represents 1 library sequences
90      2       1:+ACo-
92      0       1:+ACo-          :+ACo-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     1       0:+AD0-          +ACoAPQ-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     1       0:+AD0-          +ACoAPQ-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.46070.0032+ADs- mu+AD0- 7.5062
0.171
mean+AF8-var+AD0-43.244912.899, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.195032
Kolmogorov-Smirnov statistic: 0.1059 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 26.7      0.47
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   64 24.0      1.1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 24.8      1.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)    56 21.7      4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.7      5.2
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.7      5.2
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)    53 20.8      5.9
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)   61 23.4      6.4

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.2 9.9
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.2 10
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.2 10

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 108.3 bits: 26.7 E(): 0.47
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (28-58:246-276)

10 20 30 40 50
 AAD-12 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
 :::: :: . :: : . : ::
 gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTQGVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
 220 230 240 250 260 270

60 70 80
 AAD-12 GDVVVWDNRCLLHRAEPWDFKLP
 :
 gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
 280 290 300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 64 Z-score: 101.9 bits: 24.0 E(): 1.1
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (8-64:79-133)

10 20 30
 AAD-12 LRPLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
 :::: :: : : : ::
 gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
 50 60 70 80 90 100

40 50 60 70 80
 AAD-12 ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLP
 :: :::: : : ::
 gi+AHw-121 EEFRASLVDYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
 110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 97.7 bits: 24.8 E(): 1.8
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (28-58:247-277)

10 20 30 40 50
 AAD-12 LRPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
 :::: :: . :: : . : ::
 gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGYDLDFKNPESDPSKWLS
 220 230 240 250 260 270

AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
:
gi+AHw-184 YVWKISEFYGRKPEGTTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF

70 80
AAD-12 CLLHRAEPWDFKLP

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 53 Z-score: 88.6 bits: 20.8 E(): 5.9
Smith-Waterman score: 53+ADs- 30.769+ACU- identity (43.590+ACU- similar)
in 39 aa overlap (42-80:29-63)

20 30 40 50 60 70
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
: ::: : .. : . :: : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
10 20 30 40 50

80
AAD-12 AEPWDFKLP
:: :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
60 70 80 90

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 initl: 43 opt: 61 Z-score: 87.9 bits: 23.4 E(): 6.4
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (10-74:424-492)

10 20 30
AAD-12 LRPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
: : . : . : . : . : . :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
400 410 420 430 440 450

40 50 60 70 80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLP
: . . : : . . : . : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKTKCTESLVNRRPCFS
460 470 480 490 500 510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQLKTVMG
520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.5 bits: 21.2 E(): 9.9
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (59-73:122-138)

30 40 50 60 70 80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLP

```

                                : .....: ...:
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100          110          120          130          140          150

```

```

gi+AHw-162 RKELAAVDCSEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160          170          180          190          200

```

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
  initn: 49 initl: 49 opt: 54 Z-score: 84.4 bits: 21.2 E(): 10
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (59-73:122-138)

```

```

              30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLL--HRAEPWDFKLP
                                : .....: ...:
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100          110          120          130          140          150

```

```

gi+AHw-124 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160          170          180          190          200          210

```

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
  initn: 49 initl: 49 opt: 54 Z-score: 84.4 bits: 21.2 E(): 10
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (59-73:122-138)

```

```

              30          40          50          60          70          80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLL--HRAEPWDFKLP
                                : .....: ...:
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100          110          120          130          140          150

```

```

gi+AHw-209 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160          170          180          190          200          210

```

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
Total Scan time: 0.090 Total Display time: 0.010

```

```

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

```

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```

```
1+AD4APgA+-AAD-12: 195 - 274 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

opt      E()
+ADw- 20    2    0: +AD0-
22      0    0:           one +AD0- represents 4 library sequences
24      0    0:
26      0    0:
28      0    0:
30      0    2: +ACo-
32      1    8: +AD0AKg-
34      3   21: +AD0-     +ACo-
36     27   44: +AD0APQA9AD0APQA9AD0-     +ACo-
38     34   72: +AD0APQA9AD0APQA9AD0APQA9-     +ACo-
40     73  101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
42     90
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
44    121
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0-   +ACo-
46    186
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
48    161
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQ-
50    139
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0APQ-
52    127
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0APQ-
54     95
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9-
56     61   76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-   +ACo-
58     60   62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60     48   50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62     53   40: +AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
64     39   32: +AD0APQA9AD0APQA9AD0AKgA9AD0-
66     36   25: +AD0APQA9AD0APQA9ACoAPQA9-
68     18   20: +AD0APQA9AD0AKg-
70     11   16: +AD0APQA9ACo-
72     13   12: +AD0APQAqAD0-
74      8   10: +AD0APQAq-
76     16    7: +AD0AKgA9AD0-
78     25    6: +AD0AKgA9AD0APQA9AD0-
80      7    4: +ACoAPQ-
82      6    3: +ACoAPQ-

```

```

84      3      3:+ACo-
86      0      2:+ACo-
88      2      2:+ACo-      inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      1      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     0      0:      +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     1      0:+AD0-      +ACoAPQ-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-
118     0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.54970.00323+ADs- mu+AD0- 7.0204
0.172
mean+AF8-var+AD0-42.564813.042, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196584
Kolmogorov-Smirnov statistic: 0.1072 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:      opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.8      0.44
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.1      1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8      1.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.8      3.8
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8      5
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8      5
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)  53 20.9      5.5
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.4      6.3
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.3      9.5
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210)  54 21.3      9.6
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210)  54 21.3      9.6

```



```

              10              20              30              40              50
AAD-12      RPLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
              :::: :: . .: : . :. .: .
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
            220            230            240            250            260            270

            60            70            80
AAD-12      GDVVVWDNRCLLHRAEPWDFKLPR
            :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFFERVGDKIQIVGDDLTVTNPTRIKT
            280            290            300            310            320            330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.0 bits: 21.8 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (38-54:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : ..... :: ... ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKLPR

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 89.8 bits: 21.8 E(): 5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (38-54:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : ..... :: ... ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKLPR

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 89.8 bits: 21.8 E(): 5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (38-54:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : ..... :: ... ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKLPR

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150
```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:

Full+AD0-Chiti (91 aa)

initn: 43 initl: 43 opt: 53 Z-score: 89.0 bits: 20.9 E(): 5.5

Smith-Waterman score: 53+ADs- 30.769+ACU- identity (43.590+ACU- similar)

in 39 aa overlap (41-79:29-63)

```

                20      30      40      50      60      70
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLLHR
                :   :::   : .. : ..   :: : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
                10      20      30      40      50

```

```

                80
AAD-12 AEPWDFKLPR
                :: :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                60      70      80      90

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:

Full+AD0-Serum (608 aa)

initn: 43 initl: 43 opt: 61 Z-score: 88.0 bits: 23.4 E(): 6.3

Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)

in 69 aa overlap (9-73:424-492)

```

                        10      20      30
AAD-12 RPLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                        : : . : . : . : . : . : . :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCLEFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
                400      410      420      430      440      450

```

```

                40      50      60      70      80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWDFKLPR
                : . . : : . . : . : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
                460      470      480      490      500      510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
                520      530      540      550      560      570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid

+AFs-Gallus gal (208 aa)

initn: 49 initl: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)

in 17 aa overlap (58-72:122-138)

```

                30      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVDNRCLL--HRAEPWDFKLPR
                : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100      110      120      130      140      150

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
                160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
 Full+AD0-Ovomuco (210 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.6
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (58-72:122-138)

```

      30      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPR
      : .....: ...:
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

gi+AHw-124 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
 gallus+AF0- (210 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.6
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (58-72:122-138)

```

      30      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPR
      : .....: ...:
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

gi+AHw-209 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200      210

```

80 residues in 1 query sequences
 331323 residues in 1471 library sequences
 Scomplib +AFs-34t26+AF0-
 start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
 Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
 +ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
 FASTA searches a protein or DNA sequence data bank
 version 3.4t26 July 7, 2006
 Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
 /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
 searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 196 - 275 80 aa - 80 aa
 vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

opt E()

```

+ADw- 20      2      0:+AD0-
22      0      0:          one +AD0- represents 4 library sequences
24      0      0:
26      0      0:
28      0      0:
30      0      2:+ACo-
32      1      8:+AD0AKg-
34      2      21:+AD0-      +ACo-
36      24      44:+AD0APQA9AD0APQA9-      +ACo-
38      34      72:+AD0APQA9AD0APQA9AD0APQA9-      +ACo-
40      73      101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
42      96
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
44      120
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9-      +ACo-
46      182
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0-
48      168
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9-
50      143
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0APQA9-
52      121
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0-
54      91
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
56      61      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-      +ACo-
58      61      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60      48      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      53      40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
64      38      32:+AD0APQA9AD0APQA9AD0AKgA9AD0-
66      37      25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68      19      20:+AD0APQA9AD0AKg-
70      11      16:+AD0APQA9ACo-
72      12      12:+AD0APQAq-
74      9      10:+AD0APQAq-
76      15      7:+AD0AKgA9AD0-
78      26      6:+AD0AKgA9AD0APQA9AD0-
80      7      4:+ACoAPQ-
82      5      3:+ACoAPQ-
84      4      3:+ACo-
86      0      2:+ACo-
88      2      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      1      1:+ACo-          :+ACo-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-

```

```

100      0      0:      +ACo-
102      1      0:+AD0-      +ACoAPQ-
104      0      0:      +ACo-
106      0      0:      +ACo-
108      1      0:+AD0-      +ACoAPQ-
110      0      0:      +ACo-
112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.58960.00324+ADs- mu+AD0- 6.7803
0.172
mean+AF8-var+AD0-42.573413.035, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196564
Kolmogorov-Smirnov statistic: 0.1065 (N+AD0-28) at 44

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.070
The best scores are:
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 26.8 0.44
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 64 24.1 1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 24.8 1.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 21.8 3.8
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8 5
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8 5
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 53 20.9 5.5
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608) 61 23.4 6.3
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208) 54 21.3 9.5
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210) 54 21.3 9.6
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210) 54 21.3 9.6

```

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 108.7 bits: 26.8 E(): 0.44
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (26-56:246-276)

```

```

10      20      30      40      50
AAD-12      PLVKVHPETGRPSLLIGRHAHAIPGMDAEESERFLEGLVDWACQAPRVHAHQWAA

```

```

                :::: :: . .:: : . : .::
gi+AHw-370 APDIKTAEALDLIVSAIEAAGYTGGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
                220      230      240      250      260      270

```

```

        60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRV
:

```

```

gi+AHw-370 GPQLAELEYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 64 Z-score: 102.4 bits: 24.1 E(): 1
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (6-62:79-133)

```

                                10      20      30
AAD-12                        PLVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                                :::: :: : : :::
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100

```

```

                40      50      60      70      80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRV
                :: .::: : : :::
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 97.9 bits: 24.8 E(): 1.8
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (26-56:247-277)

```

                10      20      30      40      50
AAD-12      PLVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                :::: :: . : : . :. :.
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

        60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRV
:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.1 bits: 21.8 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (37-53:68-86)

```

                10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR

```

```

                                : . . . . : :: ... ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
              40          50          60          70          80          90

```

```

              70          80
AAD-12 CLLHRAEPWDFKLPRV

```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
              100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.9 bits: 21.8 E(): 5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (37-53:68-86)

```

              10          20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : . . . . : :: ... ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
              40          50          60          70          80          90

```

```

              70          80
AAD-12 CLLHRAEPWDFKLPRV

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
              100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.9 bits: 21.8 E(): 5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (37-53:68-86)

```

              10          20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : . . . . : :: ... ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
              40          50          60          70          80          90

```

```

              70          80
AAD-12 CLLHRAEPWDFKLPRV

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
              100          110          120          130          140          150

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-Chiti (91 aa)

initn: 43 init1: 43 opt: 53 Z-score: 89.1 bits: 20.9 E(): 5.5
 Smith-Waterman score: 53+ADs- 30.769+ACU- identity (43.590+ACU- similar)
 in 39 aa overlap (40-78:29-63)

```

              10          20          30          40          50          60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR

```



```

                                :   :::   : .. : ..   :: : .
gi+AHw-323  QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
                                10         20         30         40         50

```

```

      70         80
AAD-12  AEPWDFKLPRV

```

```

      ::   :
gi+AHw-323  CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
              60         70         80         90

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 init1: 43 opt: 61 Z-score: 88.0 bits: 23.4 E(): 6.3
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (8-72:424-492)

```

                                10         20         30
AAD-12                                PLVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
                                :   :   . :: :... :: ...   . :   :
gi+AHw-135  YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
              400         410         420         430         440         450

```

```

      40         50         60         70         80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRV
      :   . . :   :... . :   . :   :: :... :
gi+AHw-135  LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSESVTKCCTESLVNRRPCFS
              460         470         480         490         500         510

```

```

gi+AHw-135  ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQQLKTVMG
              520         530         540         550         560         570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (57-71:122-138)

```

      30         40         50         60         70         80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRV
                                :   ::...::... :... :
gi+AHw-162  MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100         110         120         130         140         150

```

```

gi+AHw-162  RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160         170         180         190         200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (57-71:122-138)

```

      30         40         50         60         70         80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRV

```

```

                                : .....:
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100      110      120      130      140      150

```

```

gi+AHw-124 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (57-71:122-138)

```

              30      40      50      60      70      80
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLL--HRAEPWDFKLPRV
                                : .....:
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100      110      120      130      140      150

```

```

gi+AHw-209 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160      170      180      190      200      210

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
Total Scan time: 0.070 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 197 - 276 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      1      8:+AD0AKg-
      34      2      21:+AD0-   +ACo-

```

```

36      24      44:+AD0APQA9AD0APQA9-      +ACo-
38      32      72:+AD0APQA9AD0APQA9AD0APQ-      +ACo-
40      73      101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
42      85      123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQ-      +ACo-
44      113
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ-      +ACo-
46      190
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
48      172
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0-
50      152
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0APQA9AD0APQ-
52      126
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0APQ-
54      84
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
56      57      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
58      67      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
60      45      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      50      40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
64      38      32:+AD0APQA9AD0APQA9-+AD0AKgA9AD0-
66      41      25:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
68      19      20:+AD0APQA9AD0AKg-
70      13      16:+AD0APQA9ACo-
72      13      12:+AD0APQAqAD0-
74      8      10:+AD0APQAq-
76      14      7:+AD0AKgA9AD0-
78      25      6:+AD0AKgA9AD0APQA9AD0-
80      7      4:+ACoAPQ-
82      6      3:+ACoAPQ-
84      4      3:+ACo-
86      0      2:+ACo-
88      1      2:+ACo-      inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      1      1:+ACo-      :+ACo-
94      0      1:+ACo-      :+ACo-
96      0      1:+ACo-      :+ACo-
98      1      0:+AD0-      +ACoAPQ-
100     0      0:      +ACo-
102     1      0:+AD0-      +ACoAPQ-
104     0      0:      +ACo-
106     0      0:      +ACo-
108     1      0:+AD0-      +ACoAPQ-
110     0      0:      +ACo-
112     0      0:      +ACo-
114     0      0:      +ACo-
116     0      0:      +ACo-

```

```

118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.67290.00321+ADs- mu+AD0- 6.2279
0.171
mean+AF8-var+AD0-42.208112.937, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.197413
Kolmogorov-Smirnov statistic: 0.1202 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.9  0.43
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  64 24.2  0.94
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.9  1.7
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.9  3.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9  4.7
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9  4.7
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)  53 21.0  5.2
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  61 23.5  6.2
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.4  9.1
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210)  54 21.4  9.2
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210)  54 21.4  9.2

