

**Report Title**

**Updated Bioinformatics Evaluation of  $\Delta 6$  and  $\Delta 15$  Desaturases Utilizing the  
AD\_2009, TOX\_2009 and PRT\_2009 Databases**

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## 1.0 Summary

Monsanto has developed soybean, MON 87769, which produces stearidonic acid (SDA), an omega-3 fatty acid. Production of SDA in soybean seed was achieved through the introduction of genes encoding *Neurospora crassa*  $\Delta 15$  desaturase (Nc $\Delta 15$ D) and *Primula juliae*  $\Delta 6$  desaturase (Pj $\Delta 6$ D) via *Agrobacterium*-mediated transformation.

The bioinformatic evaluation of the Pj $\Delta 6$ D and Nc $\Delta 15$ D contained in MON 87769 was previously conducted by Silvanovich and McClain (2008). In the 2008 analysis it was concluded that the bioinformatic search data indicated the lack of both structurally and immunologically relevant similarities between the Pj $\Delta 6$ D and Nc $\Delta 15$ D protein sequences and known allergens, toxins, or other biologically active proteins that may have an adverse effect on the health of animals or humans.

The results of these most recent bioinformatics evaluations using the AD\_2009, TOX\_2009 and PRT\_2009 databases contained herein parallel those of Silvanovich and McClain (2008). When combined, these new data confirm the previously reported conclusion (Silvanovich and McClain, 2008) that no meaningful sequence or inferred structural similarity exists between Pj $\Delta 6$ D and Nc $\Delta 15$ D and allergenic or toxic proteins or proteins of concern to human or animal health.

## 2.0 Sequence Database Preparation

The allergen, gliadin, and glutenin sequence database (AD\_2009) was obtained from the Food Allergy Research and Resource Program Database (FARRP, 2009)<sup>1</sup> and was used as provided. The AD\_2009 database contains 1,386 sequences. A complete description of the AD\_2009 database can be found in Silvanovich (2009).

GenBank protein database, release 169.0 (December 16, 2008), was downloaded from NCBI (National Center for Biotechnology Information) and formatted for use. It is referred to herein as the PRT\_2009 database and contains 14,717,352 sequences. A complete description of the PRT\_2009 database can be found in Silvanovich (2009).

The toxin database is a subset of sequences derived from the PRT\_2009 database that was selected using a keyword search and filtered to remove likely non-toxin proteins. It is referred to herein as the TOX\_2009 database and contains 7,651 sequences. A complete description of the TOX\_2009 database can be found in Silvanovich (2009).

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<sup>1</sup> located at <http://www.allergenonline.com>

### 3.0 Sequence Database Searches

The PjΔ6D and NcΔ15D query sequences used in this analysis were the same as previously described in Silvanovich and McClain (2008). FASTA analyses using the AD\_2009, TOX\_2009, and PRT\_2009 databases were performed on a desktop computer loaded with a SUSE LINUX version 10.1 operating system. The structural similarity between the query peptides and sequences in the AD\_2009, TOX\_2009, and PRT\_2009 databases was assessed using the FASTA algorithm (Lipman and Pearson, 1985; Pearson and Lipman, 1988). FASTA comparisons are initiated by aligning the first match of a specific wordsize. The alignment is then extended based on the chosen scoring matrix. Specific FASTA comparison parameters used in this study included a wordsize (k-tuple) of two, a gap creation penalty of 10, a gap extension penalty of two, and an expectation threshold (*E*-score) of one. FASTA comparisons were performed using the BLOSUM50 scoring matrix (Henikoff and Henikoff, 1992). The BLOSUM matrix series (Henikoff and Henikoff, 1992) was derived from a set of aligned, ungapped regions from protein families, called the BLOCKS database. Sequences from each block were clustered based on the percent of identical residues in the alignments (Henikoff and Henikoff, 1996). The BLOSUM50 matrix will identify blocks of conserved residues that are at least 50% identical. BLOSUM50 works well for identifying sequence similarities that include gaps, and thus recognizes distant evolutionary relationships (Pearson, 2000). In instances where greater than 25 alignments displaying an *E*-score less than one were recovered, alignment data is only shown for the top 25 alignments.

In addition to the FASTA comparisons of each query sequence to allergens (to assess overall structural similarity), an eight amino acid sliding window search was performed. An algorithm was developed to identify whether or not a linearly contiguous match of eight amino acids existed between the query sequence and sequences within the allergen database (AD\_2009). This program compares the query sequence to each protein sequence in the allergen database using a sliding-window of eight amino acids; that is, with a seven amino acid overlap relative to the preceding window.

### 4.0 Significance of the Alignment

An *E*-score of  $1 \times 10^{-5}$  was set as an initial high cut-off value for alignment significance. Although all alignments were inspected visually, any aligned sequence that yielded an *E*-score less than or equal to  $1 \times 10^{-5}$  was analyzed further to determine if such an alignment represented significant sequence homology.

### 5.0 Results and Discussion

Bioinformatics analysis was performed on PjΔ6D and NcΔ15D protein sequences (Figures 1 and 2) to assess the potential for structural similarity with known allergens, toxins, or other biologically active proteins. Summaries of the top alignments from the analyses are shown

in Tables 1-6. The supporting dataset output files for all of the analyses are presented in Appendices 1 and 2. The results of these assessments parallel those described in Silvanovich and McClain (2008).

### 5.1 *Assessment of Potential Allergenicity for the PjΔ6D protein sequence*

Potential structural identity and similarity shared between the PjΔ6D protein (Figure 1) and proteins in the allergen database were evaluated using the FASTA sequence alignment program. Identified proteins were ranked according to their degree of similarity (Appendix 1). None of these aligned proteins yielded an *E*-score of less than  $1 \times 10^{-5}$  nor did any alignments meet the Codex Alimentarius (2003) threshold for potential allergenicity.

No immunologically relevant sequences of eight contiguous amino acid identities were detected when the PjΔ6D protein sequence was compared to the AD\_2009 sequence using a sliding window search (Appendix 1).

### 5.2 *Assessment of Potential Toxicity for the PjΔ6D protein sequence:*

Potential structural identity and similarity shared between the PjΔ6D protein and proteins in the TOX\_2009 database was evaluated using the FASTA sequence alignment program. No alignments displaying an *E*-score of 1 or less were observed (Table 2 and Appendix 1).

### 5.3 *Assessment of Potential Adverse Biological Activity for the PjΔ6D protein sequence:*

Potential structural similarities shared between the PjΔ6D protein and proteins in the PRT\_2009 database were evaluated using the FASTA sequence alignment program. Identified proteins were ranked according to their degree of similarity (Table 3 and Appendix 1).

The FASTA algorithm identified and aligned a total of 2566 proteins in the PRT\_2009 database that yielded an alignment *E*-score of 1 or less and of those, 779 displayed an *E*-score of  $1 \times 10^{-5}$  or less. Visual inspection of these alignments revealed that many alignments were with proteins described as being fatty acid desaturases. The top alignment observed for the PjΔ6D sequence was to an unnamed protein product (GI-151416086) from *Primula luteola* (Table 2). The alignment demonstrated 89.438% identity over the full length of both the query and aligned proteins with an *E*-score of  $6.2 \times 10^{-188}$ . The next six alignments were identical to one another and one of these, with GI -30350277, was identified as being a delta-6 desaturase. Based upon the top seven alignments, it is concluded that the PjΔ6D is a Δ6 desaturase and that there is no indication of the potential for harmful biological activity.

#### 5.4 *Assessment of Potential Allergenicity for the NcΔ15D protein sequence:*

Potential structural identity and similarity shared between the NcΔ15D protein (Figure 2) and proteins in the allergen database were evaluated using the FASTA sequence alignment program. Identified proteins were ranked according to their degree of similarity (Appendix 2). None of these aligned proteins yielded an *E*-score of less than or equal to  $1 \times 10^{-5}$  nor did any alignments meet the Codex Alimentarius (2003) threshold for potential allergenicity.

As was described in Silvanovich and McClain (2008), a single potential immunologically relevant sequence of eight contiguous amino acid identities was detected when the NcΔ15D protein sequence (Figure 2) was compared to the AD\_2009 sequence database (Appendix 2) using a sliding window search. The alignment consisted of eight consecutive serine residues (SSSSSSSS) in the NcΔ15D query sequence with a region of nine consecutive serine residues in *Triticum aestivum* serine carboxypeptidase. Polyserine tracts such as that contained in the NcΔ15D are a common motif that are found in numerous proteins. Proteins containing stretches of eight or more serine residue represent functionally diverse classes, including enzymes, signaling molecules, structural proteins and transport molecules (Faux et al., 2005).

#### 5.5 *Assessment of Potential Toxicity for the NcΔ15D protein sequence:*

Potential structural identity and similarity shared between the NcΔ15D protein and proteins in the TOX\_2009 database was evaluated using the FASTA sequence alignment program. No alignments displaying an *E*-score of 1 or less were observed (Table 5 and Appendix 2).

#### 5.6 *Assessment of Potential Adverse Biological Activity for the NcΔ15D protein sequence:*

Potential structural similarities shared between the NcΔ15D protein and proteins in the PRT\_2009 database were evaluated using the FASTA sequence alignment program. Identified proteins were ranked according to their degree of similarity (Table 6 and Appendix 2).

The FASTA algorithm identified and aligned a total of 1,786 proteins in the PRT\_2009 database that yielded an alignment *E*-score of  $\leq 1$  and of those 1,303 displayed an *E*-score less than  $1 \times 10^{-5}$ . Visual inspection of these alignments revealed that most alignments were with proteins described as being a fatty acid desaturase. The top alignment observed for the NcΔ15D sequence was to a hypothetical protein CHGG\_0 (GI-88181398) from *Chaetomium globosum* (Table

6). Annotation associated with GI-88181398 describes the protein sequence as being Delta12 Fatty Acid Desaturase-like. The alignment demonstrated 67.519% identity over the 391 amino acids with an *E*-score of  $1.2 \times 10^{-120}$ . Based upon the top alignment, it is concluded that the NcΔ15D is a Δ15 desaturase and that there is no indication of the potential for harmful biological activity.

## 6.0 Conclusions

A bioinformatics analysis of PjΔ6D and NcΔ15D protein sequences was conducted to determine if either protein shared significant structural similarities with known allergens, toxins, or biologically active protein sequences contained in the AD\_2009, TOX\_2009 and PRT\_2009 databases, respectively. The bioinformatics results indicate that no biologically relevant sequence similarities were observed between the PjΔ6D and NcΔ15D protein sequences and any known allergens, biologically active proteins, or human and animal toxins. These results and conclusions of this current analysis parallel those described in Silvanovich and McClain (2008).

## 7.0 References

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- Silvanovich, A. (2009). The assembly of AD\_2009, TOX\_2009 and PRT\_2009. Monsanto Technical Report MSL0021840, St. Louis, MO.
- Silvanovich, A. and McClain, J. S. (2008). Bioinformatics Evaluation of Delta 6 and Delta 15 desaturases Utilizing the AD8, TOXIN6 and PROTEIN Databases. Monsanto Technical Report MSL0021252, St. Louis, MO.

Figure 1 Amino Acid Sequence of *Primula juliae* PjΔ6D Protein

```
>del_6
MTKTIIYITSSELEKHNKPGDLWISIHGQVDVSSWAALHPGGIAPLLALAGHDVTD AFL
AYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLLDSFHKMG MFRARGHTAYATFVIM
ILMLVSSVTGVLCS ENPWVHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWN RFAQIL
SSNCLQGISIGWWKWNHNAHHIACNSLEYD PDLQYIPLL VVSPKFFNSLTSRFYDKKLN
FDGVS RFLVQYQHWSFY PVMCVARLNMLAQS FILLFSRREVANRVQEILGLAVFWLWFP
LLL SCLPNWGERIMFLLASYSVTGIQH VQFSLNHFSSDVYVGPPVGN DWFKKQTAGTLN
ISCPAWMDW FHGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYN IASFTKANV
LTLET LRNTAIEARDLSNPIPKNMVWEAVKNVG
```

Figure 2 Amino Acid Sequence of the *Neurospora crassa* Nc $\Delta$ 15D Protein

```
>del_15  
MAVTTRSHKAAAATEPEVVSTGVDAVSAAAPSSSSSSSSSQKSAEPIEYPDIKTIRD  
AIPDHCFRPRVWISMAFYIRDFAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTG  
IWILAHECGHGAFSRHTWFNNVMGWIGHSFLLVPYFSWKFSHHRHHRFTGHMEKDMAFV  
PATEADRNRKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKGSK  
QWETGKGGMGWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYILYQAAQVVGWQMVG  
LLYFQQYFWVHHWLVAITYLHHTHEEVHHFDADSWTFVKGALATVDRDFGFIGKHLFHN  
IIDHHVVHHLFPRI PFYAAEEATNSIRPMLGPLYHRDDRSFMGQLWYNFTHCKWVVPDP  
QVPGALIWAHTVQSTQ
```

**Table 1** Top alignment observed for the Pj $\Delta$ 6D protein sequence from a FASTA search against the AD\_2009 allergen database.

Database	GI #	Description	E-score	% Identity	aa Overlap
AD_2009	82492267	major pollen allergen Phl p 4 precursor [Phleum pratense]	0.09	24.038	208

**Table 2** Top alignment observed for the Pj $\Delta$ 6D protein sequence from a FASTA search against the TOX\_2009 database.

Database	Accession #	Description	E-score	% Identity	aa Overlap
TOX_2009	-	-	-	-	-

**Table 3** Top alignment observed for the Pj $\Delta$ 6D desaturase protein sequence from a FASTA search against the PRT\_2009 database.

Database	GI #	Description	E-score	% Identity	aa Overlap
PRT_2009	151416086	unnamed protein product	6.2e-188	89.438	445

**Table 4** Top alignment observed for the Nc $\Delta$ 15D protein sequence from a FASTA search against the AD\_2009 allergen database.

Database	GI #	Description	E-score	% Identity	aa Overlap
AD_2009	30794292	lactotransferrin [Bos taurus]	0.25	25.225	111

**Table 5** Top alignment observed for the Nc $\Delta$ 15D protein sequence from a FASTA search against the TOX\_2009 database.

Database	Accession #	Description	E-score	% Identity	aa Overlap
TOX_2009	-	-	-	-	-

**Table 6** Top alignment observed for the Nc $\Delta$ 15 $\Delta$ Dprotein sequence from a FASTA search against the PRT\_2009 database.

Database	GI #	Description	E-score	% Identity	aa Overlap
PRT_2009	88181398	hypothetical protein CHGG_0	1.2e-120	67.519	391

## Appendix 1. Bioinformatic analysis of PjΔ6D (polypeptide del\_6)

```
>del_6
MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTD AFLAYHPPSTSRLLPPFSTNLL
LEKHSVSETSSDYRKL LDFHKMG MFRARGHTAYATFVIMILMLVSSVTGVLCSEN PWVHLVCGAAMGFAWIQC GWIG
HDSGHYRIMTDRKWRNFAQILSSNCLQG ISIGWKKWNHNAHHIACNSLEYD PDLYIPLL VVSPKFFNSLT SRFYDKK
LNF DGVSRFLVQYQHWSFY PVMCVARLNMLAQSFILLESRRE VANRVQEILGLAVFWLWFP LLLSCLPNWGERIMFLL
ASYSVTGIQHVFSLNHFSSDVYVGP PVGNDWFKKQTAGTLNISC PAWMDWFGGLQFQVEHHLFPRM PRGQFRKISP
FVRDLCKKHNLTYNIASF TKANVLTLET LRNTAIEARDLSNP IPKNMVWEAVKNVG
```

---

```
Sliding 8 amino acid window search
Database searched = AD_2009
Query = del_6
```

```
Start time: Tue Oct 20 14:14:08 CDT 2009 Finish time: Tue Oct 20 14:14:08 CDT 2009
```

```
No 8 amino acid matches exist between del_6 and the AD_2009 database
```

---

```
# fasta34 del_6.pep /home/andre/db/AD_2009 -Q -E 1 -O del_6.pep_ad.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006
```

Please cite:

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

```
del_6, 446 aa
vs /home/andre/db/AD_2009 library
```

	opt	E()	
< 20	3	0:=	
22	0	0:	one = represents 3 library sequences
24	0	0:	
26	0	0:	
28	4	0:==	
30	2	2:*	
32	4	7:==*	
34	13	20:===== *	
36	36	41:===== *	
38	57	68:===== *	
40	82	95:===== *	
42	122	116:=====*	
44	146	128:=====*	
46	114	130:===== *	
48	109	125:===== *	
50	115	114:=====*	
52	100	100:=====*	
54	106	85:=====*	
56	72	71:=====*	
58	62	59:=====*	
60	58	47:=====*	
62	48	38:=====*	

```
64 22 30:===== *
66 23 24:=====*
68 17 19:=====*
70 10 15:=====*
72 15 12:=====*
74 14 9:=====*
76 1 7:== *
78 11 5:=====
80 7 4:=====
82 1 3:==
84 4 3:=====
86 1 2:==
88 2 2:== inset = represents 1 library sequences
90 0 1:==
92 0 1:== :*
94 0 1:== :*
96 0 1:== :*
98 1 0:= *=
100 3 0:= =====
102 0 0:== *
104 0 0:== *
106 0 0:== *
108 0 0:== *
110 0 0:== *
112 0 0:== *
114 0 0:== *
116 0 0:== *
118 0 0:== *
>120 1 0:= *=
307888 residues in 1386 sequences
Expectation_n fit: rho(ln(x))= 3.45140.00395; mu= 17.5972 0.204
mean_var=51.640512.245, 0's: 3 Z-trim: 4 B-trim: 0 in 0/44
Lambda= 0.178476
Kolmogorov-Smirnov statistic: 0.0308 (N=29) at 48

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 37, opt: 25, open/ext: -10/-2, width: 16
The best scores are: opt bits E(1386)
gi|82492267|gb|ABB78007.1| major pollen allergen P ( 525) 90 31.7 0.09

>>gi|82492267|gb|ABB78007.1| major pollen allergen Phl p (525 aa)
initn: 53 initl: 53 opt: 90 Z-score: 120.7 bits: 31.7 E(): 0.09
Smith-Waterman score: 90; 24.038% identity (48.558% similar) in 208 aa
overlap (68-262:246-440)

40 50 60 70 80 90
del_6 LHPGGIAPLLALAGHDVTD AFLAYHPPSTSRLLP-PFSTNLLLEKHSVSETSSD----YR
gi|824 HDKKSMDGDDHFWAVRGGGSGSFGIVVAWQVKLLPVPPTVTIFKISKTVSEGAVDIINKWQ
220 230 240 250 260 270

100 110 120 130 140 150
del_6 KLLDSFHKMG MFRARGHTAYATFVIMILMLVSSVTGVLCSEN PWVHLVCGAAMGFAWIQC
gi|824 VVAPQLPADLMIRIIAQGPKATFEAMYLGTCKTLTPLMSSKFPPELGMNPSHCNEMSWIQS
280 290 300 310 320 330
```

```

      160      170      180      190      200
del_6  GWIGHDSGHYRIMTRKWNR-----FAQILSSNCLQGISIGWVKWNHNAHHIACNS--L
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|824  IPFVH-LGHRDALEDDLLNRNNSFKPFAEYKSDYVYQPFKTVWEQILNTWLVKPGAGIM
      340      350      360      370      380      390

      210      220      230      240      250      260
del_6  EYDPLQYIPLLVSPKFFNSLTSRFYDKKLNFDGVSRLFVQYQHSFYPMCVARLNML
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|824  IFDP---YGATISATPE---SATP-FPHRK---GVL-FNIQYVNYWFAPGAAAAPLSWS
      400      410      420      430      440

      270      280      290      300      310      320
del_6  AQSFIILLFSRREVANRVQEILGLAVFWLWFPLLLSCLPNWGERIMFLASYSVTGIQHVQ
gi|824  KDIYNYMEFYVSKNPRQAYANYRIDLGRNEVVNDVSTYASGKVKWQKYFKGNFERLAIT
      450      460      470      480      490      500

```

446 residues in 1 query sequences  
307888 residues in 1386 library sequences  
Scomplib [34t26]  
start: Tue Oct 20 14:14:07 2009 done: Tue Oct 20 14:14:07 2009  
Total Scan time: 0.130 Total Display time: 0.010

Function used was FASTA [version 3.4t26 July 7, 2006]

```
# fasta34 del_6.pep /home/andre/db/TOX_2009 -Q -E 1 -O del_6.pep_tx.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006
```

Please cite:

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

del\_6, 446 aa  
vs /home/andre/db/TOX\_2009 library

```

      opt      E()
< 20      61      0:=====
22      0      0:
24      0      0:
26      1      0:=
28      4      2:*
30      18     11:*=
32      169     41:====*=====
34      223     110:====*=====
36      189     227:====*=====
38      260     375:====*=====
40      397     523:====*=====
42      583     639:====*=====
44      610     705:====*=====
46      697     718:====*=====
48      683     688:====*=====
50      491     627:====*=====
52      553     552:====*=====

```

one = represents 12 library sequences

```

54 632 471:====*=====
56 470 394:====*=====
58 316 323:====*=====
60 240 262:====*
62 216 210:====*
64 238 167:====*
66 122 132:====*
68 90 104:====*
70 66 81:====*
72 61 64:====*
74 55 50:====*
76 41 39:====*
78 59 30:====*
80 24 23:====*
82 30 18:====*
84 11 14:====*
86 4 11:*
88 7 8:*
90 13 7:*=
92 4 5:*
94 3 4:*
96 4 3:*
98 1 2:*
100 0 2:*
102 0 1:*
104 0 1:*
106 0 1:*
108 0 1:*
110 0 1:*
112 0 0:*
114 0 0:*
116 0 0:*
118 0 0:*
>120 0 0:*

```

inset = represents 1 library sequences

1891534 residues in 7651 sequences  
Expectation\_n fit: rho(ln(x))= 4.69740.000632; mu= 11.8328 0.032  
mean\_var=46.976210.284, 0's: 59 Z-trim: 60 B-trim: 317 in 2/60  
Lambda= 0.187127  
Kolmogorov-Smirnov statistic: 0.0450 (N=29) at 50

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 37, opt: 25, open/ext: -10/-2, width: 16  
!! No sequences with E() < 1.000000

446 residues in 1 query sequences  
1891534 residues in 7651 library sequences  
Scomplib [34t26]  
start: Tue Oct 20 14:14:08 2009 done: Tue Oct 20 14:14:09 2009  
Total Scan time: 0.740 Total Display time: 0.000

Function used was FASTA [version 3.4t26 July 7, 2006]

```
# fasta34 del_6.pep /home/andre/db/PRT_2009 -Q -E 1 -O del_6.pep_prt.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006
```

Please cite:

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

del\_6, 446 aa  
vs /home/andre/db/PRT\_2009 library

```

      opt      E()
< 20 221466    0:=====
 22  193      0:=
 24  349     14:*
 26  741    309:*
 28 3029   3336:*
 30 14774 20264:*
 32 57974 78356:====*
 34 163664 212491:===== *
 36 359115 436407:===== *
 38 623546 721218:===== *
 40 911007 1006036:===== *
 42 1157242 1229756:===== *
 44 1320669
1356536:=====*
 46 1364349
1381665:=====*
 48 1322937
1322785:=====*
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 90 14466 12565:=====*
 92 11005 9722:=====*
 94 7810 7523:=====*
 96 5804 5821:=====*
 98 4266 4504:=====*
100 3246 3485:=====*
102 2586 2696:=====*
104 1921 2086:=====*
106 1675 1614:=====*
108 1214 1249:=====*
110 1002 966:=====*
112 756 748:=====*
114 526 579:=====*
```

one = represents 22740 library sequences

inset = represents 221 library sequences

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116 520 448:*      :==*
118 520 346:*      :==*
>120 5672 268:*    :=*=====
3787527556 residues in 14717352 library sequences
statistics sampled from 60000 to 14708932 sequences
Expectation_n fit: rho(ln(x))= 5.13510.000191; mu= 11.0947 0.010
mean_var=64.341913.335, 0's: 845 Z-trim: 861 B-trim: 2610 in 1/63
Lambda= 0.159892
Kolmogorov-Smirnov statistic: 0.0324 (N=29) at 46
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FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 37, opt: 25, open/ext: -10/-2, width: 16  
The best scores are:

	opt bits
E(14717352)	
gi 151416086 emb CAO78348.1  unnamed protein produ ( 449)	2838 663.3 6.2e-188
gi 118627908 emb CAL85354.1  unnamed protein produ ( 453)	2836 662.8 8.6e-188
gi 126633766 emb CAM55839.1  unnamed protein produ ( 453)	2836 662.8 8.6e-188
gi 39750753 emb CAE84827.1  unnamed protein produc ( 453)	2836 662.8 8.6e-188
gi 60220786 emb CAI58892.1  unnamed protein produc ( 453)	2836 662.8 8.6e-188
gi 30350277 gb AAP23034.1  fatty acid delta-6 desa ( 453)	2836 662.8 8.6e-188
gi 76059286 emb CAJ30837.1  unnamed protein produc ( 453)	2836 662.8 8.6e-188
gi 118627910 emb CAL85355.1  unnamed protein produ ( 453)	2821 659.4 9.5e-187
gi 39750755 emb CAE84828.1  unnamed protein produc ( 453)	2821 659.4 9.5e-187
gi 126633768 emb CAM55840.1  unnamed protein produ ( 453)	2813 657.5 3.4e-186
gi 30350281 gb AAP23036.1  fatty acid delta-6 desa ( 453)	2813 657.5 3.4e-186
gi 60220788 emb CAI58893.1  unnamed protein produc ( 453)	2813 657.5 3.4e-186
gi 76059288 emb CAJ30838.1  unnamed protein produc ( 453)	2813 657.5 3.4e-186
gi 30350275 gb AAP23033.1  sphingolipid delta-8 de ( 452)	2504 586.3 9.8e-165
gi 30350279 gb AAP23035.1  sphingolipid delta-8 de ( 452)	2486 582.1 1.7e-163
gi 129593742 gb ABO31111.1  sphingolipid delta-8 d ( 447)	2189 513.6 7.2e-143
gi 144583293 gb ABP01349.1  D8-sphingolipid desatu ( 447)	2175 510.4 6.8e-142
gi 157339279 emb CAO43820.1  unnamed protein produ ( 447)	2166 508.3 2.9e-141
gi 4101626 gb AAD01240.1  desaturase/cytochrome b5 ( 446)	2143 503.0 1.1e-139
gi 37727301 gb AAO13090.1  delta-6-desaturase [Cam ( 448)	2136 501.4 3.5e-139
gi 4102021 gb AAD01410.1  delta 6-desaturase [Bora ( 448)	2120 497.7 4.5e-138
gi 126633756 emb CAF55834.1  unnamed protein produ ( 448)	2120 497.7 4.5e-138
gi 70795233 gb AAZ08559.1  delta-6 desaturase [Ech ( 448)	2120 497.7 4.5e-138
gi 76059232 emb CAJ30813.1  unnamed protein produc ( 448)	2120 497.7 4.5e-138
gi 156141045 gb ABU51607.1  delta 6-desaturase [Bo ( 448)	2120 497.7 4.5e-138
gi 60220732 emb CAI58865.1  unnamed protein produc ( 448)	2120 497.7 4.5e-138
gi 71068111 gb AAZ23035.1  delta-6 desaturase [Ech ( 448)	2119 497.5 5.3e-138
gi 56664937 gb AAW18134.1  Sequence 15 from patent ( 448)	2114 496.3 1.2e-137
gi 197038257 gb ACH17687.1  Sequence 15 from paten ( 448)	2114 496.3 1.2e-137
gi 17223795 gb AAL23580.1  delta-6-desaturase [Ech ( 448)	2114 496.3 1.2e-137
gi 40781920 emb CAF55407.1  unnamed protein produc ( 448)	2114 496.3 1.2e-137
gi 62780293 gb AAZ05063.1  Sequence 11 from patent ( 448)	2114 496.3 1.2e-137
gi 2062403 gb AAC49700.1  delta 6 desaturase [Bora ( 448)	2114 496.3 1.2e-137
gi 42689976 gb AAS32275.1  Sequence 5 from patent ( 448)	2112 495.8 1.6e-137
gi 158508159 gb ABW65783.1  Sequence 5 from patent ( 448)	2112 495.8 1.6e-137
gi 3999225 gb AAC92657.1 AR021719 Sequence 5 from ( 448)	2112 495.8 1.6e-137
gi 145009144 gb ABP23376.1  Sequence 5 from patent ( 448)	2112 495.8 1.6e-137
gi 2096441 gb AAB55273.1  Sequence 5 from patent U ( 448)	2112 495.8 1.6e-137
gi 20251303 gb AAE96306.1  Sequence 5 from patent ( 448)	2112 495.8 1.6e-137
gi 17223797 gb AAL23581.1  delta-6-desaturase [Ech ( 448)	2111 495.6 1.9e-137
gi 89077589 gb ABD60318.1  delta-6 fatty acid desa ( 448)	2110 495.4 2.2e-137
gi 10056257 gb AAE33163.1  Sequence 5 from patent ( 446)	2104 494.0 5.8e-137
gi 12808274 gb AAE43494.1  Sequence 15 from patent ( 446)	2104 494.0 5.8e-137
gi 33757665 gb AAQ51238.1  Sequence 5 from patent ( 446)	2104 494.0 5.8e-137

gi 67592982 gb AAAY74580.1	Sequence 7 from patent	( 447)	2098	492.6	1.5e-136	gi 194702868 gb ACF85518.1	unknown [Zea mays]	( 194)	925	221.8	2.2e-55
gi 156972231 gb ABU98945.1	delta-8 lipid desatura	( 455)	2080	488.5	2.7e-135	gi 148372324 gb ABQ63083.1	delta-6-fatty acid des	( 522)	868	208.9	4.4e-51
gi 22296826 gb AAM94345.1	delta-6-desaturase [Arg	( 448)	2042	479.7	1.2e-132	gi 71068119 gb AAZ23038.1	delta-8 desaturase rela	( 169)	852	204.9	2.3e-50
gi 157349838 emb CAO39694.1	unnamed protein produ	( 447)	2017	473.9	6.3e-131	gi 11527281 gb AAG36959.1	AF290983_1 delta-6 desat	( 523)	854	205.7	4.1e-50
gi 22652111 gb AANO3619.1	AF406816_1 sphingolipid	( 446)	2000	470.0	9.6e-130	gi 28557112 dbj BACS7562.1	delta-6 fatty acid des	( 523)	854	205.7	4.1e-50
gi 118487585 gb ABK95618.1	unknown [Populus trich	( 447)	1962	461.2	4.2e-127	gi 11527283 gb AAG36960.1	AF296076_1 delta-6 desat	( 523)	854	205.7	4.1e-50
gi 33330963 gb AAQ10732.1	delta-8-sphingolipid de	( 446)	1948	458.0	3.9e-126	gi 189498326 gb ACE06759.1	delta-6 fatty acid des	( 523)	853	205.5	4.9e-50
gi 62780291 gb AAAY05061.1	Sequence 8 from patent	( 450)	1938	455.7	2e-125	gi 71068117 gb AAZ23037.1	delta-8 desaturase rela	( 169)	833	200.6	4.7e-49
gi 76803801 gb ABA55805.1	delta-8 sphingolipid de	( 469)	1938	455.7	2e-125	gi 71068115 gb AAZ23036.1	delta-8 desaturase rela	( 169)	802	193.4	6.7e-47
gi 3702328 gb AAC62885.1	putative fatty acid desa	( 449)	1925	452.7	1.6e-124	gi 150850711 gb EDN25904.1	hypothetical protein B	( 542)	800	193.2	2.4e-46
gi 71068109 gb AAZ23034.1	delta-6 desaturase-rela	( 448)	1924	452.5	1.8e-124	gi 154699578 gb EDN99316.1	hypothetical protein S	( 538)	793	191.6	7.3e-46
gi 9995127 emb CAC07391.1	unnamed protein product	( 458)	1910	449.2	1.7e-123	gi 150409733 gb EDN05173.1	hypothetical protein H	( 567)	793	191.6	7.6e-46
gi 62780295 gb AAAY05065.1	Sequence 13 from patent	( 458)	1910	449.2	1.7e-123	gi 144976092 gb ABP13187.1	Sequence 10 from paten	( 178)	775	187.2	5.2e-45
gi 1040729 emb CAA60621.1	delta-8 sphingolipid de	( 458)	1910	449.2	1.7e-123	gi 57223843 gb AAW41886.1	delta 8-sphingolipid de	( 535)	757	183.3	2.3e-43
gi 6850849 emb CAB71088.1	delta-8 sphingolipid de	( 449)	1904	447.9	4.5e-123	gi 160707466 gb EAT91028.2	hypothetical protein S	( 575)	755	182.9	3.4e-43
gi 28059272 gb AAO30042.1	delta-8 sphingolipid de	( 449)	1904	447.9	4.5e-123	gi 49650087 emb CAG79813.1	YALIOE21131p [Yarrowia	( 535)	748	181.2	9.7e-43
gi 16226517 gb AAL16189.1	AF428420_1 AT3g61580/F2A	( 449)	1904	447.9	4.5e-123	gi 146449687 gb EDK43943.1	hypothetical protein L	( 597)	748	181.3	1.1e-42
gi 9995108 emb CAC07390.1	unnamed protein product	( 449)	1904	447.9	4.5e-123	gi 60172958 gb AAX14504.1	sphingolipid delta-8 de	( 493)	747	180.1	1.1e-42
gi 3819710 emb CAA11858.1	delta-8 sphingolipid de	( 449)	1904	447.9	4.5e-123	gi 90304858 gb EAS34489.1	hypothetical protein CI	( 640)	747	181.1	1.3e-42
gi 23306384 gb AAN17419.1	delta-8 sphingolipid de	( 449)	1904	447.9	4.5e-123	gi 211589395 emb CAP95536.1	Pc21g06390 [Penicilli	( 553)	743	180.1	2.2e-42
gi 3819708 emb CAA11857.1	delta-8 sphingolipid de	( 449)	1901	447.2	7.2e-122	gi 12311151 emb CAC22584.1	unnamed protein produc	( 483)	742	179.8	2.3e-42
gi 9995106 emb CAC07389.1	unnamed protein product	( 449)	1901	447.2	7.2e-122	gi 144976088 gb ABP13183.1	Sequence 2 from patent	( 483)	742	179.8	2.3e-42
gi 21592945 gb AAM64895.1	delta-8 sphingolipid de	( 449)	1898	446.5	1.2e-122	gi 8670977 emb CAB94992.1	delta 6-fatty acetylena	( 483)	742	179.8	2.3e-42
gi 12002282 gb AAG43277.1	AF133728_1 delta 8-sphin	( 446)	1896	446.0	1.6e-122	gi 40781928 emb CAF05410.1	unnamed protein produc	( 483)	742	179.8	2.3e-42
gi 145009165 gb ABP23397.1	Sequence 27 from paten	( 452)	1893	445.3	2.6e-122	gi 160814759 emb CAP40224.1	unnamed protein produ	( 483)	742	179.8	2.3e-42
gi 42689997 gb AAS32296.1	Sequence 27 from patent	( 452)	1893	445.3	2.6e-122	gi 12311153 emb CAC22585.1	unnamed protein produc	( 483)	742	179.8	2.3e-42
gi 20251324 gb AAE96327.1	Sequence 27 from patent	( 452)	1893	445.3	2.6e-122	gi 40781928 emb CAF05411.1	unnamed protein produc	( 483)	742	179.8	2.3e-42
gi 158508180 gb ABW65804.1	Sequence 27 from paten	( 452)	1893	445.3	2.6e-122	gi 144976089 gb ABP13184.1	Sequence 4 from patent	( 483)	742	179.8	2.3e-42
gi 125563301 gb EAZ08681.1	hypothetical protein O	( 457)	1851	435.6	2.2e-119	gi 213504782 emb CAS91431.1	unnamed protein produ	( 538)	740	179.4	3.5e-42
gi 113631148 dbj BAF24829.1	Os09g0338500 [Oryza s	( 466)	1851	435.6	2.2e-119	gi 44984327 gb AAS53293.1	AFL079Wp [Ashbya gossyp	( 538)	740	179.4	3.5e-42
gi 215765030 dbj BAG86727.1	unnamed protein produ	( 466)	1851	435.6	2.2e-119	gi 211587722 emb CAP85769.1	Pc20g04400 [Penicilli	( 555)	739	179.2	4.2e-42
gi 50252533 dbj BAD28708.1	putative delta-6-desat	( 466)	1851	435.6	2.2e-119	gi 119413943 gb EAW23882.1	fatty acid desaturase,	( 565)	739	179.2	4.3e-42
gi 33330961 gb AAQ10731.1	delta-6-fatty acid desa	( 446)	1840	433.1	1.2e-118	gi 164651328 gb EDR15568.1	delta 8-sphingoloid de	( 541)	738	178.9	4.8e-42
gi 194703370 gb ACF85769.1	unknown [Zea mays]	( 464)	1834	431.7	3.3e-118	gi 159128761 gb EDP53875.1	fatty acid desaturase,	( 565)	731	177.3	1.5e-41
gi 194689688 gb ACF78928.1	unknown [Zea mays]	( 464)	1834	431.7	3.3e-118	gi 187973797 gb EDU41296.1	fatty acid desaturase	( 568)	731	177.3	1.5e-41
gi 62780289 gb AAAY05059.1	Sequence 4 from patent	( 462)	1833	431.5	3.9e-118	gi 119401147 gb EAW11571.1	fatty acid desaturase,	( 564)	730	177.1	1.8e-41
gi 195629792 gb ACG36537.1	desaturase/cytochrome	( 462)	1833	431.5	3.9e-118	gi 150856702 gb EDN31894.1	hypothetical protein B	( 563)	729	176.9	2.1e-41
gi 194690302 gb ACF79235.1	unknown [Zea mays]	( 462)	1833	431.5	3.9e-118	gi 135365631 gb EBH15038.1	hypothetical protein G	( 366)	726	176.1	2.4e-41
gi 195642946 gb ACG40941.1	desaturase/cytochrome	( 463)	1833	431.5	3.9e-118	gi 210070696 gb EEA24786.1	fatty acid desaturase,	( 557)	728	176.6	2.5e-41
gi 4100569 gb AAD00895.1	fatty acid desaturase/cy	( 446)	1832	431.2	4.4e-118	gi 134076236 emb CAR39522.1	unnamed protein produ	( 557)	727	176.4	2.9e-41
gi 194701904 gb ACF85036.1	unknown [Zea mays]	( 464)	1830	430.8	6.3e-118	gi 49643967 emb CAG99919.1	KLLA0E19471p [Kluyvero	( 573)	725	176.0	4.1e-41
gi 62780294 gb AAAY05064.1	Sequence 12 from patent	( 469)	1790	421.6	3.8e-115	gi 83774861 dbj BAE64984.1	unnamed protein produc	( 558)	723	175.5	5.5e-41
gi 4104056 gb AAD10250.1	S276 [Triticum aestivum]	( 469)	1790	421.6	3.8e-115	gi 190344838 gb EDK36596.2	hypothetical protein P	( 599)	720	174.8	9.4e-41
gi 62780292 gb AAAY05062.1	Sequence 10 from patent	( 469)	1788	421.1	5.3e-115	gi 114191764 gb EAU33464.1	hypothetical protein A	( 557)	718	174.3	1.2e-40
gi 62780288 gb AAE61289.1	Sequence 2 from patent	( 448)	1767	416.3	1.5e-113	gi 213504774 emb CAS91423.1	unnamed protein produ	( 597)	718	174.3	1.3e-40
gi 162670501 gb EDG57069.1	predicted protein [Phy	( 469)	1613	380.7	7.5e-103	gi 154695397 gb EDN95135.1	hypothetical protein S	( 563)	716	173.9	1.7e-40
gi 50882497 gb AAT85664.1	putative desaturase [Ma	( 464)	1579	372.9	1.7e-100	gi 50882491 gb AAT85661.1	delta6 fatty acid desat	( 481)	714	173.4	2e-40
gi 125605297 gb EAZ244333.1	hypothetical protein O	( 433)	1553	366.9	1e-98	gi 160814735 emb CAP40212.1	unnamed protein produ	( 481)	714	173.4	2e-40
gi 194702890 gb ACF85529.1	unknown [Zea mays]	( 330)	1495	353.4	8.8e-95	gi 159124031 gb EDP49150.1	fatty acid desaturase,	( 560)	713	173.2	2.7e-40
gi 217073182 gb ACJ84950.1	unknown [Medicago trun	( 331)	1490	352.3	2e-94	gi 119409837 gb EAW19784.1	fatty acid desaturase	( 507)	712	172.9	2.9e-40
gi 14477726 gb AAE61289.1	Sequence 7 from patent	( 252)	1228	291.8	2.4e-76	gi 51831765 gb AAU10084.1	delta 8-(E)-sphingolipi	( 542)	711	172.7	3.6e-40
gi 10055434 gb AAE32340.1	Sequence 7 from patent	( 252)	1228	291.8	2.4e-76	gi 90304908 gb EAS34539.1	hypothetical protein CI	( 560)	711	172.7	3.7e-40
gi 12808267 gb AAE43487.1	Sequence 8 from patent	( 252)	1228	291.8	2.4e-76	gi 199433823 emb CAG90058.2	DEHA2G01628p [Debaryo	( 582)	710	172.5	4.5e-40
gi 23313405 gb AAN19963.1	Sequence 7 from patent	( 252)	1228	291.8	2.4e-76	gi 21104520 dbj BAB93117.1	putative delta 8-sphin	( 568)	708	172.0	6.1e-40
gi 156227752 gb EDO48554.1	predicted protein [Nem	( 455)	1173	279.2	2.6e-72	gi 21104522 dbj BAB93118.1	putative delta 8-sphin	( 573)	705	171.3	9.9e-40
gi 190588831 gb EDV28853.1	hypothetical protein T	( 472)	1152	274.4	7.7e-71	gi 145009867 gb EDJ94523.1	hypothetical protein M	( 568)	702	170.6	1.6e-39
gi 144577779 gb ABO95845.1	predicted protein [Ost	( 498)	1063	253.9	1.2e-64	gi 46406034 gb AAS93682.1	delta-6-fatty acid desa	( 458)	698	169.7	2.5e-39
gi 62780290 gb AAAY05060.1	Sequence 6 from patent	( 253)	935	224.2	5.4e-56	gi 217271823 gb ACK28004.1	Sequence 38 from paten	( 458)	698	169.7	2.5e-39