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 109.0 bits: 26.9 E(): 0.43
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (25-55:246-276)

```

          10          20          30          40          50
AAD-12      LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
          ....: . . . . .
gi+AHw-370  APDIKTAKEALDLIVSAIEAAGYTGVQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
          220          230          240          250          260          270

          60          70          80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPRVM
          :
gi+AHw-370  GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 64 Z-score: 102.8 bits: 24.2 E(): 0.94
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (5-61:79-133)

```

                                10          20          30
AAD-12                      LVKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                                ....  ....  :  :  ...  .
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                   50          60          70          80          90          100

```

```

                   40          50          60          70          80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVM
                   ..  .....  :  .  ...
gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                   110          120          130          140          150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.2 bits: 24.9 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (25-55:247-277)

```

                                10          20          30          40          50
AAD-12          LVKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                ....  ::  .  .  :  :  .  .  .  .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                   220          230          240          250          260          270

```

```

                   60          70          80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVM
                   :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                   280          290          300          310          320          330

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.5 bits: 21.9 E(): 3.6
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (36-52:68-86)

```

                   10          20          30          40          50          60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                   :  ....  ::  ...  ...
gi+AHw-219 YVWKISEFYGRKPEGTTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                   40          50          60          70          80          90

```

```

                   70          80
AAD-12 CLLHRAEPWDFKLPRVM

gi+AHw-219 SFDSDRSGLLLKQKVSDE
                   100          110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (36-52:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKLPRVM

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100     110     120     130     140     150
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (36-52:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      70      80
AAD-12 CLLHRAEPWDFKLPRVM

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100     110     120     130     140     150
```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 53 Z-score: 89.5 bits: 21.0 E(): 5.2
Smith-Waterman score: 53+ADs- 30.769+ACU- identity (43.590+ACU- similar)
in 39 aa overlap (39-77:29-63)

```

      10      20      30      40      50      60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
      : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
      10      20      30      40      50

      70      80
AAD-12 AEPWDFKLPRVM
      : : :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60      70      80      90
```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)
 initn: 43 initl: 43 opt: 61 Z-score: 88.2 bits: 23.5 E(): 6.2
 Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
 in 69 aa overlap (7-71:424-492)

```

                                10      20      30
AAD-12      LVKVHPETGRPSLLIGRHAHAIPGMDA---AESERF
              : : . :. :... .: ... .: :
gi+AHw-135  YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
              400      410      420      430      440      450

              40      50      60      70      80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVM
              : . . : :... .: .: : : : : :
gi+AHw-135  LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
              460      470      480      490      500      510

gi+AHw-135  ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
              520      530      540      550      560      570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
 +AFs-Gallus gal (208 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 85.1 bits: 21.4 E(): 9.1
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (56-70:122-138)

```

              30      40      50      60      70      80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVM
              : : : : : : : : : :
gi+AHw-162  MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100      110      120      130      140      150

gi+AHw-162  RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
 Full+AD0-Ovomuco (210 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 85.1 bits: 21.4 E(): 9.2
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (56-70:122-138)

```

              30      40      50      60      70      80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVM
              : : : : : : : : : :
gi+AHw-124  MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100      110      120      130      140      150

gi+AHw-124  RKELAAVSDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
 gallus+AF0- (210 aa)

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8: +ACo-
      34      3      21:+AD0-      +ACo-
      36      22     44:+AD0APQA9AD0APQA9-      +ACo-
      38      30     72:+AD0APQA9AD0APQA9AD0APQ-      +ACo-
      40      77    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      42      88
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-

```



```
mean+AF8-var+AD0-42.807412.995, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
```

Lambda+AD0- 0.196027

Kolmogorov-Smirnov statistic: 0.1236 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.070

The best scores are: opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
(439) 73 26.8 0.44

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 64 24.1 0.98

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
(440) 66 24.8 1.8

gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(91) 55 21.5 3.6

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
56 21.8 3.7

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
56 21.9 4.9

gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
56 21.9 4.9

gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
(608) 61 23.4 6.3

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
(208) 54 21.3 9.3

gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
(210) 54 21.3 9.4

gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
54 21.3 9.4

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)
initn: 73 init1: 73 opt: 73 Z-score: 108.7 bits: 26.8 E(): 0.44
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (24-54:246-276)

	10	20	30	40	50
AAD-12	VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA				
	::: :: . :: : . : .:				
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTQGVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT				
	220	230	240	250	260 270
	60	70	80		
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMW				
	:				
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK				
	280	290	300	310	320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 64 Z-score: 102.5 bits: 24.1 E(): 0.98
Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
in 61 aa overlap (4-60:79-133)

```

                                10          20
AAD-12          VKVHPETGRPSL--LIGRHA--HAIPGMDAAES
                                .... : : : :
gi+AHw-121 DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
          50          60          70          80          90          100

```

```

          30          40          50          60          70          80
AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMW
          :: : : : : : : : :
gi+AHw-121 EEFRASLVDYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
          110          120          130          140          150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 init1: 66 opt: 66 Z-score: 98.0 bits: 24.8 E(): 1.8
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (24-54:247-277)

```

                                10          20          30          40          50
AAD-12          VKVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                : : : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPKWLS
          220          230          240          250          260          270

```

```

          60          70          80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVMW
          :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
          280          290          300          310          320          330

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 92.3 bits: 21.5 E(): 3.6
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (38-80:29-70)

```

          10          20          30          40          50          60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
          : : : : : : : :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
          10          20          30          40          50

```

```

          70          80
AAD-12 AEPWDFKLP---RVMW
          :: : : :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
          60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 92.2 bits: 21.8 E(): 3.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (35-51:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      70      80
AAD-12 CLLHRAEPWDFKLPRVMW

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.9 E(): 4.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (35-51:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

```

      70      80
AAD-12 CLLHRAEPWDFKLPRVMW

gi+AHw-456 SFGSDRSGLLLKQKVSDDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.9 E(): 4.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (35-51:68-86)

```

      10      20      30      40      50      60
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      : . . . . : : : . . . : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      70      80
AAD-12 CLLHRAEPWDFKLPRVMW

gi+AHw-184 SFDSDRSGLLLKQKVSDDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
      100      110      120      130      140      150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 43 init1: 43 opt: 61 Z-score: 88.0 bits: 23.4 E(): 6.3
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (6-70:424-492)

```

                                10      20      30
AAD-12      VKVHPETGRPSLLIGRHAHAIPGMDA--AESERF
                                : : . : . : . : . : . :
gi+AHw-135  YAHVFDEFKPLVEEPHNLVKTNCELFEKLG EYGFQNALLVRYTKKVPQVSTPTLVEVSRS
              400      410      420      430      440      450

```

```

              40      50      60      70      80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPVMMW
              : . . : : . . : . : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
              460      470      480      490      500      510

```

```

gi+AHw-135  ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
              520      530      540      550      560      570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.3
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (55-69:122-138)

```

              30      40      50      60      70      80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMW
                                : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVITYDNECLLCAHKVEQGASVDKRDGGC
              100      110      120      130      140      150

```

```

gi+AHw-162  RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
              160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (55-69:122-138)

```

              30      40      50      60      70      80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMW
                                : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVITYDNECLLCAHKVEQGASVDKRDGGC
              100      110      120      130      140      150

```

```

gi+AHw-124  RKELAAVSVCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
              160      170      180      190      200      210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 init1: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (55-69:122-138)

```

              30      40      50      60      70      80
AAD-12  DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPVMMW

```

```

                                : .....: ...
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100          110          120          130          140          150

gi+AHw-209 RKELAAVSVDCEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160          170          180          190          200          210

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:28 2010 done: Fri Feb 5 12:56:28 2010
Total Scan time: 0.070 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 199 - 278 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0:          one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      0      8: +ACo-
      34      3      21:+AD0-      +ACo-
      36      33      44:+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      38      25      72:+AD0APQA9AD0APQA9AD0-      +ACo-
      40      70      101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42      90
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      44      110      136:+AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-      +ACo-
      46      185
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
      48      185
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-

```

```

50      142
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
52      134
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQAqAD0APQA9AD0APQA9AD0-
54      72      91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
56      58      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
58      58      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60      52      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      56      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
64      38      32:+AD0APQA9AD0APQA9AD0AKgA9AD0-
66      41      25:+AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
68      21      20:+AD0APQA9AD0AKgA9-
70      12      16:+AD0APQA9ACo-
72      11      12:+AD0APQAq-
74      10      10:+AD0APQAq-
76      15       7:+AD0AKgA9AD0-
78      24       6:+AD0AKgA9AD0APQA9-
80        7       4:+ACoAPQ-
82        6       3:+ACoAPQ-
84        3       3:+ACo-
86        0       2:+ACo-
88        1       2:+ACo-          inset +AD0- represents 1 library sequences
90        2       1:+ACo-
92        2       1:+ACo-          :+ACoAPQ-
94        0       1:+ACo-          :+ACo-
96        0       1:+ACo-          :+ACo-
98        1       0:+AD0-          +ACoAPQ-
100       0       0:              +ACo-
102       1       0:+AD0-          +ACoAPQ-
104       0       0:              +ACo-
106       0       0:              +ACo-
108       1       0:+AD0-          +ACoAPQ-
110       0       0:              +ACo-
112       0       0:              +ACo-
114       0       0:              +ACo-
116       0       0:              +ACo-
118       0       0:              +ACo-
+AD4-120    0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.62070.00329+ADs- mu+AD0- 6.4987
0.175
mean+AF8-var+AD0-43.308113.146, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.194890
Kolmogorov-Smirnov statistic: 0.1195 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
 (439) 73 26.7 0.47
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 64 24.0 1
 gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
 (440) 66 24.8 1.8
 gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
 (91) 55 21.4 3.8
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 21.8 3.8
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 21.8 5.1
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 21.8 5.1
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
 (608) 61 23.4 6.5
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.6
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.7
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.3 9.7

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.3 bits: 26.7 E(): 0.47
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (23-53:246-276)

	10	20	30	40	50
AAD-12	KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA				
	::: :: . : : . : .				
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYT	QGVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT			
	220	230	240	250	260 270

	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWH		
	:		
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK		
	280	290	300 310 320 330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 102.1 bits: 24.0 E(): 1
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (3-59:79-133)

	10	20
AAD-12	KVHPETGRPSL--LIGRHA--HAIPGMDAAES	
	::: ::: :: : : : . .	
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF	
	50	60 70 80 90 100

	30	40	50	60	70	80
--	----	----	----	----	----	----

AAD-12 ERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWH

gi+AHw-121 EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
110 120 130 140 150

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)
initn: 66 initl: 66 opt: 66 Z-score: 97.7 bits: 24.8 E(): 1.8
Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (23-53:247-277)

AAD-12 KVHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
220 230 240 250 260 270

AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVMWH
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
280 290 300 310 320 330

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 55 Z-score: 92.0 bits: 21.4 E(): 3.8
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (37-79:29-70)

AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
10 20 30 40 50 60
10 20 30 40 50

AAD-12 AEPWDFKLP---RVMWH
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
70 80
60 70 80 90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 91.9 bits: 21.8 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (34-50:68-86)

AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

70 80

AAD-12
 K V H P E T G R P S L L I G R H A H A I P G M D A --- A E S E R F
 : : . : . : . . : . . . : :
 gi+AHw-135 Y A H V F D E F K P L V E E P H N L V K T N C E L F E K L G E Y G F Q N A L L V R Y T K K V P Q V S T P T L V E V S R S
 400 410 420 430 440 450
 40 50 60 70 80

gi+AHw-209 RKELAAVSVCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
160 170 180 190 200 210

[illegible]

```

56      66      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58      63      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60      46      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      58      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQA9-
64      43      32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66      39      25:+AD0APQA9AD0APQA9ACoAPQA9AD0-
68      19      20:+AD0APQA9AD0AKg-
70      14      16:+AD0APQA9ACo-
72      10      12:+AD0APQAq-
74       9      10:+AD0APQAq-
76      15       7:+AD0AKgA9AD0-
78      24       6:+AD0AKgA9AD0APQA9-
80       7       4:+ACoAPQ-
82       6       3:+ACoAPQ-
84       3       3:+ACo-
86       0       2:+ACo-
88       1       2:+ACo-          inset +AD0- represents 1 library sequences
90       2       1:+ACo-
92       2       1:+ACo-          :+ACoAPQ-
94       0       1:+ACo-          :+ACo-
96       0       1:+ACo-          :+ACo-
98       1       0:+AD0-          +ACoAPQ-
100      0       0:              +ACo-
102      1       0:+AD0-          +ACoAPQ-
104      0       0:              +ACo-
106      0       0:              +ACo-
108      1       0:+AD0-          +ACoAPQ-
110      0       0:              +ACo-
112      0       0:              +ACo-
114      0       0:              +ACo-
116      0       0:              +ACo-
118      0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.56650.0033+ADs- mu+AD0- 6.6904
0.175
mean+AF8-var+AD0-43.585313.347, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.194269
Kolmogorov-Smirnov statistic: 0.1174 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 26.7      0.46
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   64 24.0      1
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 24.8      1.8
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)   55 21.4      3.8

```

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 21.7 3.8
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 21.8 5.1
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 21.8 5.1
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.4 6.4
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.3 9.6
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.3 9.7
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.3 9.7

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 108.4 bits: 26.7 E(): 0.46
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (22-52:246-276)

	10	20	30	40	50	
AAD-12	VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA					
			::: :: . ::: :	. :	:: .	
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT					
	220	230	240	250	260	270

	60	70	80			
AAD-12	GDVVVWDNRCLLHRAEPWDFKLPRVMWHS					
	:					
gi+AHw-370	GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK					
	280	290	300	310	320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 64 Z-score: 102.1 bits: 24.0 E(): 1
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (2-58:79-133)

	10	20				
AAD-12	VHPETGRPSL--LIGRHA--HAIPGMDAAES					
 ::: :: :	: : :.. ::				
gi+AHw-121	DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF					
	50	60	70	80	90	100

	30	40	50	60	70	80
AAD-12	ERFLEGLVDWACQAPRVHAHQWAAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHS					
	:: .:::	:	::	:::		
gi+AHw-121	EEFRASLVDYLS----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ					
	110	120	130	140	150	

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 97.7 bits: 24.8 E(): 1.8

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (22-52:247-277)

```

                10      20      30      40      50
AAD-12      VHPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                : : : : : : : : : : : :
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

                60      70      80
AAD-12  GDVVVWDNRCLLHRAEPWDFKLPRVMWHS
                :
gi+AHw-232  GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 92.0 bits: 21.4 E(): 3.8
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (36-78:29-70)

```

                10      20      30      40      50      60
AAD-12  GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
                : : : : : : : : : : : :
gi+AHw-323  QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAY
                10      20      30      40      50

```

```

                70      80
AAD-12  AEPWDFKLPR--RVMWHS
                : : : :
gi+AHw-323  CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                60      70      80      90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 91.9 bits: 21.7 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (33-49:68-86)

```

                10      20      30      40      50      60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                : : : : : : : : : : : :
gi+AHw-219  YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40      50      60      70      80      90

```

```

                70      80
AAD-12  CLLHRAEPWDFKLPRVMWHS
gi+AHw-219  SFDSDRSGLLLKQKVSDE
                100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1

Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (33-49:68-86)