gi 160814737 emb CAP40213.1  unnamed protein produ ( 458) 698 169.7 2.5e-39	gi 14477727 gb AAE61290.1  Sequence 8 from patent ( 125) 582 142.6 9.9e-32
gi 32481183 gb AAP83964.1  delta-6 fatty acid desa ( 458) 698 169.7 2.5e-39	gi 10055435 gb AAE32341.1  Sequence 8 from patent ( 125) 582 142.6 9.9e-32
gi 83772354 dbj BAE62484.1  unnamed protein produc ( 560) 698 169.7 3e-39	gi 23313406 gb AAN19964.1  Sequence 8 from patent ( 125) 582 142.6 9.9e-32
gi 111068756 gb EAT89876.1  hypothetical protein S ( 566) 695 169.0 4.9e-39	gi 12808268 gb AAE43488.1  Sequence 9 from patent ( 125) 582 142.6 9.9e-32
gi 187979846 gb EDU46472.1  delta 8-(E)-sphingolip ( 570) 692 168.3 7.9e-39	gi 140999045 gb ECO95070.1  hypothetical protein G ( 289) 575 141.2 6e-31
gi 167277335 gb ABZ30199.1  Sequence 4137 from pat ( 366) 687 167.1 1.2e-38	gi 139205567 gb ECE13361.1  hypothetical protein G ( 269) 569 139.8 1.5e-30
gi 134083492 emb CAK46969.1  unnamed protein produ ( 539) 686 166.9 2e-38	gi 217271830 gb ACK28011.1  Sequence 45 from paten ( 467) 570 140.1 2e-30
gi 60499697 gb AAX22051.1  delta-6-fatty acid desa ( 459) 685 166.7 2e-38	gi 15823620 dbj BAB69055.1  delta-6 fatty acid des ( 467) 570 140.1 2e-30
gi 160814727 emb CAP40208.1  unnamed protein produ ( 459) 685 166.7 2e-38	gi 160814739 emb CAP40214.1  unnamed protein produ ( 467) 570 140.1 2e-30
gi 60499699 gb AAX22052.1  delta-6-fatty acid desa ( 459) 685 166.7 2e-38	gi 38708284 gb AAR27297.1  delta-6 desaturase [Amy ( 467) 570 140.1 2e-30
gi 160814725 emb CAP40207.1  unnamed protein produ ( 459) 680 165.5 4.5e-38	gi 5639724 gb AAD45877.1 AF139720_1 delta8 fatty a ( 419) 554 136.4 2.3e-29
gi 83027409 gb ABB96724.1  delta-6 fatty acid desa ( 459) 680 165.5 4.5e-38	gi 158457283 gb ABW41477.1  Sequence 6 from patent ( 419) 554 136.4 2.3e-29
gi 162680220 gb EDQ66658.1  predicted protein [Phy ( 529) 679 165.3 5.9e-38	gi 155291439 gb ABT47043.1  Sequence 134513 from p ( 461) 549 135.3 5.6e-29
gi 83775486 dbj BAE65606.1  unnamed protein produc ( 583) 679 165.3 6.4e-38	gi 6434321 emb CAA94233.2  C. elegans protein W08D ( 443) 537 132.5 3.7e-28
gi 40781930 emb CAF05412.1  unnamed protein produc ( 520) 677 164.9 8.1e-38	gi 126633764 emb CAM55838.1  unnamed protein produ ( 443) 537 132.5 3.7e-28
gi 126633758 emb CAM55835.1  unnamed protein produ ( 520) 677 164.9 8.1e-38	gi 76059240 emb CAJ30817.1  unnamed protein produc ( 443) 537 132.5 3.7e-28
gi 12311158 emb CAC22586.1  unnamed protein produc ( 520) 677 164.9 8.1e-38	gi 56664936 gb AAW18133.1  Sequence 14 from patent ( 443) 537 132.5 3.7e-28
gi 76059234 emb CAJ30814.1  unnamed protein produc ( 520) 677 164.9 8.1e-38	gi 60220740 emb CAI58869.1  unnamed protein produc ( 443) 537 132.5 3.7e-28
gi 60220734 emb CAI58866.1  unnamed protein produc ( 520) 677 164.9 8.1e-38	gi 9927414 emb CAC04885.1  unnamed protein product ( 443) 537 132.5 3.7e-28
gi 40781934 emb CAF05414.1  unnamed protein produc ( 520) 677 164.9 8.1e-38	gi 67592977 gb AAY74575.1  Sequence 2 from patent ( 443) 537 132.5 3.7e-28
gi 160814757 emb CAP40223.1  unnamed protein produ ( 520) 677 164.9 8.1e-38	gi 197038256 gb ACH17686.1  Sequence 14 from paten ( 443) 537 132.5 3.7e-28
gi 8670979 emb CAB94993.1  delta 6-fatty acid desa ( 520) 677 164.9 8.1e-38	gi 67592981 gb AAY74579.1  Sequence 6 from patent ( 443) 537 132.5 3.7e-28
gi 144976093 gb ABP13188.1  Sequence 12 from paten ( 520) 677 164.9 8.1e-38	gi 3088520 gb AAC15586.1  delta6-fatty-acid-desatu ( 443) 537 132.5 3.7e-28
gi 27803034 emb CAD60737.1  unnamed protein produc ( 590) 675 164.4 1.2e-37	gi 157354159 emb CAO46726.1  unnamed protein produ ( 220) 532 132.1 4.7e-28
gi 188219276 emb CAP49256.1  unnamed protein produ ( 590) 675 164.4 1.2e-37	gi 56664932 gb AAW18129.1  Sequence 2 from patent ( 447) 534 131.8 6.1e-28
gi 149386657 gb ABN66573.2  predicted protein [Pic ( 573) 668 162.8 3.7e-37	gi 60220722 emb CAI58860.1  unnamed protein produc ( 447) 534 131.8 6.1e-28
gi 116055137 emb CAL57533.1  S68358 Delta8 sphingo ( 473) 650 158.6 5.6e-36	gi 4235626 gb AAD13294.1  delta5-fatty acid desatu ( 447) 534 131.8 6.1e-28
gi 40781963 emb CAF05424.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 126633738 emb CAM55825.1  unnamed protein produ ( 447) 534 131.8 6.1e-28
gi 3790209 emb CAA11033.1  delta6-acyl-lipid desat ( 525) 633 154.7 9.2e-35	gi 76059230 emb CAJ30812.1  unnamed protein produc ( 447) 534 131.8 6.1e-28
gi 76059238 emb CAJ30816.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 6434326 emb CAB61031.1  C. elegans protein T13F ( 447) 534 131.8 6.1e-28
gi 12579152 emb CAC27296.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 40781942 emb CAF05418.1  unnamed protein produc ( 447) 534 131.8 6.1e-28
gi 22316697 emb CAD44447.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 126633746 emb CAM55829.1  unnamed protein produ ( 447) 534 131.8 6.1e-28
gi 55163951 emb CAH68800.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 60220730 emb CAI58864.1  unnamed protein produc ( 447) 534 131.8 6.1e-28
gi 55163940 emb CAH68796.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 4003523 gb AAC95143.1  delta 5 fatty acid desat ( 447) 534 131.8 6.1e-28
gi 40781936 emb CAF05415.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 50831508 emb CAH05234.1  unnamed protein produc ( 447) 534 131.8 6.1e-28
gi 52748017 emb CAH56933.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 76059222 emb CAJ30808.1  unnamed protein produc ( 447) 534 131.8 6.1e-28
gi 22316543 emb CAD44416.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 197038252 gb ACH17682.1  Sequence 2 from patent ( 447) 534 131.8 6.1e-28
gi 22316675 emb CAD44440.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 116001263 emb CAL49883.1  unnamed protein produ ( 456) 531 131.1 1e-27
gi 40781966 emb CAF05426.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 167279305 gb ABZ32169.1  Sequence 6107 from pat ( 454) 525 129.8 2.6e-27
gi 52748006 emb CAH56929.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 67592979 gb AAY74577.1  Sequence 4 from patent ( 443) 523 129.3 3.5e-27
gi 22316521 emb CAD44410.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 167279306 gb ABZ32170.1  Sequence 6108 from pat ( 473) 521 128.8 5.1e-27
gi 22316540 emb CAD44414.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 40161450 gb AAR67463.1  Sequence 14 from patent ( 453) 518 128.1 7.9e-27
gi 60220738 emb CAI58868.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 155709334 gb ABU33983.1  Sequence 14 from paten ( 453) 518 128.1 7.9e-27
gi 22316694 emb CAD44445.1  unnamed protein produc ( 525) 633 154.7 9.2e-35	gi 112053839 gb ABH96551.1  Sequence 14 from paten ( 453) 518 128.1 7.9e-27
gi 3790207 emb CAA11032.1  delta6-acyl-lipid desat ( 525) 633 154.7 9.2e-35	gi 67592980 gb AAY74578.1  Sequence 5 from patent ( 471) 511 126.5 2.5e-26
gi 126633762 emb CAM55837.1  unnamed protein produ ( 525) 633 154.7 9.2e-35	gi 22316517 emb CAD44408.1  unnamed protein produc ( 477) 510 126.3 3e-26
gi 162684935 gb EDQ71334.1  predicted protein [Phy ( 525) 633 154.7 9.2e-35	gi 19879689 gb AAL92563.1  delta 6 fatty acid desa ( 477) 510 126.3 3e-26
gi 197038253 gb ACH17683.1  Sequence 4 from patent ( 421) 619 151.4 7.2e-34	gi 60220736 emb CAI58867.1  unnamed protein produc ( 477) 510 126.3 3e-26
gi 56664933 gb AAW18130.1  Sequence 4 from patent ( 421) 619 151.4 7.2e-34	gi 55163965 emb CAH68803.1  unnamed protein produc ( 477) 510 126.3 3e-26
gi 158457281 gb ABW41475.1  Sequence 2 from patent ( 421) 619 151.4 7.2e-34	gi 22316671 emb CAD44438.1  unnamed protein produc ( 477) 510 126.3 3e-26
gi 158457282 gb ABW41476.1  Sequence 4 from patent ( 421) 619 151.4 7.2e-34	gi 160814745 emb CAP40217.1  unnamed protein produ ( 477) 510 126.3 3e-26
gi 158457285 gb ABW41479.1  Sequence 113 from pate ( 422) 619 151.4 7.2e-34	gi 40781932 emb CAF05413.1  unnamed protein produc ( 477) 510 126.3 3e-26
gi 60220716 emb CAI58857.1  unnamed protein produc ( 421) 599 146.8 1.8e-32	gi 126633760 emb CAM55836.1  unnamed protein produ ( 477) 510 126.3 3e-26
gi 76059216 emb CAJ30805.1  unnamed protein produc ( 421) 599 146.8 1.8e-32	gi 55163963 emb CAH68802.1  unnamed protein produc ( 477) 510 126.3 3e-26
gi 50831502 emb CAH05231.1  unnamed protein produc ( 421) 599 146.8 1.8e-32	gi 217271822 gb ACK28003.1  Sequence 37 from paten ( 477) 510 126.3 3e-26
gi 148917592 emb CAO00487.1  unnamed protein produ ( 421) 599 146.8 1.8e-32	gi 52748031 emb CAH56936.1  unnamed protein produc ( 477) 510 126.3 3e-26
gi 126633732 emb CAM55822.1  unnamed protein produ ( 421) 599 146.8 1.8e-32	gi 52748029 emb CAH56935.1  unnamed protein produc ( 477) 510 126.3 3e-26
gi 158457284 gb ABW41478.1  Sequence 7 from patent ( 422) 591 145.0 6.4e-32	gi 145244841 gb ABP49078.1  delta 6 fatty acid des ( 477) 510 126.3 3e-26

gi 76059236 emb CAJ30815.1  unnamed protein produc ( 477)	510	126.3	3e-26	gi 160814753 emb CAP40221.1  unnamed protein produ ( 457)	481	119.6	3e-24
gi 160814743 emb CAP40216.1  unnamed protein produ ( 458)	509	126.1	3.4e-26	gi 147843618 emb CAN79879.1  hypothetical protein ( 326)	475	118.1	5.8e-24
gi 34221930 dbj BAC82359.1  delta6 fatty acid desa ( 458)	509	126.1	3.4e-26	gi 48596231 gb AAT46029.1  delta-6 fatty acyl desa ( 357)	463	115.4	4.3e-23
gi 34221932 dbj BAC82360.1  delta6 fatty acid desa ( 458)	509	126.1	3.4e-26	gi 12007244 gb AAG45093.1 AF307941_1 delta 6-fatty ( 357)	452	112.9	2.5e-22
gi 111572541 gb ABH10627.1  delta-6 desaturase [Ph ( 456)	506	125.4	5.4e-26	gi 12007246 gb AAG45094.1 AF307942_1 delta 6-fatty ( 357)	452	112.9	2.5e-22
gi 160814755 emb CAP40222.1  unnamed protein produ ( 457)	503	124.7	8.8e-26	gi 134025932 gb AAI34688.1  FADS3 protein [Bos tau ( 443)	451	112.7	3.5e-22
gi 11559824 gb AAG38104.1 AF306634_1 delta6-fatty ( 457)	503	124.7	8.8e-26	gi 98375714 gb ABF58684.1  delta8-desaturase [Perk ( 457)	448	112.0	5.8e-22
gi 126013646 gb ABN69091.1  delta-6 fatty acid des ( 457)	502	124.5	1e-25	gi 148917608 emb CAO00495.1  unnamed protein produ ( 457)	448	112.0	5.8e-22
gi 160814747 emb CAP40218.1  unnamed protein produ ( 457)	502	124.5	1e-25	gi 160783195 emb CAP40166.1  unnamed protein produ ( 457)	448	112.0	5.8e-22
gi 18483177 gb AAL73948.1 AF465282_1 delta 6 fatty ( 457)	502	124.5	1e-25	gi 13436176 gb AAH04901.1  Fatty acid desaturase 3 ( 445)	444	111.1	1.1e-21
gi 157677391 emb CAL69819.1  delta6 fatty acid des ( 386)	501	124.2	1.1e-25	gi 29693077 gb AAO93498.1  Sequence 1 from patent ( 445)	444	111.1	1.1e-21
gi 126013644 gb ABN69090.1  delta-6 fatty acid des ( 457)	501	124.2	1.2e-25	gi 119594382 gb EAW73976.1  fatty acid desaturase ( 445)	444	111.1	1.1e-21
gi 34221934 dbj BAC82361.1  delta6 fatty acid desa ( 457)	501	124.2	1.2e-25	gi 119594384 gb EAW73978.1  fatty acid desaturase ( 445)	444	111.1	1.1e-21
gi 160814763 emb CAP40226.1  unnamed protein produ ( 457)	501	124.2	1.2e-25	gi 10798853 gb AAG23122.1 AF084560_1 fatty acid de ( 445)	444	111.1	1.1e-21
gi 217271825 gb ACK28006.1  Sequence 40 from paten ( 457)	501	124.2	1.2e-25	gi 4868366 gb AAD31282.1 AF134404_1 delta-6 fatty ( 445)	444	111.1	1.1e-21
gi 6070340 dbj BAA85588.1  delta-6 fatty acid desa ( 457)	501	124.2	1.2e-25	gi 217115831 gb ACJ97546.1  Sequence 524 from pate ( 445)	444	111.1	1.1e-21
gi 76059312 emb CAJ30850.1  unnamed protein produc ( 484)	501	124.2	1.3e-25	gi 197722765 gb EDY66673.1  fatty acid desaturase ( 362)	441	110.3	1.5e-21
gi 160814733 emb CAP40211.1  unnamed protein produ ( 484)	501	124.2	1.3e-25	gi 210117575 gb EEA65312.1  hypothetical protein B ( 428)	433	108.5	6e-21
gi 60220812 emb CAI58905.1  unnamed protein produc ( 484)	501	124.2	1.3e-25	gi 38490061 gb AAR21624.1  delta-6 fatty acyl desa ( 454)	428	107.4	1.4e-20
gi 126633772 emb CAM55842.1  unnamed protein produ ( 484)	501	124.2	1.3e-25	gi 52424053 gb AAU47273.1  delta-6 fatty acyl desa ( 454)	428	107.4	1.4e-20
gi 60172984 gb AAX14505.1  delta-6 fatty acid desa ( 484)	501	124.2	1.3e-25	gi 149062366 gb EDM12789.1  fatty acid desaturase ( 449)	427	107.1	1.6e-20
gi 217271824 gb ACK28005.1  Sequence 39 from paten ( 459)	498	123.5	2e-25	gi 21742819 emb CAD38527.1  putative fatty acid de ( 449)	427	107.1	1.6e-20
gi 160814751 emb CAP40220.1  unnamed protein produ ( 459)	498	123.5	2e-25	gi 26348537 dbj BAC37908.1  unnamed protein produc ( 449)	427	107.1	1.6e-20
gi 16033737 gb AAL13310.1 AF419296_1 delta-6 fatty ( 459)	498	123.5	2e-25	gi 149062365 gb EDM12788.1  fatty acid desaturase ( 449)	427	107.1	1.6e-20
gi 21900891 emb CAD42499.1  unnamed protein produc ( 459)	498	123.5	2e-25	gi 148709391 gb EDL41337.1  fatty acid desaturase ( 449)	426	106.9	1.9e-20
gi 27278518 gb AAN93256.1  Sequence 18 from patent ( 457)	497	123.3	2.3e-25	gi 74192499 dbj BAE43041.1  unnamed protein produc ( 449)	426	106.9	1.9e-20
gi 155080898 gb ABS94492.1  Sequence 67 from paten ( 457)	497	123.3	2.3e-25	gi 148709390 gb EDL41336.1  fatty acid desaturase ( 449)	426	106.9	1.9e-20
gi 23313401 gb AAN19959.1  Sequence 2 from patent ( 457)	497	123.3	2.3e-25	gi 74181920 dbj BAE32659.1  unnamed protein produc ( 469)	426	106.9	2e-20
gi 12808262 gb AAE43482.1  Sequence 2 from patent ( 457)	497	123.3	2.3e-25	gi 7670385 dbj BAA95044.1  unnamed protein product ( 449)	425	106.7	2.3e-20
gi 10055430 gb AAE32336.1  Sequence 2 from patent ( 457)	497	123.3	2.3e-25	gi 26325278 dbj BAC26393.1  unnamed protein produc ( 449)	424	106.5	2.6e-20
gi 155070718 gb ABS91063.1  Sequence 43 from paten ( 457)	497	123.3	2.3e-25	gi 51860651 gb AAU11445.1  fatty acid desaturase [ ( 465)	424	106.5	2.7e-20
gi 155707464 gb ABU33113.1  Sequence 2 from patent ( 457)	497	123.3	2.3e-25	gi 51860649 gb AAU11444.1  fatty acid desaturase [ ( 465)	424	106.5	2.7e-20
gi 12808273 gb AAE43493.1  Sequence 14 from patent ( 457)	497	123.3	2.3e-25	gi 160814731 emb CAP40210.1  unnamed protein produ ( 465)	424	106.5	2.7e-20
gi 182916823 gb ACC10858.1  Sequence 2 from patent ( 457)	497	123.3	2.3e-25	gi 16904665 dbj BAB71963.1  putative delata 6-desa ( 452)	420	105.5	5e-20
gi 145025091 gb ABP24248.1  Sequence 31 from paten ( 457)	497	123.3	2.3e-25	gi 156617902 gb ABU87822.1  delta5-desaturase-like ( 452)	417	104.8	8.1e-20
gi 14477722 gb AAE61285.1  Sequence 2 from patent ( 457)	497	123.3	2.3e-25	gi 13447755 gb AAK26745.1 AF301910_1 putative delt ( 454)	416	104.6	9.6e-20
gi 10056256 gb AAE33162.1  Sequence 4 from patent ( 457)	497	123.3	2.3e-25	gi 23313403 gb AAN19961.1  Sequence 5 from patent ( 355)	404	101.8	5.3e-19
gi 33757664 gb AAQ51237.1  Sequence 4 from patent ( 457)	497	123.3	2.3e-25	gi 10055432 gb AAE32338.1  Sequence 5 from patent ( 355)	404	101.8	5.3e-19
gi 160814761 emb CAP40225.1  unnamed protein produ ( 457)	497	123.3	2.3e-25	gi 12808265 gb AAE43485.1  Sequence 6 from patent ( 355)	404	101.8	5.3e-19
gi 6448796 gb AAF08685.1 AF110510_1 delta-6 fatty ( 457)	497	123.3	2.3e-25	gi 14477724 gb AAE61287.1  Sequence 5 from patent ( 355)	404	101.8	5.3e-19
gi 158475487 gb ABW48563.1  Sequence 24 from paten ( 457)	497	123.3	2.3e-25	gi 61207418 gb AAX40418.1  delta-6-fatty acid desa ( 459)	403	101.6	7.7e-19
gi 144998355 gb ABP16928.1  Sequence 17 from paten ( 457)	497	123.3	2.3e-25	gi 72398639 gb AAZ72733.1  delta-6-fatty acid desa ( 459)	403	101.6	7.7e-19
gi 40781950 emb CAF05422.1  unnamed protein produc ( 457)	497	123.3	2.3e-25	gi 170937447 emb CAP62105.1  unnamed protein produ ( 573)	403	101.7	9.3e-19
gi 118822321 gb ABL20743.1  Sequence 2 from patent ( 457)	497	123.3	2.3e-25	gi 15281354 dbj BAB63440.1  putative delata 6-desa ( 454)	395	99.8	2.8e-18
gi 62774622 gb AAY02015.1  Sequence 41 from patent ( 458)	497	123.3	2.3e-25	gi 55846441 gb AAK82631.2 AF478472_1 delta-5 fatty ( 454)	395	99.8	2.8e-18
gi 23329313 gb AAN26147.1  Sequence 44 from patent ( 458)	497	123.3	2.3e-25	gi 157918419 gb ABV99846.1  fatty acid desaturase ( 347)	389	98.3	5.8e-18
gi 62774608 gb AAY02001.1  Sequence 11 from patent ( 458)	497	123.3	2.3e-25	gi 88176241 gb EAQ83709.1  hypothetical protein CH ( 540)	391	98.9	6e-18
gi 23329295 gb AAN26129.1  Sequence 10 from patent ( 458)	497	123.3	2.3e-25	gi 111150824 emb CAJ62528.1  putative delta fatty ( 365)	388	98.1	7.1e-18
gi 160814723 emb CAP40206.1  unnamed protein produ ( 459)	496	123.1	2.7e-25	gi 66474461 gb AAY46796.1  delta-6 fatty acyl desa ( 447)	389	98.4	7.1e-18
gi 76059402 emb CAJ30866.1  unnamed protein produc ( 459)	496	123.1	2.7e-25	gi 148790756 gb ABR12315.1  delta-6 desaturase [Si ( 445)	387	97.9	9.7e-18
gi 160814741 emb CAP40215.1  unnamed protein produ ( 457)	495	122.8	3.2e-25	gi 126633770 emb CAM55841.1  unnamed protein produ ( 456)	387	97.9	9.9e-18
gi 46559566 emb CAE53093.1  delta6 fatty acid desa ( 457)	495	122.8	3.2e-25	gi 160814767 emb CAP40228.1  unnamed protein produ ( 456)	387	97.9	9.9e-18
gi 210099241 gb EEA47338.1  hypothetical protein B ( 435)	487	121.0	1.1e-24	gi 60220804 emb CAI58901.1  unnamed protein produc ( 456)	387	97.9	9.9e-18
gi 217271810 gb ACK27991.1  Sequence 2 from patent ( 359)	481	119.5	2.4e-24	gi 116061047 emb CAL56435.1  delta-6-desaturase (I ( 456)	387	97.9	9.9e-18
gi 184831751 gb AAL73947.1 AF465281_1 delta 6 fatty ( 457)	482	119.8	2.5e-24	gi 76059304 emb CAJ30846.1  unnamed protein produc ( 456)	387	97.9	9.9e-18
gi 160814749 emb CAP40219.1  unnamed protein produ ( 457)	482	119.8	2.5e-24	gi 58294486 gb AAW70159.1  delta-6-desaturase [Ost ( 456)	387	97.9	9.9e-18
gi 184831791 gb AAL73949.1 AF465283_1 delta 6 fatty ( 457)	481	119.6	3e-24	gi 110565253 emb CAL23343.1  unnamed protein produ ( 456)	387	97.9	9.9e-18
gi 12007242 gb AAG45092.1 AF307940_1 delta 6-fatty ( 457)	481	119.6	3e-24	gi 190582402 gb EDV22475.1  hypothetical protein T ( 430)	382	96.8	2.1e-17