```

          10          20          30          40          50          60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
          :  . . . . :  ::  . . .  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

```

          70          80
AAD-12  CLLHRAEPWDFKLPRVMWHS

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (33-49:68-86)

```

          10          20          30          40          50          60
AAD-12  PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVDNR
          :  . . . . :  ::  . . .  ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          70          80
AAD-12  CLLHRAEPWDFKLPRVMWHS

gi+AHw-184 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:

Full+AD0-Serum (608 aa)

initn: 43 initl: 43 opt: 61 Z-score: 87.9 bits: 23.4 E(): 6.4
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (4-68:424-492)

```

          10          20          30
AAD-12  VHPETGRPSLLIGRHAHAIPGMDA---AESERF
          :  :  .  . .  . . .  . . .  . :  :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
          400          410          420          430          440          450

```

```

          40          50          60          70          80
AAD-12  LEGLVDWACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWDFKLPRVMWHS
          :  . .  :  . . .  . :  . :  ::  . . . . :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
          460          470          480          490          500          510

```

```

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
          520          530          540          550          560          570

```


Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 201 - 280 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      1      8: +AD0AKg-
      34      20     21: +AD0APQA9AD0APQAq-
      36      17     44: +AD0APQA9AD0APQ- +ACo-
      38      25     72: +AD0APQA9AD0APQA9AD0- +ACo-
      40      72    101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42      99
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      44      104    136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9- +ACo-
      46      189
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      48      188
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
      50      135
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0-
      52      128
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0APQ-
      54      62     91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      56      65     76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      58      61     62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      60      50     50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      62      55     40: +AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      64      46     32: +AD0APQA9AD0APQA9AD0AKgA9AD0APQA9-
      66      42     25: +AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      68      20     20: +AD0APQA9AD0AKg-
      70      14     16: +AD0APQA9ACo-
      72       8     12: +AD0APQAq-
```

```

74      5      10:+AD0APQAq-
76     14      7:+AD0AKgA9AD0-
78     25      6:+AD0AKgA9AD0APQA9AD0-
80      7      4:+ACoAPQ-
82      5      3:+ACoAPQ-
84      4      3:+ACo-
86      0      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:              +ACo-
102     1      0:+AD0-          +ACoAPQ-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     1      0:+AD0-          +ACoAPQ-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120    0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.58200.0033+ADs- mu+AD0- 6.6331
0.175
mean+AF8-var+AD0-42.776013.219, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196098
Kolmogorov-Smirnov statistic: 0.1147 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 26.8      0.44
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   64 24.1      0.98
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 24.8      1.7
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)   55 21.5      3.6
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.8      3.7
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9      4.8
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9      4.8
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)   61 23.5      6.1
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)   54 21.3      9.2

```

gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.3
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.3 9.3

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 108.8 bits: 26.8 E(): 0.44
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (21-51:246-276)

```

                                10      20      30      40      50
AAD-12      HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . :: : . : . : .
gi+AHw-370  APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNNSDKSKWIT
                220      230      240      250      260      270

```

```

                        60      70      80
AAD-12  GDVVVDNRCLLHRAEPWDFKLPRVMWHSR
:
gi+AHw-370  GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 64 Z-score: 102.6 bits: 24.1 E(): 0.98
 Smith-Waterman score: 64+ADs- 32.787+ACU- identity (50.820+ACU- similar)
 in 61 aa overlap (1-57:79-133)

```

                                10      20
AAD-12      HPETGRPSL--LIGRHA--HAIPGMDAAES
                                .... :: : : ... ::
gi+AHw-121  DLDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQF
                50      60      70      80      90      100

                30      40      50      60      70      80
AAD-12  ERFLEGLVDWACQAPRVHAHQWAAAGDVVVVDNRCLLHRAEPWDFKLPRVMWHSR
                :: .::: . : . : . :
gi+AHw-121  EEFRASLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.1 bits: 24.8 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (21-51:247-277)

```

                                10      20      30      40      50
AAD-12      HPETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . :: : . : . : .
gi+AHw-232  APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

                        60      70      80

```

AAD-12 GDVVVWDNRCLLHRAEPWDFKLPVVMWHSR

```

      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:

Full+AD0-Chiti (91 aa)

initn: 43 initl: 43 opt: 55 Z-score: 92.3 bits: 21.5 E(): 3.6
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (35-77:29-70)

```

      10      20      30      40      50      60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
      :   :::   : .. : ..   :: : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
      10      20      30      40      50

```

```

      70      80
AAD-12 AEPWDFKLP---RVMWHSR
      ::   :   :   :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60      70      80      90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.2 bits: 21.8 E(): 3.7
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (32-48:68-86)

```

      10      20      30      40      50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :   .:::   :: ... ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      60      70      80
AAD-12 CLLHRAEPWDFKLPVVMWHSR
gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (32-48:68-86)

```

      10      20      30      40      50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :   .:::   :: ... ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

```

      60      70      80

```

AAD-12 CLLHRAEPWDFKLPRVMWHSR

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.1 bits: 21.9 E(): 4.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (32-48:68-86)

10 20 30 40 50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: : : . . . :
gi+AHw-184 YVWKISEFYGRKPEGTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

60 70 80
AAD-12 CLLHRAEPWDFKLPRVMWHSR

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.2 bits: 23.5 E(): 6.1
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (3-67:424-492)

10 20
AAD-12 HPETGRPSLLIGRHAHAIPGMDA---AESERF
: : . . . : : . . . : :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
400 410 420 430 440 450

30 40 50 60 70 80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSR
: . . : : . . : : : : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSESVTKCTESLVNRRPCFS
460 470 480 490 500 510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)

initn: 49 init1: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.2
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (52-66:122-138)

30 40 50 60 70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
: : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC


```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 202 - 281 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      0      8: +ACo-
      34      21     21: +AD0APQA9AD0APQAq-
      36      17     44: +AD0APQA9AD0APQ- +ACo-
      38      24     72: +AD0APQA9AD0APQA9- +ACo-
      40      73    101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      42      97
123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      44      112
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0- +ACo-
      46      182
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0-
      48      188
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
      50      141
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACoAPQA9AD0APQA9-
      52      123
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0-
      54      63     91: +AD0APQA9AD0APQA9AD0APQ- +AD0APQA9AD0APQA9AD0APQ-
+ACo-
      56      66     76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      58      64     62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      60      47     50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      62      53     40: +AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
      64      49     32: +AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0-
      66      39     25: +AD0APQA9AD0APQA9ACoAPQA9AD0-
      68      20     20: +AD0APQA9AD0AKg-
```



```

70      14      16:+AD0APQA9ACo-
72      7      12:+AD0APQAq-
74      6      10:+AD0APQAq-
76     14      7:+AD0AKgA9AD0-
78     24      6:+AD0AKgA9AD0APQA9-
80      7      4:+ACoAPQ-
82      6      3:+ACoAPQ-
84      4      3:+ACo-
86      0      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     1      0:+AD0-          +ACoAPQ-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120    0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.57120.00334+ADs- mu+AD0- 6.6678
0.177
mean+AF8-var+AD0-42.451213.163, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196847
Kolmogorov-Smirnov statistic: 0.1106 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 26.9    0.42
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   63 23.9    1.2
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 24.9    1.7
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)    55 21.5    3.5
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)    56 21.9    3.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9    4.7
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9    4.7
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)   61 23.5    6

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.4 9
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.4 9.1
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.4 9.1

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 init1: 73 opt: 73 Z-score: 109.1 bits: 26.9 E(): 0.42
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (20-50:246-276)

```

                10      20      30      40
AAD-12          PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                :::: :: . ::: : . :      :: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220      230      240      250      260      270

```

```

                50      60      70      80
AAD-12          GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRL
                :
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 init1: 51 opt: 63 Z-score: 101.3 bits: 23.9 E(): 1.2
 Smith-Waterman score: 63+ADs- 33.333+ACU- identity (50.000+ACU- similar)
 in 60 aa overlap (1-56:80-133)

```

                10      20
AAD-12          PETGRPSL--LIGRHA--HAIPGMDAAESE
                :: :::: :: : : :: . ::
gi+AHw-121 LDSIKDSADFAVHSGRIVGFFSEVIGLIGNPEN-RPALKTLIDGLASSHKARGIEKAQFE
                50      60      70      80      90      100

```

```

                30      40      50      60      70      80
AAD-12          RFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRL
                .: :::: : .: ::
gi+AHw-121 EFRASLVDYLS-----HHLWDNDTMKSTWDLALNNMFFYILHALEVAQ
                110      120      130      140      150

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 init1: 66 opt: 66 Z-score: 98.4 bits: 24.9 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (20-50:247-277)

```

                10      20      30      40
AAD-12          PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                :::: :: . ::: : . :      :: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

      50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRL
      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
  initn: 43 initl: 43 opt: 55 Z-score: 92.5 bits: 21.5 E(): 3.5
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (34-76:29-70)

      10      20      30      40      50      60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
      :   ::   :   ..   :   .   ::   :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCPDNNCQATY-HYYNPAQNN---WDLRAVSAY
      10      20      30      40      50

      70      80
AAD-12 AEPWDFKLP---RVMWHSRL
      ::   :   :   :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60      70      80      90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 92.4 bits: 21.9 E(): 3.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (31-47:68-86)

      10      20      30      40      50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :   .:::   ::   ...   ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRL

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
  initn: 40 initl: 40 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (31-47:68-86)

      10      20      30      40      50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :   .:::   ::   ...   ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

60 70 80
AAD-12 CLLHRAEPWDFKLPRVMWHSRL

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.2 bits: 21.9 E(): 4.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (31-47:68-86)

10 20 30 40 50
AAD-12 PETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

60 70 80
AAD-12 CLLHRAEPWDFKLPRVMWHSRL

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:

Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.4 bits: 23.5 E(): 6
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (2-66:424-492)

10 20
AAD-12 PETGRPSLLIGRHAHAIPGMDA---AESERF
: : . : . : . : . :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
400 410 420 430 440 450

30 40 50 60 70 80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRL
: . . : : . . : . : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFS
460 470 480 490 500 510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKKTVMG
520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid

+AFs-Gallus gal (208 aa)

initn: 49 init1: 49 opt: 54 Z-score: 85.2 bits: 21.4 E(): 9
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (51-65:122-138)

30 40 50 60 70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:29 2010 done: Fri Feb 5 12:56:29 2010
Total Scan time: 0.080 Total Display time: 0.010

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

70      13      16:+AD0APQA9ACo-
72      11      12:+AD0APQAq-
74       7      10:+AD0APQAq-
76      13       7:+AD0AKgA9AD0-
78      25       6:+AD0AKgA9AD0APQA9AD0-
80       8       4:+ACoAPQ-
82       4       3:+ACo-
84       4       3:+ACo-
86       0       2:+ACo-
88       1       2:+ACo-          inset +AD0- represents 1 library sequences
90       2       1:+ACo-
92       2       1:+ACo-          :+ACoAPQ-
94       1       1:+ACo-          :+ACo-
96       0       1:+ACo-          :+ACo-
98       1       0:+AD0-          +ACoAPQ-
100      0       0:              +ACo-
102      0       0:              +ACo-
104      0       0:              +ACo-
106      0       0:              +ACo-
108      1       0:+AD0-          +ACoAPQ-
110      0       0:              +ACo-
112      0       0:              +ACo-
114      0       0:              +ACo-
116      0       0:              +ACo-
118      0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.43670.00337+ADs- mu+AD0- 7.3394
0.179
mean+AF8-var+AD0-43.006113.196, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.195573
Kolmogorov-Smirnov statistic: 0.1065 (N+AD0-28) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 26.8      0.43
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 24.9      1.7
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   59 22.7      2.6
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)   55 21.5      3.7
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.8      3.7
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8      4.9
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8      4.9
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)   61 23.5      6

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.2
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.3
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.3 9.3

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 109.0 bits: 26.8 E(): 0.43
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (19-49:246-276)

	10	20	30	40
AAD-12	ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . : : . : . : .			
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYT	QGV	DIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT	
	220	230	240	250
				260
				270

	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLA			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSI	EDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNP	IRIKK	
	280	290	300	310
				320
				330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.3 bits: 24.9 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (19-49:247-277)

	10	20	30	40
AAD-12	ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . : : . : . : .			
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYK	KGKVG	IAMDVASSEFYKD	KGKYLDFKPNPESDPSKWLS
	220	230	240	250
				260
				270

	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLA			
	:			
gi+AHw-232	GPQLADLYEQLISEYPIVSI	EDPFAEDDWD	AWVHFFERVGDKIQIVGDDLTVTNP	TRIKT
	280	290	300	310
				320
				330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 59 Z-score: 94.8 bits: 22.7 E(): 2.6
 Smith-Waterman score: 59+ADs- 32.143+ACU- identity (48.214+ACU- similar)
 in 56 aa overlap (4-55:83-133)

	10	20
AAD-12	ETGRPSL--LIGRHA--HAIPGMDAAESERFLE	
	::: :: : : : . . . :	
gi+AHw-121	IKDSADFAVHSGRIVGFFSEVIGLIGNPENRPA	LKTLIDGLASSHKARGIEKAQFEEFRA
	60	70
		80
		90
		100
		110


```

      30      40      50      60      70      80
AAD-12 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLA
      .:.:.      :      .:      .:.
gi+AHw-121 SLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                  120      130      140      150

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 55 Z-score: 92.2 bits: 21.5 E(): 3.7
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (33-75:29-70)

```

      10      20      30      40      50      60
AAD-12 GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
                  :      :::      :      .:      .:      .:      .:
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCPDNNCQATY-HYYNPAQNN--WDLRAVSAY
                  10      20      30      40      50

```

```

      70      80
AAD-12 AEPWDFKLP---RVMWHSRLA
      ::      :      :      :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                  60      70      80      90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.1 bits: 21.8 E(): 3.7
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (30-46:68-86)

```

      10      20      30      40      50
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                  :      .:.:.      ::      ...      .:.
gi+AHw-219 YVWKISEFYGRKPEGTTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                  40      50      60      70      80      90

```

```

      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLA
gi+AHw-219 SFDSDRSGLLLKQKVSDE
                  100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 90.0 bits: 21.8 E(): 4.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (30-46:68-86)

```

      10      20      30      40      50
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                  :      .:.:.      ::      ...      .:.
gi+AHw-456 YVWKISEFYGRKPEGTTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
                  40      50      60      70      80      90

```

60 70 80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLA

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.8 E(): 4.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (30-46:68-86)

10 20 30 40 50
AAD-12 ETGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGNFKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

60 70 80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLA

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:

Full+AD0-Serum (608 aa)

initn: 43 init1: 43 opt: 61 Z-score: 88.5 bits: 23.5 E(): 6
Smith-Waterman score: 61+ADs- 26.087+ACU- identity (53.623+ACU- similar)
in 69 aa overlap (1-65:424-492)

10 20
AAD-12 ETGRPSLLIGRHAHAIPGMDA---AESERF
: : . : . : . : . :
gi+AHw-135 YAHVFDEFKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS
400 410 420 430 440 450

30 40 50 60 70 80
AAD-12 LEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLA
: . . : : . . : . : : : : :
gi+AHw-135 LGKVGSKCCTHPEAERLSAEDYLSVVLNRLCVLHEKTPVSESVTKCTESLVNRRPCFS
460 470 480 490 500 510

gi+AHw-135 ALQVDETYVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMG
520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid

+AFs-Gallus gal (208 aa)

initn: 49 init1: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.2
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (50-64:122-138)

20 30 40 50 60 70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:29 2010 done: Fri Feb 5 12:56:29 2010
Total Scan time: 0.080 Total Display time: 0.000

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

```

68      18      20:+AD0APQA9AD0AKg-
70      13      16:+AD0APQA9ACo-
72      12      12:+AD0APQAq-
74       7      10:+AD0APQAq-
76      16       7:+AD0AKgA9AD0-
78      22       6:+AD0AKgA9AD0APQA9-
80       8       4:+ACoAPQ-
82       3       3:+ACo-
84       3       3:+ACo-
86       0       2:+ACo-
88       0       2:+ACo-          inset +AD0- represents 1 library sequences
90       3       1:+ACo-
92       1       1:+ACo-          :+ACo-
94       1       1:+ACo-          :+ACo-
96       0       1:+ACo-          :+ACo-
98       1       0:+AD0-          +ACoAPQ-
100      0       0:              +ACo-
102      0       0:              +ACo-
104      0       0:              +ACo-
106      0       0:              +ACo-
108      1       0:+AD0-          +ACoAPQ-
110      0       0:              +ACo-
112      0       0:              +ACo-
114      0       0:              +ACo-
116      0       0:              +ACo-
118      0       0:              +ACo-
+AD4-120      0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.38670.00339+ADs- mu+AD0- 7.5819
0.180
mean+AF8-var+AD0-43.897513.052, 0's: 2 Z-trim: 3 B-trim: 0 in 0/43
Lambda+AD0- 0.193577
Kolmogorov-Smirnov statistic: 0.1086 (N+AD0-26) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.7      0.46
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8      1.8
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  59 22.6      2.8
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.4      3.9
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.7      3.9
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8      5.1
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8      5.1

```

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.6
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.3 9.7
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.7

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 108.5 bits: 26.7 E(): 0.46
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (18-48:246-276)

	10	20	30	40
AAD-12	TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
		::: :: . ::: : . : .: .		
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYT	QGQVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT		
	220	230	240	250
			260	270

	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSI	EDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK		
	280	290	300	310
			320	330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 97.9 bits: 24.8 E(): 1.8
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (18-48:247-277)

	10	20	30	40
AAD-12	TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
		::: :: . .: : . : .: .		
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKPNPESDPSKWLS			
	220	230	240	250
			260	270

	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAG			
	:			
gi+AHw-232	GPQLADLYEQLISEYPIVSI	EDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT		
	280	290	300	310
			320	330

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 59 Z-score: 94.4 bits: 22.6 E(): 2.8
 Smith-Waterman score: 59+ADs- 32.143+ACU- identity (48.214+ACU- similar)
 in 56 aa overlap (3-54:83-133)

	10	20
AAD-12	TGRPSL--LIGRHA--HAIPGMDAAESERFLE	
	::: :: : : : . . . :	
gi+AHw-121	IKDSADFAVHSGRIVGFFSEVIGLIGNPENRPA	LTIDGLASSHKARGIEKAQFEFRA
	60	70
	80	90
	100	110

```

      30      40      50      60      70      80
AAD-12  GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAG
      .:.:.      :  .:      .:.
gi+AHw-121 SLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      120      130      140      150

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 55 Z-score: 91.7 bits: 21.4 E(): 3.9
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (32-74:29-70)

```

      10      20      30      40      50      60
AAD-12  GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHR
      :  :::      :  .:  .:  .:  .:
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAY
      10      20      30      40      50

```

```

      70      80
AAD-12  AEPWDFKLP---RVMWHSRLAG
      ::  :  :  :
gi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60      70      80      90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 91.7 bits: 21.7 E(): 3.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (29-45:68-86)

```

      10      20      30      40      50
AAD-12  TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  .:.:.      ::  ...  .:.
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMDF
      40      50      60      70      80      90

```

```

      60      70      80
AAD-12  CLLHRAEPWDFKLPRVMWHSRLAG
gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100      110

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 89.6 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (29-45:68-86)

```

      10      20      30      40      50
AAD-12  TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  .:.:.      ::  ...  .:.
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMNF
      40      50      60      70      80      90

```

60 70 80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAG

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 89.6 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (29-45:68-86)

10 20 30 40 50
AAD-12 TGRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

60 70 80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAG

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)

initn: 49 initl: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (49-63:122-138)

20 30 40 50 60 70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
: : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

80
AAD-12 RLAG

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
160 170 180 190 200

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)

initn: 49 initl: 49 opt: 54 Z-score: 84.7 bits: 21.3 E(): 9.7
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (49-63:122-138)

20 30 40 50 60 70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
: : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	0	0:	
26	0	0:	
28	0	0:	

```

30      0      2:+ACo-
32      1      8:+AD0AKg-
34     21     21:+AD0APQA9AD0APQAq-
36     18     44:+AD0APQA9AD0APQ-      +ACo-
38     32     72:+AD0APQA9AD0APQA9AD0APQ-      +ACo-
40     77    101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
42     82
123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
44    131
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACo-
46    162
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQ-
48    186
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
50    123
121:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACo-
52    131    106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+AD0APQA9AD0APQA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9-
54    66     91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
56    66     76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
58    73     62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
60    53     50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQ-
62    49     40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
64    43     32:+AD0APQA9AD0APQA9AD0AKgA9AD0APQ-
66    38     25:+AD0APQA9AD0APQA9-+ACoAPQA9AD0-
68    19     20:+AD0APQA9AD0AKg-
70    17     16:+AD0APQA9ACoAPQ-
72     9     12:+AD0APQAq-
74    11     10:+AD0APQAq-
76    14      7:+AD0AKgA9AD0-
78    20      6:+AD0AKgA9AD0APQ-
80     9      4:+ACoAPQA9-
82     7      3:+ACoAPQ-
84     3      3:+ACo-
86     1      2:+ACo-
88     0      2:+ACo-      inset +AD0- represents 1 library sequences
90     2      1:+ACo-
92     2      1:+ACo-      :+ACoAPQ-
94     0      1:+ACo-      :+ACo-
96     1      1:+ACo-      :+ACo-
98     1      0:+AD0-      +ACoAPQ-
100    0      0:      +ACo-
102    0      0:      +ACo-
104    0      0:      +ACo-
106    0      0:      +ACo-
108    0      0:      +ACo-
110    1      0:+AD0-      +ACoAPQ-

```

```

112      0      0:      +ACo-
114      0      0:      +ACo-
116      0      0:      +ACo-
118      0      0:      +ACo-
+AD4-120      0      0:      +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.39680.00337+ADs- mu+AD0- 7.5565
0.179
mean+AF8-var+AD0-41.635212.859, 0's: 2 Z-trim: 3 B-trim: 44 in 1/42
Lambda+AD0- 0.198767
Kolmogorov-Smirnov statistic: 0.0984 (N+AD0-28) at 44

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

```

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.0 0.38
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.0 1.5
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151) 59 22.8 2.4
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 55 21.6 3.4
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115) 56 21.9 3.4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.0 4.5
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.0 4.5
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208) 54 21.4 8.6
gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (
210) 54 21.4 8.7
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210) 54 21.4 8.7

```

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:

Full+AD0-Enolas (439 aa)

initn: 73 initl: 73 opt: 73 Z-score: 110.0 bits: 27.0 E(): 0.38

Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (17-47:246-276)

```

                                10      20      30      40
AAD-12      GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . :: : . : . :
gi+AHw-370  APDIKTAKEALDLIVSAIEAAGYTQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220      230      240      250      260      270

                50      60      70      80
AAD-12  GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGR
:
gi+AHw-370  GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK

```

```

              70              80
AAD-12 AEPWDFKLP--RVMWHSRLAGR
      ::  :  :  :
qi+AHw-323 CSTWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR

```

60 70 80 90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.7 bits: 21.9 E(): 3.4
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (28-44:68-86)

	10	20	30	40	50
AAD-12	GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR				
	: : : : . . . : :				
gi+AHw-219	YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF				
	40	50	60	70	80
	60	70	80		
AAD-12	CLLHRAEPWDFKLPRVMWHSRLAGR				
gi+AHw-219	SFDSDRSGLLLKQKVSDE				
	100	110			

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 90.6 bits: 22.0 E(): 4.5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (28-44:68-86)

	10	20	30	40	50
AAD-12	GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR				
	: : : : . . . : :				
gi+AHw-456	YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF				
	40	50	60	70	80
	60	70	80		
AAD-12	CLLHRAEPWDFKLPRVMWHSRLAGR				
gi+AHw-456	SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS				
	100	110	120	130	140

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 90.6 bits: 22.0 E(): 4.5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (28-44:68-86)

	10	20	30	40	50
AAD-12	GRPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR				
	: : : : . . . : :				
gi+AHw-184	YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF				
	40	50	60	70	80
	60	70	80		
AAD-12	CLLHRAEPWDFKLPRVMWHSRLAGR				
gi+AHw-184	SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS				

80
AAD-12 RLAGR
gi+AHw-124 RKELAAVSVCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC

160 170 180 190 200 210

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:29 2010 done: Fri Feb 5 12:56:29 2010

Total Scan time: 0.080 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1

FASTA searches a protein or DNA sequence data bank

version 3.4t26 July 7, 2006

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs

/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 206 - 285 80 aa - 80 aa

vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      0      8: +ACo-
      34     16     21: +AD0APQA9AD0- +ACo-
      36     19     44: +AD0APQA9AD0APQ- +ACo-
      38     27     72: +AD0APQA9AD0- +AD0APQA9- +ACo-
      40    101
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AK
g-
      42     76    123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+ACo-
      44    127
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQ- +ACo-
      46    172
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
      48    185    132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9A
D0APQA9AD0APQA9AD0-
      50    121
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACo-

```

```

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
  join: 42, opt: 30, open/ext: -10/-2, width: 32
  Scan time: 0.080
The best scores are:
                                     opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)    73 26.8    0.44
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)    66 24.8    1.7

```


gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 59 22.6 2.7
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
 (608) 64 24.3 3.4
 gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
 (91) 55 21.4 3.8
 gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
 56 21.7 3.8
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 21.8 5
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 21.8 5
 gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
 (607) 60 23.2 7.3
 gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (607)
 60 23.2 7.3
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.4
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.3 9.5

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 108.7 bits: 26.8 E(): 0.44
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (16-46:246-276)

	10	20	30	40
AAD-12	RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . .:: : . : .:			
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYT	QGV	DIAMD	VASSEFYKDGLYDLDFKNPN
	220	230	240	250 260 270
	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRP			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIV	SIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK		
	280	290	300	310 320 330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.1 bits: 24.8 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (16-46:247-277)

	10	20	30	40
AAD-12	RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . .: : . : .:			
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMD	VASSEFYKDGKYDLDFKNPESDPSKWLS		
	220	230	240	250 260 270
	50	60	70	80

AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP

```

      :
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
      280      290      300      310      320      330

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 59 Z-score: 94.6 bits: 22.6 E(): 2.7
Smith-Waterman score: 59+ADs- 32.143+ACU- identity (48.214+ACU- similar)
in 56 aa overlap (1-52:83-133)

```

                                10      20
AAD-12                        RPSL--LIGRHA--HAIPGMDAAESERFLE
                                :::  ::  :  :  ::.  ::  :::
gi+AHw-121 IKDSADFAVHSGRIVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRA
      60      70      80      90      100     110

```

```

      30      40      50      60      70      80
AAD-12 GLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRP
      .:::.  :  .:  ::
gi+AHw-121 SLVDYLS-----HHLDWNDTMKSTWDLALNNMFFYILHALEVAQ
      120     130     140     150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 53 init1: 53 opt: 64 Z-score: 92.9 bits: 24.3 E(): 3.4
Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
in 80 aa overlap (5-80:431-510)

```

                                10      20      30
AAD-12                        RPSLLIGRHAHAIPGMDA---AESERFLEGLVDW
                                .. :... .: ...  .:  :  :  .
gi+AHw-135 FKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
      410     420     430     440     450     460

```

```

      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRP
      :  :...  .:  .:  :: :...  :  .  .  .:  .  ::
gi+AHw-135 CCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSESVTKCCTESLVNRRPCFSALQVDET
      470     480     490     500     510     520

```

```

gi+AHw-135 YVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKKTVMGDFGSFVD
      530     540     550     560     570     580

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 91.9 bits: 21.4 E(): 3.8
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (30-72:29-70)

```

      10      20      30      40      50      60
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRA
      :  :::  :  .  :  .  ::  :  .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYPNQNN---WDLRAVSAYC

```

```

10          20          30          40          50
70          80
AAD-12 EPWDFKLP---RVMWHSRLAGRP
      ::  :  :  :
gi+AHw-323 STWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60          70          80          90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
  initn: 40 init1: 40 opt: 56 Z-score: 91.9 bits: 21.7 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (27-43:68-86)

10          20          30          40          50
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  ....  ::  ...  ::
gi+AHw-219 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
      40          50          60          70          80          90

60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRP

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100          110

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
  initn: 40 init1: 40 opt: 56 Z-score: 89.8 bits: 21.8 E(): 5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (27-43:68-86)

10          20          30          40          50
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  ....  ::  ...  ::
gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
      40          50          60          70          80          90

60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRP

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
      100          110          120          130          140          150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
  initn: 40 init1: 40 opt: 56 Z-score: 89.8 bits: 21.8 E(): 5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (27-43:68-86)

10          20          30          40          50
AAD-12 RPSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
      :  ....  ::  ...  ::
gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF

```

40 50 60 70 80 90

60 70 80

AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRP

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS

100 110 120 130 140 150

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName:
Full+AD0-Serum (607 aa)
initn: 51 initl: 51 opt: 60 Z-score: 86.8 bits: 23.2 E(): 7.3
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (5-80:430-509)

10 20 30

AAD-12 RPSLLIGRHAHAIPGMDA---AESERFLEGLVDW

:: :... :: ... :: : : .

gi+AHw-135 LKHLVDEPQNLIKQNCQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR

400 410 420 430 440 450

40 50 60 70 80

AAD-12 ACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWDFKLPRVMWHSRLAGRP

: :. . . . :: :... : . : . . : : . :

gi+AHw-135 CCTKPESERMPCTEDYLSLIILNRLCVLHEKTPVSEKVTCKCTESLVNRRPCFSALTPDET

460 470 480 490 500 510

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD

520 530 540 550 560 570

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin
+AFs-Bos t (607 aa)
initn: 51 initl: 51 opt: 60 Z-score: 86.8 bits: 23.2 E(): 7.3
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (5-80:430-509)

10 20 30

AAD-12 RPSLLIGRHAHAIPGMDA---AESERFLEGLVDW

:: :... :: ... :: : : .

gi+AHw-333 LKHLVDEPQNLIKQNCQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR

400 410 420 430 440 450

40 50 60 70 80

AAD-12 ACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWDFKLPRVMWHSRLAGRP

: :. . . . :: :... : . : . . : : . :

gi+AHw-333 CCTKPESERMPCTEDYLSLIILNRLCVLHEKTPVSEKVTCKCTESLVNRRPCFSALTPDET

460 470 480 490 500 510

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD

520 530 540 550 560 570

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (47-61:122-138)

```
      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150
```

```
      80
AAD-12 RLAGRP

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
      160      170      180      190      200
```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (47-61:122-138)

```
      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150
```

```
      80
AAD-12 RLAGRP

gi+AHw-124 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
      160      170      180      190      200      210
```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 84.8 bits: 21.3 E(): 9.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (47-61:122-138)

```
      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : ~
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150
```

```
      80
AAD-12 RLAGRP

gi+AHw-209 RKELAAVSVDCEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTTLSHFGKC
      160      170      180      190      200      210
```