gi 14042094 dbj BAB55103.1  unnamed protein produc ( 444)	382	96.8	2.2e-17	gi 23329312 gb AAN26146.1  Sequence 43 from patent ( 444)	359	91.5	8.6e-16
gi 40034020 emb CAE90448.1  unnamed protein produc ( 444)	382	96.8	2.2e-17	gi 62774623 gb AAAY02016.1  Sequence 42 from patent ( 444)	359	91.5	8.6e-16
gi 40037121 emb CAE91519.1  unnamed protein produc ( 444)	381	96.5	2.5e-17	gi 55726256 emb CAH89900.1  hypothetical protein [ ( 444)	357	91.0	1.2e-15
gi 14042259 dbj BAB55173.1  unnamed protein produc ( 444)	381	96.5	2.5e-17	gi 10798851 gb AAG23121.1 AF084559_1 fatty acid de ( 444)	356	90.8	1.4e-15
gi 39645719 gb AAH63726.1  MGC68735 protein [Xenop ( 446)	380	96.3	3e-17	gi 4406528 gb AAD20018.1  delta-6 fatty acid desat ( 444)	356	90.8	1.4e-15
gi 14043780 gb AAH07846.1  Fatty acid desaturase 1 ( 444)	379	96.1	3.5e-17	gi 119594380 gb EAW73974.1  fatty acid desaturase ( 444)	356	90.8	1.4e-15
gi 6842050 gb AAF29378.1  delta-5 desaturase [Homo ( 444)	379	96.1	3.5e-17	gi 45502852 emb CAF86135.1  unnamed protein produc ( 444)	356	90.8	1.4e-15
gi 23329301 gb AAN26135.1  Sequence 17 from patent ( 323)	377	95.5	3.7e-17	gi 22760712 dbj BAC11305.1  unnamed protein produc ( 444)	356	90.8	1.4e-15
gi 62774613 gb AAAY02006.1  Sequence 17 from patent ( 323)	377	95.5	3.7e-17	gi 217115830 gb ACJ97545.1  Sequence 522 from pate ( 444)	356	90.8	1.4e-15
gi 145025095 gb ABP24252.1  Sequence 41 from paten ( 444)	378	95.8	4.1e-17	gi 18381019 gb AAH22139.1  Fatty acid desaturase 1 ( 447)	355	90.5	1.6e-15
gi 10798849 gb AAG23120.1 AF084558_1 fatty acid de ( 444)	378	95.8	4.1e-17	gi 20070924 gb AAH26831.1  Fatty acid desaturase 1 ( 447)	355	90.5	1.6e-15
gi 189054357 dbj BAG36877.1  unnamed protein produ ( 444)	378	95.8	4.1e-17	gi 148709393 gb EDL41339.1  fatty acid desaturase ( 447)	354	90.3	1.9e-15
gi 217115787 gb ACJ97502.1  Sequence 69 from paten ( 444)	378	95.8	4.1e-17	gi 38969781 gb AAH63053.1  Fatty acid desaturase 1 ( 447)	354	90.3	1.9e-15
gi 3169158 gb AAC23397.1  BC269730_2 [Homo sapiens ( 444)	378	95.8	4.1e-17	gi 16151829 dbj BAB69894.1  delta-5 desaturase [Mu ( 447)	354	90.3	1.9e-15
gi 12224984 emb CAC21679.1  hypothetical protein [ ( 444)	378	95.8	4.1e-17	gi 26350885 dbj BAC39079.1  unnamed protein produc ( 447)	354	90.3	1.9e-15
gi 158457079 gb ABW41443.1  Sequence 4 from patent ( 473)	378	95.9	4.3e-17	gi 197712992 gb EDY57026.1  fatty acid desaturase ( 354)	352	89.8	2.2e-15
gi 119594379 gb EAW73973.1  fatty acid desaturase ( 501)	378	95.9	4.5e-17	gi 51858588 gb AAH81776.1  Fatty acid desaturase 2 ( 444)	353	90.1	2.2e-15
gi 62897371 dbj BAD96626.1  fatty acid desaturase ( 444)	377	95.6	4.8e-17	gi 149062367 gb EDM12790.1  fatty acid desaturase ( 444)	353	90.1	2.2e-15
gi 149022448 gb EDL79342.1  rCG26407 [Rattus norve ( 487)	377	95.6	5.2e-17	gi 4514722 dbj BAA75496.1  delta-6 fatty acid desa ( 444)	353	90.1	2.2e-15
gi 145305528 gb ABP56110.1  fatty acid desaturase ( 347)	374	94.9	6.3e-17	gi 20070719 gb AAH26848.1  Fatty acid desaturase 1 ( 447)	353	90.1	2.2e-15
gi 45502630 emb CAF85923.1  unnamed protein produc ( 501)	375	95.2	7.3e-17	gi 29436933 gb AAH49438.1  Fatty acid desaturase 2 ( 444)	352	89.8	2.6e-15
gi 22760402 dbj BAC11182.1  unnamed protein produc ( 501)	375	95.2	7.3e-17	gi 74181635 dbj BAE32539.1  unnamed protein produc ( 447)	352	89.8	2.6e-15
gi 187438554 gb ACD10793.1  fatty acid delta-6 des ( 445)	374	94.9	7.8e-17	gi 158938657 gb BAB69975.1  delta-5 fatty acid des ( 445)	344	88.0	9.4e-15
gi 144962260 gb ABP06289.1  fatty acid desaturase ( 444)	373	94.7	9.1e-17	gi 149062368 gb EDM12791.1  fatty acid desaturase ( 447)	343	87.8	1.1e-14
gi 12808266 gb AAE43486.1  Sequence 7 from patent ( 104)	365	92.5	1e-16	gi 15823618 dbj BAB69054.1  delta-5 fatty acid des ( 447)	343	87.8	1.1e-14
gi 14477725 gb AAE61288.1  Sequence 6 from patent ( 104)	365	92.5	1e-16	gi 197304192 emb CAQ30479.1  Acyl-CoA dependent de ( 449)	342	87.5	1.3e-14
gi 10055433 gb AAE32339.1  Sequence 6 from patent ( 104)	365	92.5	1e-16	gi 137081505 gb EBS10199.1  hypothetical protein G ( 116)	335	85.6	1.3e-14
gi 23313404 gb AAN19962.1  Sequence 6 from patent ( 104)	365	92.5	1e-16	gi 62774621 gb AAAY02014.1  Sequence 40 from patent ( 347)	340	87.0	1.5e-14
gi 169642221 gb AAI60507.1  LOC100145314 protein [ ( 429)	372	94.5	1e-16	gi 23329311 gb AAN26145.1  Sequence 42 from patent ( 347)	340	87.0	1.5e-14
gi 86577710 gb AAI12949.1  Fads2 protein [Xenopus ( 446)	372	94.5	1.1e-16	gi 11386009 gb AAG35068.1 AF320509_1 delta-5 desat ( 447)	340	87.1	1.8e-14
gi 50417554 gb AAH77556.1  Fads2-prov protein [Xen ( 446)	372	94.5	1.1e-16	gi 124417974 emb CAR82966.1  unnamed protein produ ( 621)	341	87.4	2e-14
gi 33585851 gb AAH55950.1  Fads3 protein [Mus musc ( 404)	371	94.2	1.2e-16	gi 10954035 gb AAG25710.1 AF309556_1 putative delt ( 444)	338	86.6	2.5e-14
gi 215276658 gb ACJ65149.1  delta-6 fatty acyl des ( 442)	371	94.2	1.3e-16	gi 158457078 gb ABW41442.1  Sequence 3 from patent ( 447)	337	86.4	2.9e-14
gi 29693080 gb AAO93499.1  Sequence 3 from patent ( 444)	371	94.2	1.3e-16	gi 62780296 gb AAAY05066.1  Sequence 17 from patent ( 114)	325	83.3	6.4e-14
gi 44921596 gb AAS49163.1  delta-6 fatty acyl desa ( 445)	370	94.0	1.5e-16	gi 144061162 gb EDI58667.1  hypothetical protein G ( 422)	321	85.0	7.2e-14
gi 23428438 gb AAL17639.1  putative delta 6-desatu ( 445)	370	94.0	1.5e-16	gi 137994188 gb ECX17375.1  hypothetical protein G ( 199)	327	83.9	7.4e-14
gi 10954037 gb AAG25711.1 AF309557_1 putative delt ( 444)	369	93.8	1.7e-16	gi 148763485 gb ABR10503.1  putative delta fatty a ( 365)	330	84.7	7.5e-14
gi 62774609 gb AAAY02002.1  Sequence 12 from patent ( 444)	367	93.3	2.4e-16	gi 138904171 gb ECC58283.1  hypothetical protein G ( 287)	321	82.6	2.6e-13
gi 7861970 gb AAH570457.1 AF226273_1 delta-5 fatty ( 444)	367	93.3	2.4e-16	gi 139950162 gb ECI57875.1  hypothetical protein G ( 228)	318	81.8	3.5e-13
gi 23329296 gb AAN26130.1  Sequence 11 from patent ( 444)	367	93.3	2.4e-16	gi 124420766 emb CAR85669.1  unnamed protein produ ( 630)	323	83.2	3.6e-13
gi 23329314 gb AAN26148.1  Sequence 45 from patent ( 445)	367	93.3	2.4e-16	gi 62774606 gb AAAY01999.1  Sequence 9 from patent ( 432)	319	82.2	5e-13
gi 23329308 gb AAN26142.1  Sequence 39 from patent ( 445)	367	93.3	2.4e-16	gi 23329294 gb AAN26128.1  Sequence 9 from patent ( 432)	319	82.2	5e-13
gi 53954492 gb AAV04489.1  Sequence 16446 from pat ( 177)	362	91.9	2.5e-16	gi 62774619 gb AAAY02012.1  Sequence 38 from patent ( 465)	319	82.2	5.3e-13
gi 67969447 dbj BAE01074.1  unnamed protein produc ( 444)	366	93.1	2.8e-16	gi 23329309 gb AAN26143.1  Sequence 40 from patent ( 465)	319	82.2	5.3e-13
gi 149383938 gb ABR24806.1  delta-6 fatty acid des ( 440)	365	92.8	3.3e-16	gi 142623810 gb ECZ40384.1  hypothetical protein G ( 558)	317	81.8	8.5e-13
gi 160783196 emb CAP40167.1  unnamed protein produ ( 411)	364	92.6	3.6e-16	gi 142247848 gb ECW69868.1  hypothetical protein G ( 364)	313	80.8	1.1e-12
gi 148709392 gb EDL41338.1  fatty acid desaturase ( 444)	364	92.6	3.8e-16	gi 111979089 gb ABH83332.1  Sequence 69 from paten ( 430)	313	80.8	1.3e-12
gi 34785344 gb AAH57189.1  Fatty acid desaturase 2 ( 444)	364	92.6	3.8e-16	gi 155095521 gb ABS99976.1  Sequence 69 from paten ( 430)	313	80.8	1.3e-12
gi 4406526 gb AAD20017.1  delta-6 fatty acid desat ( 444)	364	92.6	3.8e-16	gi 155116385 gb ABT11311.1  Sequence 69 from paten ( 430)	313	80.8	1.3e-12
gi 74138023 dbj BAE25416.1  unnamed protein produc ( 444)	364	92.6	3.8e-16	gi 155082220 gb ABS94960.1  Sequence 69 from paten ( 430)	313	80.8	1.3e-12
gi 111309298 gb AAI20880.1  4833423E24Rik protein ( 487)	364	92.6	4.1e-16	gi 155116371 gb ABT11297.1  Sequence 55 from paten ( 433)	313	80.8	1.3e-12
gi 148695383 gb EDL27330.1  mCG3008 [Mus musculus] ( 487)	364	92.6	4.1e-16	gi 54307110 gb AAV33631.1  delta-4 desaturase [Iso ( 433)	313	80.8	1.3e-12
gi 123233825 emb CAM24033.1  novel protein (483342 ( 487)	364	92.6	4.1e-16	gi 155082206 gb ABS94946.1  Sequence 55 from paten ( 433)	313	80.8	1.3e-12
gi 45502702 emb CAF85988.1  unnamed protein produc ( 501)	364	92.6	4.2e-16	gi 111979075 gb ABH83318.1  Sequence 55 from paten ( 433)	313	80.8	1.3e-12
gi 22760516 dbj BAC11229.1  unnamed protein produc ( 501)	364	92.6	4.2e-16	gi 155095507 gb ABS99962.1  Sequence 55 from paten ( 433)	313	80.8	1.3e-12
gi 148917598 emb CAO00490.1  unnamed protein produ ( 411)	362	92.1	5e-16	gi 190580163 gb EDV20248.1  hypothetical protein T ( 421)	310	80.1	2.1e-12
gi 98375736 gb ABF58685.1  delta5-desaturase [Perk ( 411)	362	92.1	5e-16	gi 74422653 gb ABA06503.1  delta-6-desaturase [Cun ( 466)	310	80.2	2.2e-12
gi 133778157 gb AAI23736.1  FADS2 protein [Bos tau ( 444)	362	92.2	5.3e-16	gi 160814729 emb CAP40209.1  unnamed protein produ ( 466)	310	80.2	2.2e-12

gi 151362066 gb ABS05069.1  fatty acid desaturase ( 357) 308 79.6 2.5e-12	gi 62774610 gb AA02003.1  Sequence 14 from patent ( 287) 274 71.7 4.8e-10
gi 163778616 gb EDQ92231.1  predicted protein [Mon ( 419) 308 79.7 2.8e-12	gi 23329300 gb AAN26134.1  Sequence 16 from patent ( 288) 274 71.7 4.8e-10
gi 210090975 gb EEA39238.1  hypothetical protein B ( 423) 308 79.7 2.9e-12	gi 62774611 gb AA02004.1  Sequence 15 from patent ( 288) 274 71.7 4.8e-10
gi 135458568 gb EBH77415.1  hypothetical protein G ( 334) 306 79.2 3.2e-12	gi 23329302 gb AAN26136.1  Sequence 18 from patent ( 288) 274 71.7 4.8e-10
gi 199601714 dbj BAG71007.1  delta5-desaturase [Ob ( 435) 307 79.5 3.4e-12	gi 23329298 gb AAN26132.1  Sequence 14 from patent ( 288) 274 71.7 4.8e-10
gi 112053846 gb ABH96555.1  Sequence 33 from paten ( 456) 306 79.2 4.2e-12	gi 143742490 gb EDG55472.1  hypothetical protein G ( 347) 274 71.8 5.6e-10
gi 136160965 gb EBM29598.1  hypothetical protein G ( 362) 303 78.5 5.6e-12	gi 110282809 gb ABG60995.1  fatty acid desaturase ( 356) 274 71.8 5.7e-10
gi 112053847 gb ABH96556.1  Sequence 35 from paten ( 442) 301 78.1 9.1e-12	gi 158260127 dbj BAF82241.1  unnamed protein produ ( 360) 274 71.8 5.8e-10
gi 145025100 gb ABP24257.1  Sequence 56 from paten ( 442) 301 78.1 9.1e-12	gi 193788350 dbj BAG53244.1  unnamed protein produ ( 360) 274 71.8 5.8e-10
gi 155707474 gb ABU33123.1  Sequence 119 from pate ( 442) 301 78.1 9.1e-12	gi 124389907 gb ABN11122.1  delta-6 desaturase [Ar ( 368) 274 71.8 5.9e-10
gi 136856060 gb EBQ86244.1  hypothetical protein G ( 398) 298 77.4 1.3e-11	gi 42565443 gb AAS20991.1  desaturase [Hyacinthus ( 82) 266 69.6 6.1e-10
gi 1361659810 gb EBM28841.1  hypothetical protein G ( 363) 296 76.9 1.7e-11	gi 23329310 gb AAN26144.1  Sequence 41 from patent ( 360) 273 71.6 6.7e-10
gi 37683439 gb AAQ98793.1  delta-4 fatty acid desa ( 445) 297 77.2 1.7e-11	gi 62774620 gb AA02013.1  Sequence 39 from patent ( 360) 273 71.6 6.7e-10
gi 136500512 gb EBQ56762.1  hypothetical protein G ( 369) 295 76.6 2e-11	gi 186469986 gb ACC85611.1  delta 6 desaturase [Ar ( 368) 273 71.6 6.9e-10
gi 144581309 gb ABO99366.1  predicted protein [Ost ( 400) 295 76.7 2.2e-11	gi 50952212 gb AAT89913.1  delta fatty acid desatu ( 416) 273 71.6 7.6e-10
gi 151358713 gb ABS01716.1  fatty acid desaturase ( 375) 293 76.2 2.9e-11	gi 33757667 gb AAQ51240.1  Sequence 7 from patent ( 365) 272 71.3 8e-10
gi 142070222 gb ECV34327.1  hypothetical protein G ( 398) 293 76.2 3e-11	gi 12808276 gb AAE43496.1  Sequence 17 from patent ( 365) 272 71.3 8e-10
gi 136491773 gb EB051081.1  hypothetical protein G ( 343) 291 75.7 3.6e-11	gi 10056259 gb AAE33165.1  Sequence 7 from patent ( 365) 272 71.3 8e-10
gi 160814765 emb CAP40227.1  unnamed protein produ ( 439) 291 75.8 4.5e-11	gi 809110 emb CAA60573.1  delta 6 desaturase [Arth ( 368) 272 71.3 8.1e-10
gi 76059226 emb CAJ30810.1  unnamed protein produc ( 439) 291 75.8 4.5e-11	gi 158304495 gb ABW26112.1  linoleoyl-CoA desatura ( 369) 272 71.3 8.1e-10
gi 126633742 emb CAM55827.1  unnamed protein produ ( 439) 291 75.8 4.5e-11	gi 134889843 gb EBE10298.1  hypothetical protein G ( 356) 271 71.1 9.2e-10
gi 20069123 gb AAM09687.1 AF489588_1 delta-5 fatty ( 439) 291 75.8 4.5e-11	gi 198261491 gb EDY85781.1  fatty acid desaturase ( 356) 270 70.9 1.1e-09
gi 40781946 emb CAF05420.1  unnamed protein produc ( 439) 291 75.8 4.5e-11	gi 56752653 gb AAW24540.1  SJCHGC05823 protein [Sc ( 173) 266 69.8 1.1e-09
gi 148917604 emb CAO00493.1  unnamed protein produ ( 439) 291 75.8 4.5e-11	gi 158938655 gb ABW33674.1  delta-5 fatty acid des ( 170) 265 69.5 1.3e-09
gi 60220726 emb CAI58862.1  unnamed protein produc ( 439) 291 75.8 4.5e-11	gi 138988511 gb ECC70380.1  hypothetical protein G ( 227) 266 69.8 1.4e-09
gi 21900887 emb CAD42497.1  unnamed protein produc ( 439) 291 75.8 4.5e-11	gi 136779681 gb EBQ35346.1  hypothetical protein G ( 372) 267 70.2 1.8e-09
gi 136170160 gb EBM35588.1  hypothetical protein G ( 362) 290 75.5 4.5e-11	gi 135931467 gb EBK79039.1  hypothetical protein G ( 381) 267 70.2 1.8e-09
gi 143039367 gb EDC37030.1  hypothetical protein G ( 376) 289 75.3 5.4e-11	gi 167780872 gb ABZ99170.1  Putative fatty acid de ( 393) 267 70.2 1.9e-09
gi 166089930 dbj BAG04638.1  delta 6 acyl-lipid de ( 364) 287 74.8 7.3e-11	gi 167777164 gb ABZ95465.1  Fatty acid desaturase ( 393) 267 70.2 1.9e-09
gi 144221401 gb EDJ74889.1  hypothetical protein G ( 310) 286 74.5 7.5e-11	gi 169155987 emb CAQ01121.1  putative fatty acid d ( 371) 266 70.0 2.1e-09
gi 88184723 gb EAQ92191.1  hypothetical protein CH ( 405) 287 74.8 7.9e-11	gi 148917606 emb CAO00494.1  unnamed protein produ ( 450) 266 70.0 2.5e-09
gi 187372747 gb ACD03117.1  delta-5 fatty acid des ( 439) 287 74.8 8.5e-11	gi 142793996 gb EDA62990.1  hypothetical protein G ( 326) 264 69.5 2.6e-09
gi 135013953 gb EBE93475.1  hypothetical protein G ( 278) 284 74.0 9.4e-11	gi 23452396 gb AAN33029.1  delta 6-desaturase-like ( 169) 260 68.4 2.9e-09
gi 134368802 gb EBA94147.1  hypothetical protein G ( 362) 285 74.3 1e-10	gi 147830365 emb CAN01300.1  putative fatty acid d ( 367) 263 69.3 3.4e-09
gi 135299436 gb EBG71506.1  hypothetical protein G ( 371) 284 74.1 1.2e-10	gi 217271813 gb ACK27994.1  Sequence 8 from patent ( 456) 264 69.6 3.5e-09
gi 210118290 gb EEA66022.1  hypothetical protein B ( 255) 282 73.6 1.2e-10	gi 217271812 gb BAC27993.1  Sequence 6 from patent ( 466) 264 69.6 3.5e-09
gi 142964797 gb EDB84170.1  hypothetical protein G ( 342) 283 73.9 1.3e-10	gi 90082433 dbj BAE90398.1  unnamed protein produc ( 146) 258 67.9 3.5e-09
gi 159026904 emb CAO89155.1  desD [Microcystis aer ( 364) 283 73.9 1.4e-10	gi 217271811 gb ACK27992.1  Sequence 4 from patent ( 473) 264 69.6 3.6e-09
gi 119710109 gb ABL96295.1  delta-5 desaturase [Pa ( 425) 281 73.5 2.2e-10	gi 136790444 gb EBQ42522.1  hypothetical protein G ( 383) 262 69.0 4.1e-09
gi 135358824 gb EBH10478.1  hypothetical protein G ( 364) 280 73.2 2.2e-10	gi 136611795 gb EBP28193.1  hypothetical protein G ( 325) 261 68.8 4.2e-09
gi 136109683 gb EBL97756.1  hypothetical protein G ( 282) 277 72.4 2.9e-10	gi 85821182 gb EAQ42329.1  Fatty acid desaturase [ ( 364) 261 68.8 4.6e-09
gi 135055165 gb EBF20558.1  hypothetical protein G ( 354) 278 72.7 3e-10	gi 162953181 gb ABY22696.1  putative delta fatty a ( 385) 260 68.6 5.7e-09
gi 349563 gb AA27286.1  delta-6 desaturase ( 359) 277 72.5 3.6e-10	gi 40034123 emb CAE90492.1  unnamed protein produc ( 160) 255 67.2 6.2e-09
gi 1653589 dbj BAA18502.1  delta-6 desaturase [Syn ( 359) 277 72.5 3.6e-10	gi 193786544 dbj BAG51327.1  unnamed protein produ ( 160) 255 67.2 6.2e-09
gi 158508158 gb ABW65782.1  Sequence 2 from patent ( 359) 277 72.5 3.6e-10	gi 26328979 dbj BAC28228.1  unnamed protein produc ( 287) 258 68.0 6.2e-09
gi 167275964 gb ABZ28828.1  Sequence 2766 from pat ( 359) 277 72.5 3.6e-10	gi 29605945 dbj BAC70009.1  putative fatty acid de ( 365) 259 68.3 6.4e-09
gi 3999224 gb AAC92656.1 AR021718 Sequence 2 from ( 359) 277 72.5 3.6e-10	gi 193784729 dbj BAG53882.1  unnamed protein produ ( 168) 255 67.2 6.4e-09
gi 145009143 gb ABP23375.1  Sequence 2 from patent ( 359) 277 72.5 3.6e-10	gi 40034682 emb CAE90732.1  unnamed protein produc ( 168) 255 67.2 6.4e-09
gi 42689975 gb AAS32274.1  Sequence 2 from patent ( 359) 277 72.5 3.6e-10	gi 193786568 dbj BAG51351.1  unnamed protein produ ( 168) 255 67.2 6.4e-09
gi 10056258 gb AAE33164.1  Sequence 6 from patent ( 359) 277 72.5 3.6e-10	gi 34365279 emb CAE45971.1  hypothetical protein [ ( 196) 255 67.3 7.3e-09
gi 2096440 gb AAB55272.1  Sequence 2 from patent U ( 359) 277 72.5 3.6e-10	gi 45503662 gb CAF86845.1  unnamed protein produc ( 210) 255 67.3 7.7e-09
gi 12808275 gb AAE43495.1  Sequence 16 from patent ( 359) 277 72.5 3.6e-10	gi 193786708 dbj BAG52031.1  unnamed protein produ ( 210) 255 67.3 7.7e-09
gi 20251302 gb AAE96305.1  Sequence 2 from patent ( 359) 277 72.5 3.6e-10	gi 134059500 emb CAM41728.1  fatty acid desaturase ( 417) 257 67.9 9.8e-09
gi 33757666 gb AAQ51239.1  Sequence 6 from patent ( 359) 277 72.5 3.6e-10	gi 76875123 emb CAI86344.1  putative fatty acid de ( 350) 256 67.6 1e-08
gi 1612522 gb AAB15502.1  Sequence 2 from patent U ( 359) 277 72.5 3.6e-10	gi 12808271 gb AAE43491.1  Sequence 12 from patent ( 143) 251 66.3 1.1e-08
gi 2490943 gb AAB79079.1 I63793 Sequence 2 from pa ( 359) 277 72.5 3.6e-10	gi 10055438 gb AAE32344.1  Sequence 11 from patent ( 143) 251 66.3 1.1e-08
gi 3012071 gb AAC11519.1 I75930 Sequence 2 from pa ( 359) 277 72.5 3.6e-10	gi 23313409 gb AAN19967.1  Sequence 11 from patent ( 143) 251 66.3 1.1e-08
gi 23329297 gb AAN26131.1  Sequence 13 from patent ( 287) 274 71.7 4.8e-10	gi 14477730 gb AAE61293.1  Sequence 11 from patent ( 143) 251 66.3 1.1e-08