80 residues in 1 query sequences

56 61 76: +AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0APOA9AD0- +ACo-

```

58      56      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
60      47      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQ-+AD0AKg-
62      53      40:+AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0APQ-
64      40      32:+AD0APQA9AD0APQA9AD0AKgA9AD0-
66      36      25:+AD0APQA9AD0APQA9ACoAPQA9-
68      21      20:+AD0APQA9AD0AKgA9-
70      14      16:+AD0APQA9ACo-
72      12      12:+AD0APQAq-
74      7       10:+AD0APQAq-
76      17      7:+AD0AKgA9AD0APQ-
78      23      6:+AD0AKgA9AD0APQA9-
80      8       4:+ACoAPQ-
82      3       3:+ACo-
84      4       3:+ACo-
86      2       2:+ACo-
88      0       2:+ACo-          inset +AD0- represents 1 library sequences
90      4       1:+ACo-
92      2       1:+ACo-          :+ACoAPQ-
94      0       1:+ACo-          :+ACo-
96      0       1:+ACo-          :+ACo-
98      1       0:+AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     1       0:+AD0-          +ACoAPQ-
110     0       0:              +ACo-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.34930.00345+ADs- mu+AD0- 7.8131
0.183
mean+AF8-var+AD0-43.607913.006, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.194219
Kolmogorov-Smirnov statistic: 0.0956 (N+AD0-27) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.8      0.45
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.8      1.7
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  64 24.3      3.4
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)   55 21.4      3.9
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.7      3.9

```

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
 (151) 57 22.1 4.1
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
 56 21.8 5.1
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
 56 21.8 5.1
 gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
 (607) 60 23.2 7.3
 gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (607)
 60 23.2 7.3
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
 (208) 54 21.3 9.5
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.6
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
 54 21.3 9.6

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
 Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 108.6 bits: 26.8 E(): 0.45
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (15-45:246-276)

	10	20	30	40
AAD-12	PSLLIGRHAHAIPGMDAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . .:: : . : .::			
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYT	GQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT		
	220	230	240	250
	260	270		
	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSI	EDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK		
	280	290	300	310
	320	330		

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.0 bits: 24.8 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (15-45:247-277)

	10	20	30	40
AAD-12	PSLLIGRHAHAIPGMDAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . .: : . . .::			
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKD	GKYDLDFKNPESDPSKWLS		
	220	230	240	250
	260	270		
	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE			
	:			
gi+AHw-232	GPQLADLYEQLISEYPIVSI	EDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT		
	280	290	300	310
	320	330		

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)
initn: 53 initl: 53 opt: 64 Z-score: 92.9 bits: 24.3 E(): 3.4
Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
in 80 aa overlap (4-79:431-510)

```

                                10          20          30
AAD-12          PSLLIGRHAHAIPGMDA---AESERFLEGLVDW
                   :. .... .: ... .: : : .
gi+AHw-135 FKPLVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
                   410          420          430          440          450          460

                   40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPE
                   : :... . : . : :: :... : . . . . : : . ::
gi+AHw-135 CCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSESVTKCTESLVNRRPCFSALQVDET
                   470          480          490          500          510          520

gi+AHw-135 YVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGSFVD
                   530          540          550          560          570          580
```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 initl: 43 opt: 55 Z-score: 91.7 bits: 21.4 E(): 3.9
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (29-71:29-70)

```

                   10          20          30          40          50          60
AAD-12 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
                   : :: : : .. : .. : : : .
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAYCS
                   10          20          30          40          50

                   70          80
AAD-12 PWDFKLP---RVMWHSRLAGRPE
                   :: : : :
gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                   60          70          80          90
```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 91.7 bits: 21.7 E(): 3.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (26-42:68-86)

```

                   10          20          30          40          50
AAD-12          PSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                   : :... : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                   40          50          60          70          80          90

                   60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPE
```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
100 110

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 57 Z-score: 91.4 bits: 22.1 E(): 4.1
Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
in 43 aa overlap (9-51:96-133)

AAD-12 PSLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
.: ... :. :.: :.:.
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEFFRASLV DYLS-----H
70 80 90 100 110 120

AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPE
.: .:
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
130 140 150

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (26-42:68-86)

AAD-12 PSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: :.: :. :.:
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
40 50 60 70 80 90

AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPE

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (26-42:68-86)

AAD-12 PSLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
: :.: :. :.:
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
40 50 60 70 80 90

AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPE

[illegible]

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-

```
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
```

Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```
1+AD4APgA+-AAD-12: 208 - 287 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      1      8: +AD0AKg-
      34      14     21: +AD0APQA9AD0- +ACo-
      36      22     44: +AD0APQA9AD0APQA9- +ACo-
      38      28     72: +AD0APQA9AD0APQA9AD0- +ACo-
      40      96
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      42      69     123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
      44      142
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9-
      46      169
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0-
      48      189
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
      50      115
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQ- +ACo-
      52      133     106: +AD0APQA9AD0APQA9AD0-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9-
      54      85
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
      56      63      76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      58      51      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      60      50      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      62      48      40: +AD0APQA9AD0APQA9AD0APQA9ACoAPQA9-
      64      39      32: +AD0APQA9AD0APQA9AD0AKgA9AD0-
      66      32      25: +AD0APQA9- +AD0APQA9ACoAPQ-
      68      24      20: +AD0APQA9AD0AKgA9-
      70      14      16: +AD0APQA9ACo-
```

```

72      12      12:+AD0APQAq-
74      7      10:+AD0APQAq-
76     17      7:+AD0AKgA9AD0APQ-
78     24      6:+AD0AKgA9AD0APQA9-
80      7      4:+ACoAPQ-
82      4      3:+ACo-
84      4      3:+ACo-
86      2      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      3      1:+ACo-
92      3      1:+ACo-          :+ACoAPQA9-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     1      0:+AD0-          +ACoAPQ-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.30810.00343+ADs- mu+AD0- 8.0127
0.182
mean+AF8-var+AD0-43.495412.979, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.194470
Kolmogorov-Smirnov statistic: 0.0959 (N+AD0-28) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)   73 26.8      0.44
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)   66 24.8      1.7
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)   64 24.4      3.3
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)    55 21.4      3.9
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)    56 21.7      3.9
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)   57 22.1      4
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.8      5.1
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.8      5.1

```

gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
 (607) 60 23.2 7.2
 gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (607) 60 23.2 7.2
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.3 9.4
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.3 9.5
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.3 9.5

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 108.8 bits: 26.8 E(): 0.44
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (14-44:246-276)

	10	20	30	40
AAD-12	SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . .:: : . : .::			
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYT	QGVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT		
	220	230	240	250
				260
				270

	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSI	EDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK		
	280	290	300	310
				320
				330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.2 bits: 24.8 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (14-44:247-277)

	10	20	30	40
AAD-12	SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . .: : . : .::			
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKD	KGKYDLDFKPNPESDPSKWLS		
	220	230	240	250
				260
				270

	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET			
	:			
gi+AHw-232	GPQLADLYEQLISEYPIVSI	EDPFAEDDWDWVHFFERVGD	KIQIVGDDLTVTNPTRIKT	
	280	290	300	310
				320
				330

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)
 initn: 53 initl: 53 opt: 64 Z-score: 93.0 bits: 24.4 E(): 3.3
 Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
 in 80 aa overlap (3-78:431-510)

```

AAD-12                      SLLIGRHAHAIPGMDA---AESERFLEGLVDW
                               :. .... .: ... .: : : . .
gi+AHw-135 FKPLVEEPHNLVKTNCLEFELGEGYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
              410          420          430          440          450          460

```

```

      30          40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPET
      : :... . : . : : : : : : : . . . : : :
gi+AHw-135 CCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKCTESLVNRRPCFSALQVDET
              470          480          490          500          510          520

```

```

gi+AHw-135 YVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGSGFVD
              530          540          550          560          570          580

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 91.8 bits: 21.4 E(): 3.9
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (28-70:29-70)

```

              10          20          30          40          50
AAD-12 SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
                               : ::: : .. : .. : : :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAYCS
              10          20          30          40          50

```

```

      60          70          80
AAD-12 PWDFKLP---RVMWHSRLAGRPET
      :: : : :
gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
      60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 91.8 bits: 21.7 E(): 3.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (25-41:68-86)

```

              10          20          30          40          50
AAD-12 SLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                               : :::: : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTTYNSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMDF
              40          50          60          70          80          90

```

```

      60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPET

gi+AHw-219 SFDSDRSGLLLKQKVSDE
      100          110

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 57 Z-score: 91.5 bits: 22.1 E(): 4

Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
in 43 aa overlap (8-50:96-133)

```

                                10      20      30
AAD-12                      SLLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
                                .:    ... ..: .: .: .: .:
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRASLVDYLS-----H
                                70      80      90      100     110     120

```

```

                                40      50      60      70      80
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPET
                                .:    ...:
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                                130     140     150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (25-41:68-86)

```

                                10      20      30      40      50
AAD-12          SLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : .: .: .: .: .: .: .:
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMNF
                                40      50      60      70      80      90

```

```

                                60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPET

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
                                100     110     120     130     140     150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 89.7 bits: 21.8 E(): 5.1
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (25-41:68-86)

```

                                10      20      30      40      50
AAD-12          SLLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : .: .: .: .: .: .: .:
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMDF
                                40      50      60      70      80      90

```

```

                                60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPET

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
                                100     110     120     130     140     150

```

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName:

Full+AD0-Serum (607 aa)

initn: 51 init1: 51 opt: 60 Z-score: 87.0 bits: 23.2 E(): 7.2

Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (3-78:430-509)

```

                                10          20
AAD-12                      SLLIGRHAHAIPGMDA---AESERFLEGLVDW
                                :: :... :: ... :: : : .
gi+AHw-135 LKHLVDEPQNLIKQNCdqFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
           400          410          420          430          440          450

           30          40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPET
           : :. . . . . :: :... : . : . . : : . ::
gi+AHw-135 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTCKCTESLVNRRPCFSALTPDET
           460          470          480          490          500          510

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
           520          530          540          550          560          570

```

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin
+AFs-Bos t (607 aa)

initn: 51 initl: 51 opt: 60 Z-score: 87.0 bits: 23.2 E(): 7.2
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (3-78:430-509)

```

                                10          20
AAD-12                      SLLIGRHAHAIPGMDA---AESERFLEGLVDW
                                :: :... :: ... :: : : .
gi+AHw-333 LKHLVDEPQNLIKQNCdqFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
           400          410          420          430          440          450

           30          40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPET
           : :. . . . . :: :... : . : . . : : . ::
gi+AHw-333 CCTKPESERMPCTEDYLSLILNRLCVLHEKTPVSEKVTCKCTESLVNRRPCFSALTPDET
           460          470          480          490          500          510

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
           520          530          540          550          560          570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)

initn: 49 initl: 49 opt: 54 Z-score: 84.9 bits: 21.3 E(): 9.4
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (45-59:122-138)

```

           20          30          40          50          60          70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
           : :...: :...
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
           100          110          120          130          140          150

           80
AAD-12 RLAGRPET

```

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

[illegible]

```

82      4      3:+ACo-
84      4      3:+ACo-
86      2      2:+ACo-
88      0      2:+ACo-          inset +AD0- represents 1 library sequences
90      2      1:+ACo-
92      4      1:+ACo-          :+ACoAPQA9AD0-
94      0      1:+ACo-          :+ACo-
96      0      1:+ACo-          :+ACo-
98      1      0:+AD0-          +ACoAPQ-
100     0      0:              +ACo-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     1      0:+AD0-          +ACoAPQ-
110     0      0:              +ACo-
112     0      0:              +ACo-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120    0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.41700.00341+ADs- mu+AD0- 7.4795
0.181
mean+AF8-var+AD0-42.761712.729, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.196131
Kolmogorov-Smirnov statistic: 0.0972 (N+AD0-27) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 26.9      0.42
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 24.9      1.7
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  64 24.4      3.3
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)   55 21.5      3.7
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 21.8      3.7
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  57 22.1      3.9
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9      4.9
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9      4.9
gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
( 607)  60 23.3      7.2
gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (
607)  60 23.3      7.2
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.3      9.2

```

gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
 (210) 54 21.3 9.2
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.3 9.2

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 109.1 bits: 26.9 E(): 0.42
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (13-43:246-276)

```

                                10      20      30      40
AAD-12                      LLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . ::: : . : .: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220      230      240      250      260      270

```

```

                    50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETE
:
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.4 bits: 24.9 E(): 1.7
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (13-43:247-277)

```

                                10      20      30      40
AAD-12                      LLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . .: : . : .: .: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

                    50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETE
:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)
 initn: 53 initl: 53 opt: 64 Z-score: 93.1 bits: 24.4 E(): 3.3
 Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
 in 80 aa overlap (2-77:431-510)

```

                                10      20
AAD-12                      LLIGRHAHAIPGMDA---AESERFLEGLVDW
                                .. :... .: ... .: : : .
gi+AHw-135 FKPLVEEPHNLVKTNCLEFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
                410      420      430      440      450      460

```

```

30      40      50      60      70      80

```

AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETE

```

      :  :...  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-135 CCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSEKVTCCCTESLVNRRPCFSALQVDET
              470              480              490              500              510              520

```

```

gi+AHw-135 YVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGSFVD
              530              540              550              560              570              580

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:

Full+AD0-Chiti (91 aa)

initn: 43 initl: 43 opt: 55 Z-score: 92.2 bits: 21.5 E(): 3.7
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (27-69:29-70)

```

              10              20              30              40              50
AAD-12  LLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
              :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAYCS
              10              20              30              40              50

```

```

              60              70              80
AAD-12  PWDFKLP---RVMWHSRLAGRPETE
              :  :  :  :  :
gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
              60              70              80              90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1

+AFs-Alte (115 aa)

initn: 40 initl: 40 opt: 56 Z-score: 92.1 bits: 21.8 E(): 3.7
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (24-40:68-86)

```

              10              20              30              40              50
AAD-12  LLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
              :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
              40              50              60              70              80              90

```

```

              60              70              80
AAD-12  CLLHRAEPWDFKLPRVMWHSRLAGRPETE

```

```

gi+AHw-219 SFDSDRSGLLLKQKVSDE
              100              110

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:

Full+AD0-Globin (151 aa)

initn: 51 initl: 51 opt: 57 Z-score: 91.8 bits: 22.1 E(): 3.9
 Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
 in 43 aa overlap (7-49:96-133)

```

              10              20              30
AAD-12  LLIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
              :  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEFRASLVVDYLS-----H

```

```

          70          80          90          100          110          120
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETE
      ..      ...
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
          130          140          150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.9 E(): 4.9
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (24-40:68-86)

```

          10          20          30          40          50
AAD-12      LLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                        : : : : : : : : : : : : : : : : : :
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
          40          50          60          70          80          90

```

```

          60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETE

gi+AHw-456 SFGSDRSGLLLKQKVSDDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.0 bits: 21.9 E(): 4.9
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (24-40:68-86)

```

          10          20          30          40          50
AAD-12      LLIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                        : : : : : : : : : : : : : : : : : :
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
          40          50          60          70          80          90

```

```

          60          70          80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETE

gi+AHw-184 SFDSDRSGLLLKQKVSDDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
          100          110          120          130          140          150

```

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName:

Full+AD0-Serum (607 aa)

initn: 51 init1: 51 opt: 60 Z-score: 87.0 bits: 23.3 E(): 7.2
 Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
 in 80 aa overlap (2-77:430-509)

```

          10          20
AAD-12      LLIGRHAHAIPGMDA---AESERFLEGLVDW
                        : : : : : : : : : : : : : : : : : :
gi+AHw-135 LKHLVDEPQNLIKQNCQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR

```



```

      400      410      420      430      440      450
      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETE
      :  :  .  .  .  .  :  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-135 CCTKPESERMPCTEDYLSLIILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDET
      460      470      480      490      500      510

```

```

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin
+AFs-Bos t (607 aa)

initn: 51 initl: 51 opt: 60 Z-score: 87.0 bits: 23.3 E(): 7.2
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (2-77:430-509)

```

                                10      20
AAD-12                        LLIGRHAHAIPGMDA---AESERFLEGLVDW
                                :  :  :  :  :  :  :  :  :  :  :
gi+AHw-333 LKHLVDEPQNLIKQNCQDFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
      400      410      420      430      440      450

```

```

      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETE
      :  :  .  .  .  .  :  :  :  :  :  :  :  :  :  :  :
gi+AHw-333 CCTKPESERMPCTEDYLSLIILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDET
      460      470      480      490      500      510

```

```

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKKTVMENFVAFVD
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)

initn: 49 initl: 49 opt: 54 Z-score: 85.1 bits: 21.3 E(): 9.2
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (44-58:122-138)

```

      20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                                :  :  :  :  :  :  :  :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
      100      110      120      130      140      150

```

```

      80
AAD-12 RLAGRPETE

```

```

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
      160      170      180      190      200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)

initn: 49 initl: 49 opt: 54 Z-score: 85.0 bits: 21.3 E(): 9.2

1+AD4APqA+-AAD-12: 210 - 289 80 aa - 80 aa

```

      opt      E()
+ADw- 20      2      0: +AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2: +ACo-
      32      0      8: +ACo-
      34      18     21: +AD0APQA9AD0APQAq-
      36      18     44: +AD0APQA9AD0APQ- +ACo-
      38      25     72: +AD0APQ- +AD0APQA9AD0APQ- +ACo-
      40      97
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AK
g-
      42      66     123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
      44      141
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQA9-
      46      176
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
      48      183     132: +AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACoAPQA9A
D0APQA9AD0APQA9AD0APQA9AD0APQ-
      50      118
121: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9ACo-
      52      134
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0APQA9AD0-
      54      89
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
      56      67      76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
      58      60      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
      60      40      50: +AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
      62      51      40: +AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
      64      32      32: +AD0APQA9AD0APQA9AD0AKg-
      66      33      25: +AD0APQA9AD0APQA9ACoAPQA9-
      68      18      20: +AD0APQA9AD0AKg-
      70      19      16: +AD0APQA9ACoAPQ-
      72      10      12: +AD0APQAq-
      74      8       10: +AD0APQAq-
      76      14      7: +AD0AKgA9AD0-
      78      23      6: +AD0AKgA9- +AD0APQA9-
      80      9       4: +ACoAPQA9-
      82      5       3: +ACoAPQ-
      84      2       3: +ACo-
      86      4       2: +ACo-
      88      1       2: +ACo- inset +AD0- represents 1 library sequences
      90      2       1: +ACo-
      92      4       1: +ACo- : +ACoAPOA9AD0-

```

```

 94      0      1:+ACo-      :+ACo-
 96      0      1:+ACo-      :+ACo-
 98      1      0:+AD0-      +ACoAPQ-
100      0      0:          +ACo-
102      0      0:          +ACo-
104      0      0:          +ACo-
106      0      0:          +ACo-
108      0      0:          +ACo-
110      1      0:+AD0-      +ACoAPQ-
112      0      0:          +ACo-
114      0      0:          +ACo-
116      0      0:          +ACo-
118      0      0:          +ACo-
+AD4-120      0      0:          +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.42160.00335+ADs- mu+AD0- 7.3913
0.178
mean+AF8-var+AD0-42.071412.335, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.197734
Kolmogorov-Smirnov statistic: 0.1000 (N+AD0-28) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.0      0.39
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.0      1.6
gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
( 608)  64 24.5      3.1
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(  91)  55 21.6      3.5
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)  56 21.9      3.5
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  57 22.2      3.6
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 21.9      4.6
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 21.9      4.6
gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName: Full+AD0-Se
( 607)  60 23.3      6.8
gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin +AFs-B (
607)  60 23.3      6.8
gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (
608)  60 23.3      6.8
gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiar (
585)  59 23.0      8
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.4      8.7
gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
( 210)  54 21.4      8.8

```

gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.4 8.8

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 109.7 bits: 27.0 E(): 0.39
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (12-42:246-276)

```

                                10      20      30      40
AAD-12                        LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . .:: : . : .: .
gi+AHw-370 APDIKTAKEALDLIVSAIEAAGYTGQVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWIT
                220      230      240      250      260      270

```

```

                    50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEG
:
gi+AHw-370 GPQLAELYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.9 bits: 25.0 E(): 1.6
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (12-42:247-277)

```

                                10      20      30      40
AAD-12                        LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                                :::: :: . .: : . : .: .
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

                    50      60      70      80
AAD-12 GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEG
:
gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDVAWVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Serum (608 aa)
 initn: 53 initl: 53 opt: 64 Z-score: 93.6 bits: 24.5 E(): 3.1
 Smith-Waterman score: 64+ADs- 23.750+ACU- identity (53.750+ACU- similar)
 in 80 aa overlap (1-76:431-510)

```

                                10      20
AAD-12                        LIGRHAHAIPGMDA---AESERFLEGLVDW
                                .. :... .: ... .: : : .
gi+AHw-135 FKPLVEEPHNLVKTNCLEFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSK
                410      420      430      440      450      460

```

```

                30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
:  :... . : . : :: :... : . . . . : . :

```

gi+AHw-135 CCTHPEAERLSCAEDYLSVVLNRLCVLHEKTPVSESVTKCCTESLVNRRPCFSALQVDET
 470 480 490 500 510 520

gi+AHw-135 YVPKEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGSFVD
 530 540 550 560 570 580

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 43 initl: 43 opt: 55 Z-score: 92.6 bits: 21.6 E(): 3.5
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (26-68:29-70)

10 20 30 40 50
 AAD-12 LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
 : ::: : .. : . :: : .
 gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAYCS
 10 20 30 40 50

60 70 80
 AAD-12 PWDFKLP---RVMWHSRLAGRPETEG
 :: : : :
 gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
 60 70 80 90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.6 bits: 21.9 E(): 3.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (23-39:68-86)

10 20 30 40 50
 AAD-12 LIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : . . . : :: ... ::
 gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

60 70 80
 AAD-12 CLLHRAEPWDFKLPVVMWHSRLAGRPETEG

gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 57 Z-score: 92.3 bits: 22.2 E(): 3.6
 Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
 in 43 aa overlap (6-48:96-133)

10 20 30
 AAD-12 LIGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
 .: ... :. :. :. :. :.
 gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEFRASLVDYLS-----H
 70 80 90 100 110 120

40 50 60 70 80
 AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEG
 .: .:
 gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
 130 140 150

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 90.5 bits: 21.9 E(): 4.6
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (23-39:68-86)

10 20 30 40 50
 AAD-12 LIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : .: .: .:
 gi+AHw-456 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
 40 50 60 70 80 90

60 70 80
 AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
 gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)
 initn: 40 init1: 40 opt: 56 Z-score: 90.5 bits: 21.9 E(): 4.6
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (23-39:68-86)

10 20 30 40 50
 AAD-12 LIGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : .: .: .:
 gi+AHw-184 YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

60 70 80
 AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
 gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1351907+AHw-sp+AHw-P02769.4+AHw-ALBU+AF8-BOVIN RecName:
 Full+AD0-Serum (607 aa)
 initn: 51 init1: 51 opt: 60 Z-score: 87.4 bits: 23.3 E(): 6.8
 Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
 in 80 aa overlap (1-76:430-509)

10 20
 AAD-12 LIGRHAHAIPGMDA---AESERFLEGLVDW
 : .: .: .:
 gi+AHw-135 LKHLVDEPQNLIKQNCQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
 400 410 420 430 440 450

```

      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
      :  :. . . . . : : : : : : : . . . : :
gi+AHw-135 CCTKPESERMPCTEDYLSLIILNRLCVLHEKTPVSEKVTCKCTESLVNRRPCFSALTPDET
      460      470      480      490      500      510

```

```

gi+AHw-135 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKLTVMENFVAFVD
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-3336842+AHw-emb+AHw-CAA76847.1+AHw- bovine serum albumin
+AFs-Bos t (607 aa)
initn: 51 init1: 51 opt: 60 Z-score: 87.4 bits: 23.3 E(): 6.8
Smith-Waterman score: 60+ADs- 23.750+ACU- identity (50.000+ACU- similar)
in 80 aa overlap (1-76:430-509)

```

                                10      20
AAD-12                                LIGRHAHAIPGMDA---AESERFLEGLVDW
                                : : : : : : : : : :
gi+AHw-333 LKHLVDEPQNLIKQNCQFEKLGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTR
      400      410      420      430      440      450

```

```

      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
      :  :. . . . . : : : : : : : . . . : :
gi+AHw-333 CCTKPESERMPCTEDYLSLIILNRLCVLHEKTPVSEKVTCKCTESLVNRRPCFSALTPDET
      460      470      480      490      500      510

```

```

gi+AHw-333 YVPKAFDEKLFTFHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKLTVMENFVAFVD
      520      530      540      550      560      570

```

+AD4APg-gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis
familiaris+AF0- (608 aa)
initn: 54 init1: 54 opt: 60 Z-score: 87.4 bits: 23.3 E(): 6.8
Smith-Waterman score: 60+ADs- 23.810+ACU- identity (50.000+ACU- similar)
in 84 aa overlap (1-80:431-514)

```

                                10      20
AAD-12                                LIGRHAHAIPGMDA---AESERFLEGLVDW
                                :. : : : : : : : : :
gi+AHw-668 FKPLVDEPQNLVKTNCLEFEKLGEYGFQNALLVRYTKKAPQVSTPTLVEVSRKLGKVGTK
      410      420      430      440      450      460

```

```

      30      40      50      60      70      80
AAD-12 ACQAPRVHAHQWAAGDVVVDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
      :. :. . . : : : : : : : : : : : : : :
gi+AHw-668 CCKKPESERMSCAEDFLSVVLNRLCVLHEKTPVSEKVTCKCTESLVNRRPCFSGLEVDET
      470      480      490      500      510      520

```

```

gi+AHw-668 YVPKEFNAETFTFHADLCTLPEAEKQVKKQTALVELLKHKPKATDEQKLTVMGDFGAFVE
      530      540      550      560      570      580

```

+AD4APg-gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis
familiaris+AF0- (585 aa)
initn: 54 init1: 54 opt: 59 Z-score: 86.1 bits: 23.0 E(): 8

Smith-Waterman score: 59+ADs- 23.810+ACU- identity (50.000+ACU- similar)
in 84 aa overlap (1-80:408-491)

```

                                10          20
AAD-12                        LIGRHAHAIPGMDA---AESERFLEGLVDW
                                :. .... : ... .: : : .
gi+AHw-331 FKPLVDEPQNLVKTNCLEFEKLGEYGFQNALLVRYTKKAPQVSTPTLVEVSRKLGKVGTK
          380          390          400          410          420          430

          30          40          50          60          70          80
AAD-12 ACQAPRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEG
          :. :. . . : . : :: :. .... : . . . . :. . : :
gi+AHw-331 CCKKPESERMSCADDFLSVVLNRLCVLHEKTPVSESRVTKCCSESLVNRRCFSGLEVDET
          440          450          460          470          480          490

gi+AHw-331 YVPKEFNAETFTFHADLCTLPEAEKQVKKQTALVELLKHKPKATDEQLKTVMGDFGAFVE
          500          510          520          530          540          550

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.5 bits: 21.4 E(): 8.7
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (43-57:122-138)

```

          20          30          40          50          60          70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                                : :. .... : :.
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

          80
AAD-12 RLAGRPETEG

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (43-57:122-138)

```

          20          30          40          50          60          70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                                : :. .... : :.
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
          100          110          120          130          140          150

          80
AAD-12 RLAGRPETEG

gi+AHw-124 RKELAAVSDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
          160          170          180          190          200          210

```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus
gallus+AF0- (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (43-57:122-138)

```

                20      30      40      50      60      70
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                : : : : : : : : : : : : : : : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100      110      120      130      140      150

                80
AAD-12 RLAGRPETEG

gi+AHw-209 RKELAAVSDCSEYKPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
                160      170      180      190      200      210

```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:32 2010 done: Fri Feb 5 12:56:32 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 211 - 290 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

```

      opt      E()
+ADw- 20      2      0:+AD0-
      22      0      0: one +AD0- represents 4 library sequences
      24      0      0:
      26      0      0:
      28      0      0:
      30      0      2:+ACo-
      32      1      8:+AD0AKg-
      34      18     21:+AD0APQA9AD0APQAq-
      36      22     44:+AD0APQA9AD0APQA9- +ACo-
      38      26     72:+AD0APQA9AD0APQA9AD0- +ACo-

```

```

40      91
101: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+ACo-
42      70      123: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-
+ACo-
44      137
136: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9ACoAPQ-
46      175
138: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQ-
48      181
132: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0-
50      119      121: +AD0APQA9AD0APQA9AD0APQA9AD0APQ-
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
52      136
106: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP
QAqAD0APQA9AD0APQA9AD0-
54      92
91: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AKg-
56      63      76: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
58      59      62: +AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
60      44      50: +AD0APQA9AD0APQA9AD0APQA9AD0APQ- +ACo-
62      49      40: +AD0APQA9AD0APQA9AD0APQA9ACoAPQA9AD0-
64      31      32: +AD0APQA9AD0APQA9AD0AKg-
66      38      25: +AD0APQA9AD0APQA9ACoAPQA9AD0-
68      14      20: +AD0APQA9AD0AKg-
70      19      16: +AD0APQA9ACoAPQ-
72      10      12: +AD0APQAq-
74      8       10: +AD0APQAq-
76      15      7: +AD0AKgA9AD0-
78      23      6: +AD0AKgA9AD0APQA9-
80      11      4: +ACoAPQA9-
82      4       3: +ACo-
84      4       3: +ACo-
86      1       2: +ACo-
88      1       2: +ACo-          inset +AD0- represents 1 library sequences
90      2       1: +ACo-
92      3       1: +ACo-          : +ACoAPQA9-
94      0       1: +ACo-          : +ACo-
96      0       1: +ACo-          : +ACo-
98      1       0: +AD0-          +ACoAPQ-
100     0       0:              +ACo-
102     0       0:              +ACo-
104     0       0:              +ACo-
106     0       0:              +ACo-
108     0       0:              +ACo-
110     1       0: +AD0-          +ACoAPQ-
112     0       0:              +ACo-
114     0       0:              +ACo-
116     0       0:              +ACo-
118     0       0:              +ACo-
+AD4-120 0       0:              +ACo-