gi 45502914 emb CAF86199.1	unnamed protein produc	( 322)	255	67.4	1.1e-08	gi 139506752 gb ECF54077.1	hypothetical protein G	( 154)	234	62.4	1.7e-07
gi 21740255 emb CAD39138.1	hypothetical protein [	( 91)	248	65.4	1.2e-08	gi 110817945 gb ABG93229.1	probable linoleoyl-CoA	( 390)	238	63.5	1.9e-07
gi 62774614 gb AA02007.1	Sequence 18 from patent	( 356)	255	67.4	1.2e-08	gi 141421268 gb ECR7099.1	hypothetical protein G	( 233)	235	62.7	2.1e-07
gi 23329303 gb AAN26137.1	Sequence 19 from patent	( 356)	255	67.4	1.2e-08	gi 148569588 gb ABQ91733.1	fatty acid desaturase	( 346)	237	63.3	2.1e-07
gi 120325829 gb ABM20144.1	fatty acid desaturase	( 357)	255	67.4	1.2e-08	gi 119951021 gb ABMO9932.1	putative delta 6 fatty	( 362)	237	63.3	2.1e-07
gi 143139481 gb EDD10306.1	hypothetical protein G	( 385)	255	67.4	1.3e-08	gi 142467276 gb ECY29127.1	hypothetical protein G	( 326)	236	63.0	2.3e-07
gi 10055436 gb AAE32342.1	Sequence 9 from patent	( 131)	249	65.8	1.4e-08	gi 158114110 gb ABW16307.1	fatty acid desaturase	( 360)	236	63.0	2.5e-07
gi 12808269 gb AAE43489.1	Sequence 10 from patent	( 131)	249	65.8	1.4e-08	gi 183580191 dbj BAG28662.1	hypothetical protein	( 370)	236	63.0	2.6e-07
gi 14477728 gb AAE61291.1	Sequence 9 from patent	( 131)	249	65.8	1.4e-08	gi 163775730 gb EDQ89353.1	predicted protein [Mon	( 453)	237	63.3	2.6e-07
gi 23313407 gb AAN19965.1	Sequence 9 from patent	( 131)	249	65.8	1.4e-08	gi 143164003 gb EDD27862.1	hypothetical protein G	( 384)	236	63.0	2.6e-07
gi 119594381 gb EAW73975.1	fatty acid desaturase	( 422)	255	67.5	1.4e-08	gi 193075956 gb ABO10536.2	putative linoleoyl-CoA	( 391)	236	63.1	2.7e-07
gi 158261605 dbj BAF82980.1	unnamed protein produ	( 422)	255	67.5	1.4e-08	gi 141237040 gb ECQ57189.1	hypothetical protein G	( 203)	232	62.0	3e-07
gi 12002125 gb AAG43192.1	AF108658_1 p5327 [Homo s	( 422)	255	67.5	1.4e-08	gi 183207976 gb ACC55374.1	Fatty acid desaturase	( 382)	235	62.8	3.1e-07
gi 144580406 gb ABO98466.1	predicted protein [Ost	( 434)	255	67.5	1.4e-08	gi 169150862 emb CAO99465.1	conserved hypothetical	( 382)	235	62.8	3.1e-07
gi 209586126 gb ACC64811.1	microsomal delta-5 des	( 477)	255	67.5	1.5e-08	gi 138069375 gb EBX56952.1	hypothetical protein G	( 215)	232	62.0	3.1e-07
gi 14042244 dbj BAB55167.1	unnamed protein produc	( 168)	248	65.6	2e-08	gi 33704153 gb AAQ28628.1	Sequence 5600 from pate	( 390)	235	62.8	3.1e-07
gi 40037090 emb CAE91508.1	unnamed protein produc	( 168)	248	65.6	2e-08	gi 110818249 gb ABG93533.1	probable fatty acid de	( 406)	235	62.8	3.2e-07
gi 111153325 emb CAJ65077.1	Linoleoyl-CoA desatur	( 381)	252	66.7	2e-08	gi 160814769 emb CAP40229.1	unnamed protein produ	( 417)	235	62.8	3.3e-07
gi 144050064 gb EDI50465.1	hypothetical protein G	( 324)	251	66.5	2.1e-08	gi 68124314 emb CAJ07076.1	fatty acid desaturase,	( 417)	235	62.8	3.3e-07
gi 86264104 gb ABC87787.1	delta-6-desaturase [Cot	( 407)	252	66.8	2.1e-08	gi 51493745 gb AAU04860.1	fatty acid desaturase 2	( 233)	232	62.0	3.3e-07
gi 54018085 dbj BAF59455.1	putative fatty acid de	( 416)	251	66.5	2.6e-08	gi 119954888 gb ABM11893.1	fatty acid desaturase	( 369)	234	62.6	3.5e-07
gi 4884144 emb CAB43280.1	hypothetical protein [H	( 311)	249	66.0	2.8e-08	gi 213986787 gb ACJ57086.1	Linoleoyl-CoA desatura	( 382)	234	62.6	3.6e-07
gi 119947604 gb ABM06515.1	putative fatty acid de	( 386)	250	66.3	2.8e-08	gi 169150677 emb CAM88587.1	conserved hypothetical	( 382)	234	62.6	3.6e-07
gi 210090977 gb EAA39240.1	hypothetical protein B	( 424)	250	66.3	3.1e-08	gi 119949221 gb ABMO8132.1	putative delta 6 fatty	( 405)	234	62.6	3.8e-07
gi 45685163 gb AAS75335.1	delta-11 fatty acid des	( 477)	250	66.3	3.4e-08	gi 110822828 gb ABG98112.1	possible fatty acid de	( 418)	234	62.6	3.9e-07
gi 156211152 gb EDO32278.1	predicted protein [Nem	( 298)	247	65.5	3.7e-08	gi 157422916 gb AAI53462.1	Fads2 protein [Danio r	( 158)	229	61.2	3.9e-07
gi 62822747 gb AAI15136.1	delta-4 desaturase [Pav	( 447)	249	66.1	3.7e-08	gi 213054610 gb ACJ39512.1	fatty acid desaturase	( 382)	233	62.4	4.2e-07
gi 119954878 gb ABM11883.1	fatty acid desaturase	( 401)	248	65.8	4e-08	gi 110819865 gb ABG95149.1	fatty acid desaturase	( 400)	233	62.4	4.4e-07
gi 152029615 gb ABS27383.1	Linoleoyl-CoA desatura	( 426)	248	65.8	4.2e-08	gi 60172939 gb AAI14503.1	putative desaturase [Th	( 515)	234	62.7	4.6e-07
gi 29605235 dbj BAC69302.1	putative fatty acid de	( 353)	247	65.6	4.2e-08	gi 15147883 dbj BAB62850.1	putative delta-6 fatty	( 445)	233	62.4	4.8e-07
gi 167349333 gb AB272068.1	fatty acid desaturase	( 342)	246	65.3	4.9e-08	gi 110820966 gb ABG96250.1	possible linoleoyl-CoA	( 329)	231	61.9	5.2e-07
gi 134898210 gb EBE15874.1	hypothetical protein G	( 290)	245	65.1	5e-08	gi 141049999 gb ECP28833.1	hypothetical protein G	( 303)	230	61.6	5.7e-07
gi 146153926 gb ABQ04780.1	Linoleoyl-CoA desatura	( 365)	245	65.1	6e-08	gi 92392651 gb ABE73926.1	fatty acid desaturase [	( 448)	232	62.2	5.7e-07
gi 149062369 gb EDM12792.1	fatty acid desaturase	( 146)	240	63.7	6.3e-08	gi 62774612 gb AAI02005.1	Sequence 16 from patent	( 315)	230	61.6	5.9e-07
gi 110589551 gb ABG77281.1	fatty acid desaturase	( 78)	236	62.6	7.1e-08	gi 23329299 gb AAN26133.1	Sequence 15 from patent	( 315)	230	61.6	5.9e-07
gi 144575966 gb ABO94035.1	predicted protein [Ost	( 459)	245	65.2	7.2e-08	gi 49529319 emb CAG7031.1	conserved hypothetical	( 383)	231	61.9	5.9e-07
gi 196193623 gb EDX88582.1	Fatty acid desaturase	( 385)	244	64.9	7.4e-08	gi 47027091 gb AAT08759.1	desaturase [Hyacinthus	( 81)	223	59.6	5.9e-07
gi 136926982 gb EBR23004.1	hypothetical protein G	( 221)	241	64.1	7.5e-08	gi 189830603 gb ACE19261.1	Sequence 5069 from pat	( 177)	227	60.8	5.9e-07
gi 54018084 dbj BAD59454.1	putative fatty acid de	( 484)	245	65.2	7.6e-08	gi 5019332 emb CAB44385.1	putative delta fatty ac	( 345)	230	61.6	6.3e-07
gi 169151651 emb CAP00440.1	putative fatty acid d	( 364)	243	64.7	8.2e-08	gi 145218257 gb ABP47661.1	fatty acid desaturase	( 360)	230	61.6	6.5e-07
gi 193077962 gb ABO12876.2	putative fatty acid de	( 364)	243	64.7	8.2e-08	gi 108770960 gb ABG09682.1	fatty acid desaturase	( 361)	230	61.6	6.5e-07
gi 213986429 gb ACJ56728.1	Linoleoyl-CoA desatura	( 364)	243	64.7	8.2e-08	gi 119695769 gb ABL92842.1	fatty acid desaturase	( 361)	230	61.6	6.5e-07
gi 183210578 gb ACC57976.1	Fatty acid desaturase	( 364)	243	64.7	8.2e-08	gi 126235957 gb ABN99357.1	fatty acid desaturase	( 361)	230	61.6	6.5e-07
gi 213057331 gb ACJ42233.1	fatty acid desaturase	( 364)	243	64.7	8.2e-08	gi 5263169 dbj BAA81814.1	fatty acid desaturase [	( 464)	231	61.9	6.9e-07
gi 169148090 emb CAM85953.1	putative fatty acid d	( 364)	243	64.7	8.2e-08	gi 85773959 gb ABC80796.1	Linoleoyl-CoA desaturas	( 364)	229	61.4	7.9e-07
gi 33702947 gb AAQ27422.1	Sequence 4394 from pate	( 368)	243	64.7	8.3e-08	gi 118174952 gb ABK75848.1	Fatty acid desaturase	( 382)	229	61.4	8e-07
gi 139178176 gb ECD94220.1	hypothetical protein G	( 188)	239	63.6	9.1e-08	gi 162696494 gb EDQ82832.1	predicted protein [Phy	( 475)	230	61.7	8.2e-07
gi 134067410 emb CAM65683.1	fatty acid desaturase	( 417)	243	64.7	9.2e-08	gi 144067825 gb EDI63603.1	hypothetical protein G	( 338)	228	61.2	8.5e-07
gi 157337268 emb CAO21614.1	unnamed protein produ	( 98)	235	62.5	1e-07	gi 144145826 gb EDJ19776.1	hypothetical protein G	( 342)	228	61.2	8.6e-07
gi 110647688 emb CAL17164.1	conserved hypothetical	( 386)	242	64.4	1e-07	gi 160773710 gb AAI55077.1	Fads2 protein [Danio r	( 421)	229	61.5	8.7e-07
gi 116610165 gb ABK02889.1	fatty acid desaturase	( 362)	241	64.2	1.1e-07	gi 14290486 gb AAH09011.1	FADS2 protein [Homo sap	( 386)	228	61.2	9.5e-07
gi 49530373 emb CAG68085.1	putative fatty acid de	( 364)	241	64.2	1.1e-07	gi 196113353 gb ACG67069.1	putative fatty acid de	( 387)	228	61.2	9.5e-07
gi 136729181 gb EBQ01866.1	hypothetical protein G	( 256)	239	63.6	1.2e-07	gi 197699371 gb EDY46304.1	delta fatty acid desat	( 350)	227	60.9	1e-06
gi 149771057 emb CAL42524.1	Fatty acid desaturase	( 365)	240	64.0	1.3e-07	gi 143064945 gb EDC55734.1	hypothetical protein G	( 369)	227	61.0	1.1e-06
gi 138510180 gb ECA09251.1	hypothetical protein G	( 276)	238	63.4	1.5e-07	gi 110822829 gb ABG98113.1	possible fatty acid de	( 412)	226	60.8	1.4e-06
gi 156232843 gb ABU57626.1	fatty acid desaturase	( 341)	239	63.7	1.5e-07	gi 119692555 gb ABL89628.1	fatty acid desaturase	( 368)	225	60.5	1.5e-06
gi 141775249 gb ECT22616.1	hypothetical protein G	( 283)	238	63.4	1.5e-07	gi 108767801 gb ABG06523.1	fatty acid desaturase	( 368)	225	60.5	1.5e-06
gi 117578080 emb CAL66549.1	transmembrane family	( 327)	238	63.5	1.7e-07	gi 9716155 emb CAC01546.1	putative delta fatty ac	( 347)	224	60.3	1.7e-06

gi 116608872 gb ABK01596.1  fatty acid desaturase ( 391)   224   60.3   1.8e-06	gi 121494859 emb CAL73341.1  Possible linoleoyl-Co ( 427)   211   57.3   1.6e-05
gi 145218283 gb ABP47687.1  fatty acid desaturase ( 382)   223   60.0   2.1e-06	gi 135102709 gb EBF50924.1  hypothetical protein G ( 360)   210   57.0   1.6e-05
gi 60220816 emb CAI58907.1  unnamed protein produc ( 482)   224   60.3   2.2e-06	gi 49609602 emb CAG73035.1  putative fatty acid de ( 381)   210   57.1   1.7e-05
gi 126633754 emb CAM55833.1  unnamed protein produ ( 482)   224   60.3   2.2e-06	gi 190580110 gb EDV20196.1  hypothetical protein T ( 464)   211   57.3   1.7e-05
gi 76059316 emb CAJ30852.1  unnamed protein produc ( 482)   224   60.3   2.2e-06	gi 76059314 emb CAJ30851.1  unnamed protein produc ( 476)   211   57.3   1.7e-05
gi 178462655 dbj BAG17175.1  putative delta-6 fatt ( 382)   222   59.8   2.5e-06	gi 126633752 emb CAM55832.1  unnamed protein produ ( 476)   211   57.3   1.7e-05
gi 140965018 gb ECO71441.1  hypothetical protein G ( 269)   220   59.3   2.5e-06	gi 60220814 emb CAI58906.1  unnamed protein produc ( 476)   211   57.3   1.7e-05
gi 140965017 gb ECO71440.1  hypothetical protein G ( 281)   220   59.3   2.6e-06	gi 136526677 gb EBO73567.1  hypothetical protein G ( 330)   209   56.8   1.7e-05
gi 145217878 gb ABP47282.1  fatty acid desaturase ( 345)   221   59.6   2.7e-06	gi 169240644 emb CAM61672.1  Probable fatty acid d ( 403)   210   57.1   1.8e-05
gi 145218274 gb ABP47678.1  fatty acid desaturase ( 357)   221   59.6   2.7e-06	gi 134068412 emb CAM66702.1  delta-6 fatty acid de ( 414)   210   57.1   1.8e-05
gi 126232803 gb ABN96203.1  fatty acid desaturase ( 368)   221   59.6   2.8e-06	gi 60172920 gb AAX14502.1  delta-8 fatty acid desa ( 476)   210   57.1   2e-05
gi 54014770 dbj BAD56140.1  putative fatty acid de ( 382)   221   59.6   2.9e-06	gi 10432462 emb CAC10296.1  putative fatty acid de ( 350)   208   56.6   2.2e-05
gi 23329304 gb AAN26138.1  Sequence 20 from patent ( 219)   218   58.8   3e-06	gi 40161452 gb AAR67465.1  Sequence 29 from patent ( 439)   209   56.9   2.2e-05
gi 62774615 gb AAY02008.1  Sequence 19 from patent ( 219)   218   58.8   3e-06	gi 155709336 gb ABU33985.1  Sequence 29 from paten ( 439)   209   56.9   2.2e-05
gi 68125348 emb CAJ03208.1  delta-6 fatty acid des ( 428)   221   59.6   3.2e-06	gi 112053843 gb ABH96553.1  Sequence 29 from paten ( 439)   209   56.9   2.2e-05
gi 140739434 gb ECN18761.1  hypothetical protein G ( 92)   212   57.1   3.8e-06	gi 155707475 gb ABU33124.1  Sequence 123 from pate ( 439)   209   56.9   2.2e-05
gi 110282811 gb ABG60997.1  fatty acid desaturase ( 363)   219   59.1   3.8e-06	gi 197038258 gb ACH17688.1  Sequence 16 from paten ( 449)   209   56.9   2.3e-05
gi 167283660 gb ABZ36524.1  Sequence 10462 from pa ( 366)   219   59.1   3.8e-06	gi 56664938 gb AAW18135.1  Sequence 16 from patent ( 449)   209   56.9   2.3e-05
gi 196171342 gb ACG72315.1  Linoleoyl-CoA desatura ( 364)   218   58.9   4.5e-06	gi 55163952 emb CAH68801.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 134984268 gb EBE73351.1  hypothetical protein G ( 364)   218   58.9   4.5e-06	gi 60220720 emb CAI58859.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 142109188 gb ECV65610.1  hypothetical protein G ( 243)   215   58.1   5.2e-06	gi 22316698 emb CAC10296.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 119693415 gb ABL90488.1  fatty acid desaturase ( 369)   217   58.7   5.3e-06	gi 190888417 gb ACE95865.1  delta 5 fatty acid des ( 469)   209   56.9   2.3e-05
gi 108768649 gb ABG07371.1  fatty acid desaturase ( 369)   217   58.7   5.3e-06	gi 52748010 emb CAH56931.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 141678995 gb ECS77487.1  hypothetical protein G ( 257)   215   58.1   5.5e-06	gi 22316544 emb CAD44417.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 118166446 gb ABK67343.1  Fatty acid desaturase ( 427)   217   58.7   6e-06	gi 145386837 gb ABP65280.1  delta 5 fatty acid des ( 469)   209   56.9   2.3e-05
gi 41398272 gb AAS05893.1  DesA3_1 [Mycobacterium ( 427)   217   58.7   6e-06	gi 52748018 emb CAH56934.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 118570156 gb ABL04907.1  linoleoyl-CoA desatura ( 428)   216   58.5   7.1e-06	gi 146762533 gb ABQ45365.1  delta-5-desaturase [Ni ( 469)   209   56.9   2.3e-05
gi 157322866 gb ABV41963.1  fatty acid desaturase ( 361)   215   58.2   7.2e-06	gi 126633736 emb CAM55824.1  unnamed protein produ ( 469)   209   56.9   2.3e-05
gi 140816700 gb ECN71323.1  hypothetical protein G ( 259)   213   57.6   7.6e-06	gi 40781967 emb CAF05427.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 138424096 gb EBZ57519.1  hypothetical protein G ( 100)   208   56.2   7.7e-06	gi 40781940 emb CAF05417.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 57228571 gb AAW45006.1  cytochrome b2, mitochon ( 593)   217   58.8   7.9e-06	gi 22316669 emb CAD44437.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 139193582 gb ECE05189.1  hypothetical protein G ( 195)   211   57.1   8.2e-06	gi 76059220 emb CAJ30807.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 126348216 emb CAJ89937.1  putative delta fatty ( 352)   214   58.0   8.3e-06	gi 209582581 gb ACI65202.1  delta 5 fatty acid des ( 469)   209   56.9   2.3e-05
gi 183174663 gb ACC39773.1  linoleoyl-CoA desatura ( 428)   215   58.2   8.3e-06	gi 55163944 emb CAH68798.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 140191202 gb ECK14420.1  hypothetical protein G ( 198)   211   57.1   8.3e-06	gi 50831506 emb CAH05233.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 62774616 gb AAY02009.1  Sequence 20 from patent ( 182)   210   56.9   9.1e-06	gi 19879687 gb EAL92562.1  delta 5 fatty acid desa ( 469)   209   56.9   2.3e-05
gi 23329305 gb AAN26139.1  Sequence 21 from patent ( 182)   210   56.9   9.1e-06	gi 22316515 emb CAD44407.1  unnamed protein produc ( 469)   209   56.9   2.3e-05
gi 140258005 gb ECK60243.1  hypothetical protein G ( 137)   208   56.3   1e-05	gi 50882495 gb AAT85663.1  polyunsaturated fatty a ( 484)   209   56.9   2.4e-05
gi 119955452 gb ABM12457.1  fatty acid desaturase ( 377)   213   57.7   1e-05	gi 212002032 gb EEB07692.1  cytochrome b5 reductas ( 124)   202   54.9   2.4e-05
gi 190347535 gb EDK39822.2  hypothetical protein P ( 335)   212   57.5   1.1e-05	gi 119955585 gb ABM12590.1  fatty acid desaturase ( 415)   208   56.6   2.5e-05
gi 196170643 gb ACG71616.1  Linoleoyl-CoA desatura ( 364)   212   57.5   1.2e-05	gi 167349344 gb ABZ72079.1  fatty acid desaturase ( 361)   207   56.3   2.6e-05
gi 143901661 gb EDH45092.1  hypothetical protein G ( 138)   207   56.1   1.2e-05	gi 207085835 gb EAD263119.1  fatty acid desaturase ( 451)   208   56.6   2.6e-05
gi 119539360 gb ABL83977.1  fatty acid desaturase ( 409)   212   57.5   1.3e-05	gi 83766989 dbj BAE57129.1  unnamed protein produc ( 474)   208   56.6   2.8e-05
gi 12808270 gb AAE43490.1  Sequence 11 from patent ( 87)   204   55.3   1.3e-05	gi 205277856 gb ACI01557.1  nitrate reductase [Sol ( 270)   205   55.8   2.8e-05
gi 10055437 gb AEE32343.1  Sequence 10 from patent ( 87)   204   55.3   1.3e-05	gi 88180680 gb EAQ88148.1  hypothetical protein CH ( 502)   208   56.7   2.9e-05
gi 23313408 gb AAN19966.1  Sequence 10 from patent ( 87)   204   55.3   1.3e-05	gi 145217762 gb ABP47166.1  fatty acid desaturase ( 418)   207   56.4   2.9e-05
gi 14477729 gb AAE61292.1  Sequence 10 from patent ( 87)   204   55.3   1.3e-05	gi 155241942 gb ABT18092.1  delta-6 fatty acid des ( 197)   203   55.3   3e-05
gi 155241962 gb ABT18093.1  delta-6 fatty acid des ( 197)   208   56.4   1.3e-05	gi 205277978 gb ACI01618.1  nitrate reductase [Sol ( 270)   204   55.6   3.3e-05
gi 137349334 gb EBT59938.1  hypothetical protein G ( 209)   208   56.4   1.4e-05	gi 140708236 gb ECM96873.1  hypothetical protein G ( 277)   204   55.6   3.4e-05
gi 46361702 gb AAS89346.1  putative delta-6 fatty ( 213)   208   56.4   1.4e-05	gi 142123983 gb ECV76534.1  hypothetical protein G ( 340)   205   55.9   3.4e-05
gi 121494767 emb CAL73248.1  Possible linoleoyl-Co ( 427)   211   57.3   1.6e-05	gi 18199570 emb CAE49221.1  Conserved hypothetical ( 426)   206   56.2   3.5e-05
gi 38490343 emb CAE55572.1  POSSIBLE LINOLEOYL-CoA ( 427)   211   57.3   1.6e-05	gi 158603254 gb EDP39249.1  Delta5 fatty acid desa ( 138)   200   54.5   3.6e-05
gi 148722958 gb ABR07583.1  hypothetical linoleoyl ( 427)   211   57.3   1.6e-05	gi 4150956 dbj BAA37090.1  delta 5 fatty acid desa ( 467)   206   56.2   3.8e-05
gi 134151369 gb EBA43414.1  hypothetical linoleoyl ( 427)   211   57.3   1.6e-05	gi 213509839 emb CAS92469.1  unnamed protein produ ( 573)   207   56.5   3.8e-05
gi 31620006 emb CAD95350.1  POSSIBLE LINOLEOYL-CoA ( 427)   211   57.3   1.6e-05	gi 2748 emb CAA34183.1  L-lactate:cytochrome c oxi ( 573)   207   56.5   3.8e-05
gi 13883146 gb AAK47669.1  linoleoyl-CoA desaturas ( 427)   211   57.3   1.6e-05	gi 110819941 gb ABG95225.1  probable fatty acid de ( 402)   205   55.9   3.9e-05
gi 124599372 gb EAY58476.1  hypothetical protein T ( 427)   211   57.3   1.6e-05	gi 49609603 emb CAG73036.1  putative fatty acid de ( 363)   204   55.7   4.2e-05
gi 148507244 gb ABQ75053.1  putative linoleoyl-CoA ( 427)   211   57.3   1.6e-05	gi 145303946 gb ABP54528.1  fatty acid desaturase ( 380)   204   55.7   4.4e-05

gi 157916653 gb ABV98080.1 fatty acid desaturase (380)	204	55.7	4.4e-05	gi 205277896 gb ACI01577.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 89287624 gb EAR85613.1 Cytochrome b5-like Heme (214)	201	54.8	4.4e-05	gi 205277976 gb ACI01617.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 210073804 gb EEA27891.1 mitochondrial cytochro (495)	205	56.0	4.6e-05	gi 205277972 gb ACI01615.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 110084610 gb ABG49441.1 fatty acid desaturase (90)	196	53.4	4.8e-05	gi 205278008 gb ACI01633.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 118570155 gb ABL04906.1 linoleoyl-CoA desaturase (428)	204	55.7	4.8e-05	gi 205277852 gb ACI01555.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 126091402 gb ABN66175.1 outer mitochondrial me (164)	199	54.3	4.9e-05	gi 205277890 gb ACI01574.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 134953667 gb EBE52727.1 hypothetical protein G (136)	198	54.0	4.9e-05	gi 205277958 gb ACI01608.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 139434429 gb ECF08979.1 hypothetical protein G (137)	198	54.0	4.9e-05	gi 205277866 gb ACI01562.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 67633944 gb AAY78896.1 delta-6 fatty acid desaturase (140)	198	54.0	5e-05	gi 205277886 gb ACI01572.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 170946111 emb CAP72912.1 unnamed protein product (460)	204	55.7	5.1e-05	gi 205277964 gb ACI01611.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 143761571 gb EDG65392.1 hypothetical protein G (212)	200	54.6	5.1e-05	gi 205277982 gb ACI01620.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 144583100 gb ABP01215.1 predicted protein [Ost (465)	204	55.7	5.2e-05	gi 205277898 gb ACI01578.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 144581334 gb ABO99391.1 predicted protein [Ost (466)	204	55.7	5.2e-05	gi 205277900 gb ACI01579.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 137166137 gb EBS57310.1 hypothetical protein G (261)	201	54.9	5.2e-05	gi 205277950 gb ACI01604.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 144581330 gb ABO99387.1 predicted protein [Ost (587)	205	56.0	5.3e-05	gi 205277846 gb ACI01552.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 144583104 gb ABP01219.1 predicted protein [Ost (587)	205	56.0	5.3e-05	gi 205277902 gb ACI01580.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277980 gb ACI01619.1 nitrate reductase [Sol (270)	201	54.9	5.3e-05	gi 205277960 gb ACI01609.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 70832613 gb EAN78117.1 delta-6 fatty acid desaturase (421)	203	55.5	5.6e-05	gi 205277928 gb ACI01593.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 145218306 gb ABP47710.1 fatty acid desaturase (464)	203	55.5	6e-05	gi 205277876 gb ACI01567.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 141112541 gb ECP71320.1 hypothetical protein G (150)	197	53.8	6.2e-05	gi 205278014 gb ACI01636.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277912 gb ACI01585.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277874 gb ACI01566.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277990 gb ACI01624.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277850 gb ACI01554.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277948 gb ACI01603.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277974 gb ACI01616.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277952 gb ACI01605.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277920 gb ACI01589.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277942 gb ACI01600.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277878 gb ACI01568.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277970 gb ACI01614.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277954 gb ACI01606.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277854 gb ACI01556.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277996 gb ACI01627.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05
gi 205277930 gb ACI01594.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 143284203 gb EDE11570.1 hypothetical protein G (421)	202	55.2	6.5e-05
gi 205277858 gb ACI01558.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 136493923 gb EB052473.1 hypothetical protein G (358)	201	55.0	6.7e-05
gi 205277924 gb ACI01591.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 121888048 gb EAX93542.1 Cytochrome b5-like Heme (94)	194	53.0	6.9e-05
gi 205278000 gb ACI01629.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 197710788 gb EDY54822.1 fatty acid desaturase (372)	201	55.0	6.9e-05
gi 205277916 gb ACI01587.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 197704570 gb EDY50382.1 fatty acid desaturase (381)	201	55.0	7.1e-05
gi 205277994 gb ACI01626.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 194348865 gb ACF51988.1 fatty acid desaturase (382)	201	55.0	7.1e-05
gi 205277848 gb ACI01553.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 190012664 emb CAQ46292.1 putative transmembrane protein (382)	201	55.0	7.1e-05
gi 205277992 gb ACI01625.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 70834807 gb EAN80309.1 cytochrome b5, putative (119)	195	53.3	7.1e-05
gi 205277934 gb ACI01596.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 108878830 gb EAT43055.1 flavo-hemoprotein B5/b5 (478)	202	55.3	7.3e-05
gi 205278016 gb ACI01637.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277884 gb ACI01571.1 nitrate reductase [Sol (270)	199	54.4	7.3e-05
gi 205277870 gb ACI01564.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277944 gb ACI01601.1 nitrate reductase [Sol (270)	199	54.4	7.3e-05
gi 205277888 gb ACI01573.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 517356 emb CAA56696.1 nitrate reductase (NADH) (900)	205	56.1	7.5e-05
gi 205277872 gb ACI01565.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 134060453 emb CAM37621.1 delta-6 fatty acid desaturase (414)	201	55.0	7.6e-05
gi 205277936 gb ACI01597.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 34102956 gb AAQ59320.1 linoleoyl-CoA desaturase (369)	200	54.7	8.1e-05
gi 205277932 gb ACI01595.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 199431473 emb CAR65620.1 DEHA2D05522p [Debaryo (552)	202	55.3	8.2e-05
gi 205277962 gb ACI01610.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 124422628 emb CAK87454.1 unnamed protein product (258)	198	54.2	8.3e-05
gi 205277908 gb ACI01583.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 163777722 gb EDQ91338.1 predicted protein [Mon (384)	200	54.7	8.3e-05
gi 205277860 gb ACI01559.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 143029156 gb EDC29503.1 hypothetical protein G (385)	200	54.7	8.4e-05
gi 205278018 gb ACI01638.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 138505134 gb ECA06792.1 hypothetical protein G (146)	195	53.3	8.4e-05
gi 205277986 gb ACI01622.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205278004 gb ACI01631.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205277880 gb ACI01569.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277918 gb ACI01588.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205277956 gb ACI01607.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277904 gb ACI01581.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205277844 gb ACI01551.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205278002 gb ACI01630.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205277894 gb ACI01576.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277914 gb ACI01586.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205277984 gb ACI01621.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277906 gb ACI01582.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205277940 gb ACI01599.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277998 gb ACI01628.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205277946 gb ACI01602.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277910 gb ACI01584.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205278006 gb ACI01632.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277864 gb ACI01561.1 nitrate reductase [Sol (270)	198	54.2	8.6e-05
gi 205277862 gb ACI01560.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 138571936 gb ECA52388.1 hypothetical protein G (239)	197	53.9	9.1e-05
gi 205277938 gb ACI01598.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 197304190 emb CAQ30478.1 Acyl-CoA dependent dehydrogenase (482)	200	54.8	0.0001
gi 205277868 gb ACI01563.1 nitrate reductase [Sol (270)	200	54.7	6.2e-05	gi 205277892 gb ACI01575.1 nitrate reductase [Sol (270)	197	54.0	0.0001