```

331323 residues in 1471 sequences

Expectation+AF8-n fit: $\rho(\ln(x))+AD0-4.45710.00337+ADs- \mu+AD0-7.21310.179$

mean+AF8-var+AD0-42.182212.320, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42

Lambda+AD0- 0.197474

Kolmogorov-Smirnov statistic: 0.0972 (N+AD0-29) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.090

The best scores are: opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En (439) 73 26.9 0.4

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno (440) 66 25.0 1.6

gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C (91) 55 21.5 3.5

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 21.9 3.5

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo (151) 57 22.2 3.7

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 21.9 4.6

gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 21.9 4.6

gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.6 5.7

gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (608) 59 23.0 8.4

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.4 8.8

gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.4 8.9

gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.4 8.9

gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiar (585) 58 22.7 9.9

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)

initn: 73 init1: 73 opt: 73 Z-score: 109.5 bits: 26.9 E(): 0.4
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (11-41:246-276)

	10	20	30	40
AAD-12	IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
	::: :: . : : . : . : .			
gi+AHw-370	APDIKTAK	EALDLIV	SAIEAAG	YTGQVDI
	220	230	240	250
				260
				270

	50	60	70	80
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGA			
	:			

gi+AHw-370 GPQLAELEYEQLLNEYPIVSIEDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK
 280 290 300 310 320 330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
 Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 98.7 bits: 25.0 E(): 1.6
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (11-41:247-277)

AAD-12 10 20 30 40
 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
 :::: :: . .: : . :.
 gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
 220 230 240 250 260 270

AAD-12 50 60 70 80
 GDVVVWDNRCLLHRAEPWDFKLPVMMWHSRLAGRPETEGA
 :
 gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVWHFFERVGDKIQIVGDDLTVTNPTRIKT
 280 290 300 310 320 330

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 43 initl: 43 opt: 55 Z-score: 92.6 bits: 21.5 E(): 3.5
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (25-67:29-70)

AAD-12 10 20 30 40 50
 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
 : :::: : . .: . . : : .
 gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAYCS
 10 20 30 40 50

AAD-12 60 70 80
 PWDFKLP---RVMWHSRLAGRPETEGA
 :: : : :
 gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
 60 70 80 90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.6 bits: 21.9 E(): 3.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (22-38:68-86)

AAD-12 10 20 30 40
 IGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : :::: :: ... ::
 gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

AAD-12 50 60 70 80
 CLLHRAEPWDFKLPVMMWHSRLAGRPETEGA

gi+AHw-219 SFDSDRSGLLLKQKVSDE
100 110

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 57 Z-score: 92.2 bits: 22.2 E(): 3.7
Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
in 43 aa overlap (5-47:96-133)

```

                                10      20      30
AAD-12                        IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
                                .:    ... ..:  .:  .:  .:
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEFFRASLVDYLS-----H
              70      80      90      100     110     120

              40      50      60      70      80
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGA
              .:    ... ..:
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
              130     140     150
```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 90.4 bits: 21.9 E(): 4.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (22-38:68-86)

```

                                10      20      30      40
AAD-12                        IGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  .:  .:  .:  .:  .:  .:
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMNF
              40      50      60      70      80      90

              50      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGA

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGNGPKDFVCQGVADAYITLVTLPKSS
              100     110     120     130     140     150
```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 90.4 bits: 21.9 E(): 4.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (22-38:68-86)

```

                                10      20      30      40
AAD-12                        IGRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                :  .:  .:  .:  .:  .:
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDTCSAQADKLEDHKWYSCGENSFMDF
              40      50      60      70      80      90

              50      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGA
```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)
 initn: 53 initl: 53 opt: 61 Z-score: 88.8 bits: 23.6 E(): 5.7
 Smith-Waterman score: 61+ADs- 23.377+ACU- identity (53.247+ACU- similar)
 in 77 aa overlap (3-75:434-510)

AAD-12 IGRHAHAIPGMDA---AESERFLEGLVDWACQ
 :... : : : : : : :
 gi+AHw-135 LVEEPHNLVKTNCLEFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSKCCT
 410 420 430 440 450 460

AAD-12 APRVHAHQWAAGDVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEGA
 :... : : : : : : : : : : : : :
 gi+AHw-135 HPEAERLSAEDYLSVVLNRLCVLHEKTPVSESVTKCCTESLVNRRPCFSALQVDETYVP
 470 480 490 500 510 520

gi+AHw-135 KEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKTKVMGDFGSFVDKCC
 530 540 550 560 570 580

+AD4APg-gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis
 familiaris+AF0- (608 aa)
 initn: 54 initl: 54 opt: 59 Z-score: 85.7 bits: 23.0 E(): 8.4
 Smith-Waterman score: 59+ADs- 26.415+ACU- identity (50.943+ACU- similar)
 in 53 aa overlap (28-79:462-514)

AAD-12 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNR-CLLHRAE
 :. :. : : : : : : : : : : : : :
 gi+AHw-668 LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCKKPESERMSCAEDFLSVVLNRLCVLHEKT
 440 450 460 470 480 490

AAD-12 PWDFKLPRVMWHSRLAGRPETEGA
 : . . . : : : : : : : : : : :
 gi+AHw-668 PVSERVTKCCSESLVNRRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
 500 510 520 530 540 550

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
 +AFs-Gallus gal (208 aa)
 initn: 49 initl: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8
 Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
 in 17 aa overlap (42-56:122-138)

AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLL--HRAEPWDFKLPRVMWHS
 : : : : : : : : : : : : : : : : : :
 gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
 100 110 120 130 140 150

10
20
30
40
50

AAD-12 IGRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAE

:
:
.
.
:
.
:
::
:::

gi+AHw-331 LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCCKKPESERMSCADDFLSVVLNRLCVLHEKT

410
420
430
440
450
460

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

```
1+AD4APgA+-AAD-12: 212 - 291 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
```

[illegible]

Kolmogorov-Smirnov statistic: 0.0963 (N+AD0-29) at 44

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1

join: 42, opt: 30, open/ext: -10/-2, width: 32

Scan time: 0.080

The best scores are: opt bits E(1471)

gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
(439) 73 27.0 0.39

gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
(440) 66 25.0 1.6

gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
(91) 55 21.6 3.4

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115)
56 21.9 3.5

gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
(151) 57 22.2 3.6

gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157)
56 21.9 4.6

gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157)
56 21.9 4.6

gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se
(608) 61 23.6 5.6

gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (608)
59 23.0 8.3

gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
(208) 54 21.4 8.7

gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo
(210) 54 21.4 8.8

gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210)
54 21.4 8.8

gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiar (585)
58 22.7 9.8

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName:
Full+AD0-Enolas (439 aa)

initn: 73 initl: 73 opt: 73 Z-score: 109.7 bits: 27.0 E(): 0.39
Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (10-40:246-276)

	10	20	30	
AAD-12	GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA			
	:	:	:	:
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYT	QGVDIAMDVASSEFYKDGLYDLDFKNPN	SDKSKWIT	
	220	230	240	250
	260	270		
	40	50	60	70
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA			
	:			
gi+AHw-370	GPQLAELYEQLLNEYPIVSI	EDPFAEDDWEAWSHFFSKVEGKTQIVGDDLT	VTNPRIKK	
	280	290	300	310
	320	330		

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName:
Full+AD0-Enolase (440 aa)

initn: 66 initl: 66 opt: 66 Z-score: 98.8 bits: 25.0 E(): 1.6

Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
in 31 aa overlap (10-40:247-277)

```

                        10      20      30
AAD-12                GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA
                        : : : : : : : : : : : :
gi+AHw-232 APDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLS
                220      230      240      250      260      270

```

```

                40      50      60      70      80
AAD-12          GDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA
                :
gi+AHw-232      GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
                280      290      300      310      320      330

```

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
Full+AD0-Chiti (91 aa)
initn: 43 init1: 43 opt: 55 Z-score: 92.7 bits: 21.6 E(): 3.4
Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
in 46 aa overlap (24-66:29-70)

```

                        10      20      30      40      50
AAD-12                GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
                        : : : : : : : : : : : :
gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN---WDLRAVSAYCS
                10      20      30      40      50

```

```

                60      70      80
AAD-12          PWDFKLP---RVMWHSRLAGRPETEGAA
                : : : :
gi+AHw-323      TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
                60      70      80      90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 init1: 40 opt: 56 Z-score: 92.7 bits: 21.9 E(): 3.5
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (21-37:68-86)

```

                        10      20      30      40
AAD-12                GRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                        : : : : : : : : : : : :
gi+AHw-219 YVWKISEFYGRKPEGTTYNSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
                40      50      60      70      80      90

```

```

                50      60      70      80
AAD-12          CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA

```

```

gi+AHw-219      SFDSDRSGLLLKQKVSDE
                100      110

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 init1: 51 opt: 57 Z-score: 92.3 bits: 22.2 E(): 3.6

Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
in 43 aa overlap (4-46:96-133)

```

                                10      20      30
AAD-12                        GRHAHAIPGMDAAESERFLEGLVDWACQAPRVH
                                .:    ... ..: .: .: .: .: .:
gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRASLVDYLS-----H
                                70      80      90      100     110     120

```

```

                                40      50      60      70      80
AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA
                                .:    ...:
gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
                                130     140     150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.5 bits: 21.9 E(): 4.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (21-37:68-86)

```

                                10      20      30      40
AAD-12                        GRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : .: .: .: .: .: .: .: .:
gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNF
                                40      50      60      70      80      90

```

```

                                50      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA

```

```

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                                100     110     120     130     140     150

```

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
subun (157 aa)

initn: 40 init1: 40 opt: 56 Z-score: 90.5 bits: 21.9 E(): 4.6
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (21-37:68-86)

```

                                10      20      30      40
AAD-12                        GRHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                                : .: .: .: .: .: .: .: .:
gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDF
                                40      50      60      70      80      90

```

```

                                50      60      70      80
AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA

```

```

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
                                100     110     120     130     140     150

```

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
Full+AD0-Serum (608 aa)

initn: 53 init1: 53 opt: 61 Z-score: 88.9 bits: 23.6 E(): 5.6

Smith-Waterman score: 61+ADs- 23.377+ACU- identity (53.247+ACU- similar)
in 77 aa overlap (2-74:434-510)

```

                                10          20
AAD-12                      GRHAHAIPGMDA---AESERFLEGLVDWACQ
                                :... :... :... :... :... :
gi+AHw-135 LVEEPHNLVKTNCLEFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSKCCT
              410          420          430          440          450          460

              30          40          50          60          70          80
AAD-12 APRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAA
              :... :... :... :... :... :... :... :... :
gi+AHw-135 HPEAERLSCAEDYLSVVLNRLCVLHEKTPVSESVTKCCTESLVNRRPCFSALQVDETYVP
              470          480          490          500          510          520

gi+AHw-135 KEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKTKVMGDFGSFVDKCC
              530          540          550          560          570          580

```

+AD4APg-gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis
familiaris+AF0- (608 aa)
initn: 54 initl: 54 opt: 59 Z-score: 85.8 bits: 23.0 E(): 8.3
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (50.943+ACU- similar)
in 53 aa overlap (27-78:462-514)

```

              10          20          30          40          50
AAD-12      GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAE
              :... :... :... :... :... :... :... :... :
gi+AHw-668 LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCKKPESERMSCAEDFLSVVLNRLCVLHEKT
              440          450          460          470          480          490

              60          70          80
AAD-12 PWDFKLPRVMWHSRLAGRPETEGAA
              :... :... :... :... :... :
gi+AHw-668 PVSESVTKCCTESLVNRRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
              500          510          520          530          540          550

```

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.5 bits: 21.4 E(): 8.7
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (41-55:122-138)

```

              20          30          40          50          60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
              :... :... :... :... :... :
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
              100          110          120          130          140          150

              70          80
AAD-12 RLAGRPETEGAA

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
              160          170          180          190          200

```

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:

Full+AD0-Ovomuco (210 aa)

initn: 49 initl: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)

in 17 aa overlap (41-55:122-138)

```

                20          30          40          50          60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                : : : : : : : : : : : : : : : : : :
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100          110          120          130          140          150
```

```

                70          80
AAD-12 RLAGRPETEGAA
```

```

gi+AHw-124 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
                160          170          180          190          200          210
```

+AD4APg-gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gallus+AF0- (210 aa)

initn: 49 initl: 49 opt: 54 Z-score: 85.4 bits: 21.4 E(): 8.8

Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)

in 17 aa overlap (41-55:122-138)

```

                20          30          40          50          60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
                : : : : : : : : : : : : : : : : : :
gi+AHw-209 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
                100          110          120          130          140          150
```

```

                70          80
AAD-12 RLAGRPETEGAA
```

```

gi+AHw-209 RKELAAVSVDCEYKPKDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC
                160          170          180          190          200          210
```

+AD4APg-gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiaris+AF0- (585 aa)

initn: 54 initl: 54 opt: 58 Z-score: 84.6 bits: 22.7 E(): 9.8

Smith-Waterman score: 58+ADs- 26.415+ACU- identity (50.943+ACU- similar)

in 53 aa overlap (27-78:439-491)

```

                10          20          30          40          50
AAD-12 GRHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAE
                : . . . . : . : : : : :
gi+AHw-331 LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCCKKPESERMSCADDFLSVVLNRLCVLHEKT
                410          420          430          440          450          460
```

```

                60          70          80
AAD-12 PWDFKLPRVMWHSRLAGRPETEGAA
                : . . . . : . : : : :
gi+AHw-331 PVSERVTKCCSESLVNRRCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
                470          480          490          500          510          520
```

80 residues in 1 query sequences
331323 residues in 1471 library sequences
Scomplib +AFs-34t26+AF0-
start: Fri Feb 5 12:56:32 2010 done: Fri Feb 5 12:56:32 2010
Total Scan time: 0.080 Total Display time: 0.010

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-
+ACM- fasta -Q -d 500 -E 10 fasta+AF8-input.txt
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta 1
FASTA searches a protein or DNA sequence data bank
version 3.4t26 July 7, 2006
Please cite:

W.R. Pearson +ACY- D.J. Lipman PNAS (1988) 85:2444-2448

Query library fasta+AF8-input.txt vs
/bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library
searching /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

1+AD4APgA+-AAD-12: 213 - 292 80 aa - 80 aa
vs /bioinformatics/Allergenicity/FARRPV10/FARRPV10.fasta library

	opt	E()	
+ADw-	20	2	0:+AD0-
22	0	0:	one +AD0- represents 4 library sequences
24	0	0:	
26	0	0:	
28	0	0:	
30	0	2:+ACo-	
32	1	8:+AD0AKg-	
34	18	21:+AD0APQA9AD0APQAq-	
36	19	44:+AD0APQA9AD0APQ- +ACo-	
38	30	72:+AD0APQA9AD0APQA9AD0APQ- +ACo-	
40	98		
101:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AK			
g-			
42	77	123:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-	
+ACo-			
44	143		
136:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9ACoAPQA9-			
46	186		
138:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQA9AD0AKgA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-			
48	177		
132:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QA9AD0APQA9AD0APQAqAD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9-			
50	110	121:+AD0APQ-	
+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQ-			
+ACo-			
52	128		
106:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0AP			
QAqAD0APQA9AD0APQ-			


```

54      84
91:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9- +ACo-
56      61      76:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
58      60      62:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0- +ACo-
60      46      50:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
62      47      40:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
64      35      32:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
66      34      25:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
68      14      20:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
70      19      16:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
72      11      12:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
74      7       10:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
76      15      7:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
78      21      6:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
80      10      4:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
82      5       3:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
84      3       3:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
86      2       2:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
88      1       2:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
90      2       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
92      3       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
94      0       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
96      0       1:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
98      1       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
100     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
102     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
104     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
106     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
108     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
110     1       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
112     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
114     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
116     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
118     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
+AD4-120     0       0:+AD0APQA9AD0APQA9AD0APQA9AD0APQA9AD0APQA9ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.38820.00339+ADs- mu+AD0- 7.5941
0.180
mean+AF8-var+AD0-41.508612.074, 0's: 2 Z-trim: 3 B-trim: 15 in 1/42
Lambda+AD0- 0.199070
Kolmogorov-Smirnov statistic: 0.0870 (N+AD0-29) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.080
The best scores are:
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439) 73 27.0 0.37
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440) 66 25.0 1.5
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91) 55 21.6 3.4

```

gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (115) 56 21.9 3.4
 gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo (151) 57 22.3 3.5
 gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 (157) 56 22.0 4.5
 gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s (157) 56 22.0 4.5
 gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName: Full+AD0-Se (608) 61 23.7 5.4
 gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (608) 59 23.1 8
 gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus (208) 54 21.5 8.5
 gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName: Full+AD0-Ovo (210) 54 21.5 8.6
 gi+AHw-209979542+AHw-gb+AHw-ACJ04729.1+AHw- ovomucoid +AFs-Gallus gall (210) 54 21.5 8.6
 gi+AHw-3319897+AHw-emb+AHw-CAA76841.1+AHw- albumin +AFs-Canis familiar (585) 58 22.8 9.5

+AD4APg-gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-Enolas (439 aa)
 initn: 73 initl: 73 opt: 73 Z-score: 110.1 bits: 27.0 E(): 0.37
 Smith-Waterman score: 73+ADs- 35.484+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (9-39:246-276)

	10	20	30
AAD-12	RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA		
	...	:	:
gi+AHw-370	APDIKTAKEALDLIVSAIEAAGYT	QGVDIAMDVASSEFYKDGLYDLDFKPNPNSDKSKWIT	
	220	230	240
	250	260	270
	40	50	60
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL		
	:		
gi+AHw-370	GPQLAELYEQLLNEYPIVSI	EDPFAEDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKK	
	280	290	300
	310	320	330

+AD4APg-gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Enolase (440 aa)
 initn: 66 initl: 66 opt: 66 Z-score: 99.2 bits: 25.0 E(): 1.5
 Smith-Waterman score: 66+ADs- 32.258+ACU- identity (54.839+ACU- similar)
 in 31 aa overlap (9-39:247-277)

	10	20	30
AAD-12	RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAA		
	...	:	:
gi+AHw-232	APDIKTPKEALDLIMDAIDKAGYKGVGIAMDVASSEFYKDGKYDLDFKPNPESDPSKWLS		
	220	230	240
	250	260	270
	40	50	60
AAD-12	GDVVVDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL		
	:		

gi+AHw-232 GPQLADLYEQLISEYPIVSIEDPFAEDDWDAAVHFFERVGDKIQIVGDDLTVTNPTRIKT
 280 290 300 310 320 330

+AD4APg-gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName:
 Full+AD0-Chiti (91 aa)
 initn: 43 initl: 43 opt: 55 Z-score: 92.9 bits: 21.6 E(): 3.4
 Smith-Waterman score: 55+ADs- 30.435+ACU- identity (41.304+ACU- similar)
 in 46 aa overlap (23-65:29-70)

AAD-12 RHAHAIPGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE
 : ::: : .. : .. :: :
 gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYNPAQNN--WDLRAVSAYCS
 10 20 30 40 50

AAD-12 PWDFKLP---RVMWHSRLAGRPETEGAAL
 :: : : :
 gi+AHw-323 TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
 60 70 80 90

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
 +AFs-Alte (115 aa)
 initn: 40 initl: 40 opt: 56 Z-score: 92.8 bits: 21.9 E(): 3.4
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (20-36:68-86)

AAD-12 RHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : :: ... ::
 gi+AHw-219 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL
 gi+AHw-219 SFDSDRSGLLLKQKVSDE
 100 110

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
 Full+AD0-Globin (151 aa)
 initn: 51 initl: 51 opt: 57 Z-score: 92.5 bits: 22.3 E(): 3.5
 Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
 in 43 aa overlap (3-45:96-133)

AAD-12 RHAHAIPGMDAAESERFLEGLVDWACQAPRVH
 .: ... :. :. :. :. :.
 gi+AHw-121 IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEFRASLVDYLS-----H
 70 80 90 100 110 120

AAD-12 AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL

gi+AHw-121 HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
 130 140 150

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
 subu (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 90.7 bits: 22.0 E(): 4.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (20-36:68-86)

 10 20 30 40
 AAD-12 RHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : : : : . . . : :
 gi+AHw-456 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
 40 50 60 70 80 90

 50 60 70 80
 AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL

gi+AHw-456 SFGSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1
 subun (157 aa)

initn: 40 initl: 40 opt: 56 Z-score: 90.7 bits: 22.0 E(): 4.5
 Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
 in 19 aa overlap (20-36:68-86)

 10 20 30 40
 AAD-12 RHAHAIPGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
 : : : : . . . : :
 gi+AHw-184 YVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
 40 50 60 70 80 90

 50 60 70 80
 AAD-12 CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL

gi+AHw-184 SFDSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS
 100 110 120 130 140 150

+AD4APg-gi+AHw-1351908+AHw-sp+AHw-P49064.1+AHw-ALBU+AF8-FELCA RecName:
 Full+AD0-Serum (608 aa)

initn: 53 initl: 53 opt: 61 Z-score: 89.2 bits: 23.7 E(): 5.4
 Smith-Waterman score: 61+ADs- 23.377+ACU- identity (53.247+ACU- similar)
 in 77 aa overlap (1-73:434-510)

 10 20
 AAD-12 RHAHAIPGMDA---AESERFLEGLVDWACQ
 : : : : . . . : :
 gi+AHw-135 LVEEPHNLVKTNCELFEKLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRLGKVGSKCCT
 410 420 430 440 450 460

 30 40 50 60 70 80
 AAD-12 APRVHAHQWAAGDVVVWDNR-CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAAL
 : : : : . . . : : : : . . . : : : : . . . : :

gi+AHw-135 HPEAERLSCAEDYLSVVLNRLCVLHEKTPVSERVTKCCTESLVNRRPCFSALQVDETYVP
470 480 490 500 510 520

gi+AHw-135 KEFSAETFTFHADLCTLPEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGSFVDKCC
530 540 550 560 570 580

+AD4APg-gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis
familiaris+AF0- (608 aa)
initn: 54 initl: 54 opt: 59 Z-score: 86.1 bits: 23.1 E(): 8
Smith-Waterman score: 59+ADs- 26.415+ACU- identity (50.943+ACU- similar)
in 53 aa overlap (26-77:462-514)

10 20 30 40 50
AAD-12 RHAAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNR-CLLHRAE
:
gi+AHw-668 LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCKKPESERMSCAEDFLSVVLNRLCVLHEKT
440 450 460 470 480 490

60 70 80
AAD-12 PWDFKLPRVMWHSRLAGRPETEGAAL
:
gi+AHw-668 PVSERVTKCCSESLVNRRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
500 510 520 530 540 550

+AD4APg-gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid
+AFs-Gallus gal (208 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.7 bits: 21.5 E(): 8.5
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (40-54:122-138)

10 20 30 40 50 60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLL--HRAEPWDFKLPRVMWHS
:
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

70 80
AAD-12 RLAGRPETEGAAL

gi+AHw-162 RKELAAVDCSEYPKPDCTAEDRPLCGSDNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
160 170 180 190 200

+AD4APg-gi+AHw-124757+AHw-sp+AHw-P01005.1+AHw-IOVO+AF8-CHICK RecName:
Full+AD0-Ovomuco (210 aa)
initn: 49 initl: 49 opt: 54 Z-score: 85.6 bits: 21.5 E(): 8.6
Smith-Waterman score: 54+ADs- 52.941+ACU- identity (82.353+ACU- similar)
in 17 aa overlap (40-54:122-138)

10 20 30 40 50 60
AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVWDNRCLL--HRAEPWDFKLPRVMWHS
:
gi+AHw-124 MNCSSYANTTSEDGKVMVLCNRAFNPVCGTDGVTYDNECLLCAHKVEQGASVDKRHDGGC
100 110 120 130 140 150

[illegible]

```

74      10      10:+AD0APQAq-
76      9       7:+AD0AKgA9-
78     19      6:+AD0AKgA9AD0APQ-
80     18      4:+ACoAPQA9AD0APQ-
82      7      3:+ACoAPQ-
84      1      3:+ACo-
86      4      2:+ACo-
88      1      2:+ACo-          inset +AD0- represents 1 library sequences
90      0      1:+ACo-
92      2      1:+ACo-          :+ACoAPQ-
94      3      1:+ACo-          :+ACoAPQA9-
96      0      1:+ACo-          :+ACo-
98      0      0:              +ACo-
100     1      0:+AD0-          +ACoAPQ-
102     0      0:              +ACo-
104     0      0:              +ACo-
106     0      0:              +ACo-
108     0      0:              +ACo-
110     0      0:              +ACo-
112     1      0:+AD0-          +ACoAPQ-
114     0      0:              +ACo-
116     0      0:              +ACo-
118     0      0:              +ACo-
+AD4-120      0      0:              +ACo-
331323 residues in 1471 sequences
Expectation+AF8-n fit: rho(ln(x))+AD0- 4.32680.00338+ADs- mu+AD0- 7.8660
0.179
mean+AF8-var+AD0-39.030511.909, 0's: 2 Z-trim: 3 B-trim: 59 in 2/41
Lambda+AD0- 0.205292
Kolmogorov-Smirnov statistic: 0.0823 (N+AD0-29) at 42

FASTA (3.5 Sept 2006) function +AFs-optimized, BL50 matrix (15:-5)+AF0-
ktup: 1
join: 42, opt: 30, open/ext: -10/-2, width: 32
Scan time: 0.090
The best scores are:                                opt bits E(1471)
gi+AHw-37078092+AHw-sp+AHw-Q870B9.1+AHw-ENO+AF8-RHORB RecName: Full+AD0-En
( 439)  73 27.4      0.29
gi+AHw-232054+AHw-sp+AHw-P30575.1+AHw-ENO1+AF8-CANAL RecName: Full+AD0-Eno
( 440)  66 25.4      1.2
gi+AHw-32363456+AHw-sp+AHw-P81729.1+AHw-CHAL+AF8-BRARA RecName: Full+AD0-C
( 91)   55 21.8      2.8
gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1 +AFs- (
115)   56 22.2      2.9
gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName: Full+AD0-Glo
( 151)  57 22.5      3
gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1 ( 157)
56 22.2      3.8
gi+AHw-1842045+AHw-gb+AHw-AAB47552.1+AHw- major allergen Alt a 1 s ( 157)
56 22.2      3.8
gi+AHw-6687188+AHw-emb+AHw-CAB64867.1+AHw- albumin +AFs-Canis familiar (
608)   59 23.3      6.8
gi+AHw-162952006+AHw-ref+AHw-NP+AF8-001106132.1+AHw- ovomucoid +AFs-Gallus
( 208)  54 21.7      7.3

```


10
20
30
40
50

AAD-12 HAHAI PGMDAAE SERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLLHRAE

:
::
:
..
:
..
::
:

gi+AHw-323 QAGGQTCAGNICCSQYGYCGTTADYCSPDNNCQATY-HYYPNQNN--WDLRAVSAYCS

10
20
30
40
50

```

        60          70          80
AAD-12  PWDFKLP---RVMWHSRLAGRPETEGAALV
        ::  :  :  :
gi+AHw-323  TWDADKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR
        60          70          80          90

```

+AD4APg-gi+AHw-21913174+AHw-gb+AHw-AAM77471.1+AHw- major allergen alt a1
+AFs-Alte (115 aa)
initn: 40 initl: 40 opt: 56 Z-score: 94.2 bits: 22.2 E(): 2.9
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (19-35:68-86)

```

                10          20          30          40
AAD-12          HAHAI PGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                :  :::::  ::  ...  ::
gi+AHw-219  YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDF
        40          50          60          70          80          90

```

```

        50          60          70          80
AAD-12  CLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV

gi+AHw-219  SFDSDRSGLLLKQKVSDE
        100          110

```

+AD4APg-gi+AHw-121237+AHw-sp+AHw-P02227.1+AHw-GLB8+AF8-CHITH RecName:
Full+AD0-Globin (151 aa)
initn: 51 initl: 51 opt: 57 Z-score: 93.9 bits: 22.5 E(): 3
Smith-Waterman score: 57+ADs- 27.907+ACU- identity (48.837+ACU- similar)
in 43 aa overlap (2-44:96-133)

```

                10          20          30
AAD-12          HAHAI PGMDAAESERFLEGLVDWACQAPRVH
                :  ::  ::  ::  ::  :::::  :
gi+AHw-121  IVGFFSEVIGLIGNPENRPALKTLIDGLASSHKARGIEKAQFEEFRASLVDYLS-----H
        70          80          90          100          110          120

```

```

        40          50          60          70          80
AAD-12  AHQWAAGDVVVWDNRCLLHRAEPWDFKLPRVMWHSRLAGRPETEGAALV
        ::  :::
gi+AHw-121  HLDWNDTMKSTWDLALNNMFFYILHALEVAQ
        130          140          150

```

+AD4APg-gi+AHw-45680856+AHw-gb+AHw-AAS75297.1+AHw- major allergen Alt a 1
subu (157 aa)
initn: 40 initl: 40 opt: 56 Z-score: 92.0 bits: 22.2 E(): 3.8
Smith-Waterman score: 56+ADs- 36.842+ACU- identity (73.684+ACU- similar)
in 19 aa overlap (19-35:68-86)

```

                10          20          30          40
AAD-12          HAHAI PGMDAAESERFLEGLVDWAC--QAPRVHAHQWAAGDVVVWDNR
                :  :::::  ::  ...  ::
gi+AHw-456  YVWKISEFYGRKPEGTYYNISLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMNF
        40          50          60          70          80          90

```

AAD-12 DAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNRCLL--HRAEPWDFKLPRVMWHS
:
gi+AHw-162 MNCSSYANTTSEDGKVMVLCNRAFNPVC GTDGV TYDNECLLCAHKVEQGASVDKRHDGGC

10
20
30
40
50

AAD-12 HAHAI PGMDAAESERFLEGLVDWACQAPRVHAHQWAAGDVVVWDNR-CLLHRAE

..
..
.
.
:
.
:
::
:::
:::

gi+AHw-331 LVRYTKKAPQVSTPTLVEVSRKLGKVGTKCCKKPESERMSCADDFLSVVLNRLCVLHEKT

410
420
430
440
450
460

```

      60      70      80
AAD-12 PWDFKLPRVMWHSRLAGRPETEGAALV
      : . . . . : . : :
gi+AHw-331 PVSERVTKCCSESLVNRRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQT
      470      480      490      500      510      520
```

80 residues in 1 query sequences

331323 residues in 1471 library sequences

Scomplib +AFs-34t26+AF0-

start: Fri Feb 5 12:56:34 2010 done: Fri Feb 5 12:56:34 2010

Total Scan time: 0.090 Total Display time: 0.000

Function used was FASTA +AFs-version 3.4t26 July 7, 2006+AF0-