gi 205277988 gb ACI01623.1  nitrate reductase [Sol ( 270) 197 54.0 0.0001	gi 19068516 emb CAD24984.1  similarity to HYPOTHET ( 94) 186 51.2 0.00025
gi 143992888 gb EDI09679.1  hypothetical protein G ( 270) 197 54.0 0.0001	gi 169117664 gb ECLA42970.1  putative fatty acid de ( 387) 193 53.1 0.00026
gi 138080494 gb EBX63372.1  hypothetical protein G ( 273) 197 54.0 0.0001	gi 140435196 gb ECL73148.1  hypothetical protein G ( 122) 187 51.5 0.00027
gi 116061092 emb CAL56480.1  Cytochrome b5 (ISS) [ ( 614) 201 55.1 0.0001	gi 3849989 emb CAA11232.1  nitrate reductase [Pich ( 859) 197 54.3 0.00026
gi 139425642 gb ECF04173.1  hypothetical protein G ( 142) 193 52.9 0.00011	gi 902626 emb CAA88925.1  nitrate reductase [Pichi ( 859) 197 54.3 0.00026
gi 124425040 emb CAK89828.1  unnamed protein produ ( 258) 196 53.7 0.00011	gi 49527995 emb CAG61646.1  unnamed protein produc ( 593) 195 53.7 0.00027
gi 119538550 gb ABL83167.1  fatty acid desaturase ( 400) 198 54.3 0.00012	gi 213509823 emb CAS92461.1  unnamed protein produ ( 593) 195 53.7 0.00027
gi 211589958 emb CAP96113.1  Pc21g12160 [Penicilli ( 488) 199 54.6 0.00012	gi 126233795 gb ABN97195.1  fatty acid desaturase ( 413) 193 53.1 0.00027
gi 116060892 emb CAL57370.1  polyunsaturated fatty ( 491) 199 54.6 0.00012	gi 177540045 gb ACB73000.1  nitrate reductase [Bet ( 905) 197 54.3 0.00027
gi 150415742 gb EDN11086.1  cytochrome b2, mitoch ( 513) 199 54.6 0.00012	gi 157932108 gb ABW05098.1  nitrate reductase [Bet ( 905) 197 54.3 0.00027
gi 183174664 gb ACC39774.1  linoleoyl-CoA desatura ( 428) 198 54.3 0.00013	gi 159124962 gb EDP50079.1  mitochondrial cytochro ( 533) 194 53.4 0.00029
gi 139726005 gb ECH04863.1  hypothetical protein G ( 243) 195 53.5 0.00013	gi 159127043 gb EDP52159.1  cytochrome b5, putativ ( 137) 187 51.5 0.00029
gi 136389516 gb EBN84143.1  hypothetical protein G ( 243) 195 53.5 0.00013	gi 135882077 gb EBK44848.1  hypothetical protein G ( 114) 186 51.2 0.00029
gi 142426436 gb ECX99050.1  hypothetical protein G ( 362) 197 54.0 0.00013	gi 178462727 dbj BAG17247.1  putative fatty acid d ( 372) 192 52.9 0.00029
gi 135737182 gb EBJ52948.1  hypothetical protein G ( 304) 196 53.8 0.00013	gi 116000840 emb CAL50520.1  cytochrome b5 isoform ( 127) 186 51.2 0.00032
gi 190348942 gb EDK41496.2  hypothetical protein P ( 547) 199 54.6 0.00013	gi 14041825 dbj BAB55002.1  nitrate reductase [Pru ( 906) 196 54.0 0.00032
gi 124425583 emb CAK90368.1  unnamed protein produ ( 313) 196 53.8 0.00013	gi 118175254 gb ABK76150.1  Fatty acid desaturase ( 418) 192 52.9 0.00032
gi 144580331 gb ABO90361.1  predicted protein [Ost ( 866) 201 55.2 0.00014	gi 190581744 gb EDV21800.1  expressed hypothetical ( 132) 186 51.2 0.00033
gi 194339836 gb EDX20802.1  delta fatty acid desat ( 270) 195 53.5 0.00014	gi 134054562 emb CAK43417.1  unnamed protein produ ( 351) 191 52.6 0.00033
gi 170945102 emb CAP71213.1  unnamed protein produ ( 498) 198 54.4 0.00014	gi 57223484 gb AAW41527.1  acyl-CoA dehydrogenase, ( 522) 193 53.2 0.00033
gi 21165531 dbj BAB93533.1  nitrate reductase [Sol ( 750) 200 54.9 0.00014	gi 138049319 gb EDP52159.1  hypothetical protein G ( 134) 186 51.2 0.00033
gi 167499 gb AAA33114.1  nitrate reductase ( 918) 201 55.2 0.00015	gi 41398476 gb AAS06096.1  DesA3_2 [Mycobacterium ( 366) 191 52.7 0.00034
gi 114192090 gb EAU33790.1  conserved hypothetical ( 773) 200 54.9 0.00015	gi 62176818 gb AAX70916.1  hypothetical protein, c ( 182) 187 51.6 0.00036
gi 140751864 gb ECN27244.1  hypothetical protein G ( 254) 194 53.3 0.00016	gi 70802212 gb AAZ12117.1  hypothetical protein, c ( 182) 187 51.6 0.00036
gi 126234693 gb ABN98093.1  fatty acid desaturase ( 464) 197 54.1 0.00016	gi 119399741 gb EAW10167.1  mitochondrial cytochro ( 495) 192 53.0 0.00037
gi 119694440 gb ABL91513.1  fatty acid desaturase ( 464) 197 54.1 0.00016	gi 108768749 gb ABG07471.1  fatty acid desaturase ( 413) 191 52.7 0.00037
gi 108769654 gb ABG08376.1  fatty acid desaturase ( 464) 197 54.1 0.00016	gi 119693516 gb ABL90589.1  fatty acid desaturase ( 413) 191 52.7 0.00037
gi 167863095 gb EDS26478.1  flavohemoprotein B5/b5 ( 688) 199 54.7 0.00016	gi 136536686 gb EBO79932.1  hypothetical protein G ( 340) 190 52.4 0.00037
gi 119538650 gb ABL83267.1  fatty acid desaturase ( 384) 196 53.8 0.00016	gi 470678 gb AAA18377.1  NADH:nitrate reductase ( 640) 193 53.3 0.00039
gi 205277926 gb ACI01592.1  nitrate reductase [Sol ( 270) 194 53.3 0.00016	gi 142586045 gb ECZ13929.1  hypothetical protein G ( 295) 189 52.1 0.00039
gi 205278012 gb ACI01635.1  nitrate reductase [Sol ( 270) 194 53.3 0.00016	gi 157335970 emb CA061800.1  unnamed protein produ ( 647) 193 53.3 0.00039
gi 205278010 gb ACI01634.1  nitrate reductase [Sol ( 270) 194 53.3 0.00016	gi 183173693 gb ACC38803.1  linoleoyl-CoA desatura ( 377) 190 52.4 0.00041
gi 205277968 gb ACI01613.1  nitrate reductase [Sol ( 270) 194 53.3 0.00016	gi 119407401 gb EAW17350.1  cytochrome b5, putativ ( 97) 183 50.5 0.00041
gi 205277966 gb ACI01612.1  nitrate reductase [Sol ( 270) 194 53.3 0.00016	gi 124426835 emb CAK91615.1  unnamed protein produ ( 215) 187 51.6 0.00041
gi 205277842 gb ACI01550.1  nitrate reductase [Sol ( 270) 194 53.3 0.00016	gi 139747378 gb ECH18288.1  hypothetical protein G ( 180) 186 51.3 0.00042
gi 205277882 gb ACI01570.1  nitrate reductase [Sol ( 270) 194 53.3 0.00016	gi 144581090 gb ABO99148.1  predicted protein [Ost ( 491) 191 52.7 0.00043
gi 205277840 gb ACI01549.1  nitrate reductase [Sol ( 270) 194 53.3 0.00016	gi 90300530 gb EAS30161.1  hypothetical protein CI ( 504) 191 52.7 0.00044
gi 205277922 gb ACI01590.1  nitrate reductase [Sol ( 272) 194 53.3 0.00016	gi 118168179 gb ABK69076.1  Fatty acid desaturase ( 366) 189 52.2 0.00047
gi 46241490 gb AAS82948.1  delta-6 fatty acid desa ( 153) 191 52.4 0.00017	gi 194344571 gb EDX25537.1  fatty acid desaturase ( 372) 189 52.2 0.00047
gi 213509817 emb CAS92457.1  unnamed protein produ ( 501) 197 54.1 0.00017	gi 138345036 gb EBZ09991.1  hypothetical protein G ( 260) 187 51.6 0.00048
gi 294114 gb AAA33713.1  nitrate reductase ( 909) 200 55.0 0.00017	gi 83634598 gb ABC30565.1  Fatty acid desaturase [ ( 388) 189 52.2 0.00049
gi 19283 emb CAA32218.1  nitrate reductase [Solanu ( 911) 200 55.0 0.00017	gi 210065295 gb EEA19389.1  cytochrome B2, putativ ( 489) 190 52.5 0.0005
gi 21165533 dbj BAB93534.1  nitrate reductase [Sol ( 911) 200 55.0 0.00017	gi 119397585 gb EAW08016.1  mitochondrial cytochro ( 495) 190 52.5 0.00051
gi 1946812 gb AAB52786.1  NADH nitrate reductase [ ( 911) 200 55.0 0.00017	gi 143664847 gb EDG15129.1  hypothetical protein G ( 408) 189 52.2 0.00051
gi 1673613 gb AAB18985.1  NADH nitrate reductase [ ( 911) 200 55.0 0.00017	gi 140226880 gb EAW17350.1  hypothetical protein G ( 188) 185 51.1 0.00051
gi 484212 gb AAA33712.1  nitrate reductase apoenzy ( 915) 200 55.0 0.00017	gi 211969281 gb EEB04477.1  cytochrome b5, putativ ( 233) 186 51.4 0.00052
gi 210092261 gb EEA40492.1  hypothetical protein B ( 527) 197 54.1 0.00017	gi 662902 emb CAA58909.1  nitrate reductase (NADH) ( 920) 193 53.4 0.00052
gi 140236009 gb ECK45013.1  hypothetical protein G ( 309) 194 53.3 0.00018	gi 1402636 dbj BAA13047.1  nitrate reductase [Spin ( 926) 193 53.4 0.00053
gi 205278020 gb ACI01639.1  nitrate reductase [Sol ( 270) 193 53.0 0.00019	gi 170119 gb AAA34033.1  NADH nitrate reductase ( 926) 193 53.4 0.00053
gi 142677129 gb ECZ78134.1  hypothetical protein G ( 356) 194 53.3 0.0002	gi 137999647 gb EBX20320.1  hypothetical protein G ( 146) 183 50.6 0.00057
gi 83772415 dbj BAE62545.1  unnamed protein produc ( 452) 195 53.6 0.00021	gi 159130941 gb EDP56054.1  mitochondrial cytochro ( 471) 189 52.3 0.00057
gi 57226795 gb AAW43255.1  conserved hypothetical ( 552) 196 53.9 0.00021	gi 119410655 gb EAW20601.1  mitochondrial cytochro ( 500) 189 52.3 0.0006
gi 118174031 gb ABK74927.1  Fatty acid desaturase ( 464) 195 53.6 0.00022	gi 134077581 emb CAK96725.1  unnamed protein produ ( 343) 187 51.7 0.00061
gi 89299034 gb EAR97022.1  Cytochrome b5-like Heme ( 697) 197 54.2 0.00022	gi 121886513 gb EAX92029.1  Cytochrome b5-like Hem ( 89) 180 49.8 0.00062
gi 138161750 gb EBY11016.1  hypothetical protein G ( 217) 191 52.5 0.00022	gi 108879915 gb EAT44140.1  cytochrome b5, putativ ( 113) 181 50.0 0.00064
gi 210069038 gb EEA23129.1  mitochondrial cytochro ( 498) 195 53.7 0.00023	gi 155707473 gb ABU33122.1  Sequence 115 from pate ( 470) 188 52.0 0.00067
gi 164644844 gb EDR09093.1  predicted protein [Lac ( 506) 195 53.7 0.00023	gi 112053841 gb ABH96552.1  Sequence 20 from paten ( 470) 188 52.0 0.00067
gi 143152211 gb EDD19579.1  hypothetical protein G ( 356) 193 53.1 0.00024	gi 40161451 gb AAR67464.1  Sequence 20 from patent ( 470) 188 52.0 0.00067

gi 155709335 gb ABU33984.1	Sequence 20 from paten	( 470)	188	52.0	0.00067	gi 29536058 emb CAD87607.1	unnamed protein produc	( 374)	183	50.8	0.0012
gi 68125846 emb CAJ04079.1	hypothetical protein,	( 179)	183	50.6	0.00068	gi 28564443 emb CAD24672.1	delta 12-acyl-lipid-co	( 374)	183	50.8	0.0012
gi 162691463 gb EDQ77825.1	predicted protein [Phy	( 150)	182	50.4	0.00069	gi 134059988 emb CAM41946.1	cytochrome b5, putati	( 142)	178	49.4	0.0012
gi 135130087 gb EBF68498.1	hypothetical protein G	( 187)	183	50.6	0.0007	gi 2385386 emb CAA04758.1	L-mandelate dehydrogena	( 565)	185	51.4	0.0013
gi 392992 gb AAA95940.1	nitrate reductase	( 890)	191	52.9	0.0007	gi 145020433 gb EDK04562.1	hypothetical protein M	( 468)	184	51.1	0.0013
gi 209556396 gb EEA06441.1	cytochrome b5-like hem	( 232)	184	50.9	0.00071	gi 29536063 emb CAD87609.1	unnamed protein produc	( 395)	183	50.8	0.0013
gi 157322867 gb ABV41964.1	fatty acid desaturase	( 360)	186	51.5	0.00074	gi 213509831 emb CAS92465.1	unnamed protein produ	( 493)	184	51.1	0.0013
gi 142975620 gb EDB91603.1	hypothetical protein G	( 137)	181	50.1	0.00075	gi 213509819 emb CAS92459.1	unnamed protein produ	( 494)	184	51.1	0.0013
gi 121913911 gb EAY18716.1	Cytochrome b5-like Hem	( 94)	179	49.5	0.00075	gi 150407977 gb EDN03518.1	predicted protein [Aje	( 337)	182	50.6	0.0013
gi 140259971 gb ECK61602.1	hypothetical protein G	( 250)	184	50.9	0.00076	gi 139566716 gb ECF95093.1	hypothetical protein G	( 105)	176	48.9	0.0013
gi 143013199 gb EDC18014.1	hypothetical protein G	( 175)	182	50.4	0.00078	gi 160814781 emb CAP40235.1	unnamed protein produ	( 519)	184	51.1	0.0014
gi 150411405 gb EDN06793.1	hypothetical protein H	( 565)	188	52.1	0.00078	gi 71842217 gb AAZ43257.1	delta-4 fatty acid desa	( 519)	184	51.1	0.0014
gi 76059224 emb CAJ30809.1	unnamed protein produc	( 480)	187	51.8	0.0008	gi 90300343 gb EAS29974.1	hypothetical protein CI	( 631)	185	51.4	0.0014
gi 60220724 emb CAI58861.1	unnamed protein produc	( 480)	187	51.8	0.0008	gi 111067352 gb EAT88472.1	hypothetical protein S	( 636)	185	51.4	0.0014
gi 162682478 gb EDQ68896.1	predicted protein [Phy	( 480)	187	51.8	0.0008	gi 170942296 emb CAP67948.1	unnamed protein produ	( 524)	184	51.1	0.0014
gi 126633740 emb CAM55826.1	unnamed protein produ	( 480)	187	51.8	0.0008	gi 139074519 gb ECD23377.1	hypothetical protein G	( 254)	180	50.0	0.0015
gi 83765628 dbj BAE55771.1	unnamed protein produc	( 480)	187	51.8	0.0008	gi 21900889 emb CAD2498.1	unnamed protein produc	( 456)	183	50.9	0.0015
gi 930002 emb CAA31787.1	nitrate reductase NR2	( 396)	186	51.5	0.0008	gi 16033740 gb AAL13311.1	delta-5 fatty acid desa	( 456)	183	50.9	0.0015
gi 136576492 gb EBP05349.1	hypothetical protein G	( 151)	181	50.1	0.00081	gi 136926981 gb EBR23003.1	hypothetical protein G	( 80)	174	48.3	0.0015
gi 138959575 gb ECC59286.1	hypothetical protein G	( 272)	184	51.0	0.00081	gi 134068897 emb CAM59831.1	hypothetical protein,	( 179)	178	49.5	0.0015
gi 136881011 gb EBR02171.1	hypothetical protein G	( 186)	182	50.4	0.00082	gi 197035436 gb ACH16336.1	Sequence 12 from paten	( 395)	182	50.6	0.0015
gi 119413109 gb EAW23050.1	mitochondrial cytochro	( 497)	187	51.8	0.00082	gi 28371825 gb AAO37753.1	fatty acid conjugase [P	( 395)	182	50.6	0.0015
gi 1762632 gb AAB39555.1	nitrate reductase	( 497)	187	51.8	0.00082	gi 138781865 gb ECB83816.1	hypothetical protein G	( 153)	177	49.2	0.0016
gi 134074829 emb CAK38943.1	unnamed protein produ	( 507)	187	51.8	0.00084	gi 150847876 gb EDN23069.1	hypothetical protein B	( 496)	183	50.9	0.0016
gi 124403861 emb CAK69321.1	unnamed protein produ	( 513)	187	51.8	0.00085	gi 135413339 gb EBH47135.1	hypothetical protein G	( 337)	181	50.3	0.0016
gi 139936283 gb ECI48758.1	hypothetical protein G	( 109)	179	49.6	0.00085	gi 24474446 gb AAN15927.1	nitrate reductase [Tili	( 894)	186	51.7	0.0016
gi 9797763 gb AAF98581.1	AC013427_24 Strong simila	( 135)	180	49.9	0.00087	gi 296099 emb CAA80270.1	nitrate reductase [Fusar	( 905)	186	51.7	0.0016
gi 26450007 dbj BAC42124.1	putative cytochrome b5	( 135)	180	49.9	0.00087	gi 150413720 gb EDN09103.1	conserved hypothetical	( 511)	183	50.9	0.0016
gi 12083238 gb AAG48778.1	AF332415_1 putative cyto	( 135)	180	49.9	0.00087	gi 14194133 gb AAK56261.1	AF367272_1 Atlg37130/F28	( 917)	186	51.7	0.0016
gi 21536989 gb AAM61330.1	cytochrome b5 [Arabidop	( 135)	180	49.9	0.00087	gi 23296643 gb AAN13137.1	putative nitrate reduct	( 917)	186	51.7	0.0016
gi 12321181 gb AAG50683.1	AC079829_16 cytochrome b	( 135)	180	49.9	0.00087	gi 16930703 gb AAL32017.1	AF436835_1 Atlg37130/F28	( 917)	186	51.7	0.0016
gi 152028791 gb ABS26559.1	fatty acid desaturase	( 370)	185	51.3	0.00089	gi 166782 gb AAA32830.1	nitrate reductase (EC 1.6	( 917)	186	51.7	0.0016
gi 58428663 gb AAW7700.1	conserved hypothetical	( 373)	185	51.3	0.0009	gi 22137030 gb AAM91360.1	Atlg37130/F28L22_2 [Ara	( 917)	186	51.7	0.0016
gi 84369783 dbj BAE70941.1	conserved hypothetical	( 373)	185	51.3	0.0009	gi 14532580 gb AAK64018.1	putative nitrate reduct	( 917)	186	51.7	0.0016
gi 188519053 gb ACD56998.1	DesA3_2 [Xanthomonas o	( 373)	185	51.3	0.0009	gi 110740277 dbj BAF02035.1	nitrate reductase [Ar	( 917)	186	51.7	0.0016
gi 156214583 gb EDO35566.1	predicted protein [Nem	( 65)	176	48.8	0.0009	gi 14335008 gb AAK59768.1	Atlg37130/F28L22_2 [Ara	( 917)	186	51.7	0.0016
gi 62088292 dbj BAD92593.1	fatty acid desaturase	( 315)	184	51.0	0.00092	gi 6623972 gb AAF19225.1	AC007505_1 nitrate reduct	( 917)	186	51.7	0.0016
gi 210123813 gb EEA71513.1	hypothetical protein B	( 469)	186	51.6	0.00092	gi 110742690 dbj BAE99256.1	nitrate reductase [Ar	( 917)	186	51.7	0.0016
gi 141169097 gb ECQ10929.1	hypothetical protein G	( 120)	179	49.6	0.00092	gi 159123640 gb EDP48759.1	fumarate reductase Osm	( 630)	184	51.2	0.0016
gi 50831510 emb CAH05235.1	unnamed protein produc	( 480)	186	51.6	0.00094	gi 187985084 gb EDU50572.1	fumarate reductase [Py	( 636)	184	51.2	0.0016
gi 142615642 gb ECZ34654.1	hypothetical protein G	( 403)	185	51.3	0.00096	gi 143254709 gb EDD92710.1	hypothetical protein G	( 356)	181	50.3	0.0016
gi 55845943 gb AAV66996.1	nitrate reductase [Phae	( 910)	189	52.4	0.00098	gi 156531881 gb ABU76707.1	hypothetical protein E	( 363)	181	50.3	0.0017
gi 32307604 gb AAP79207.1	nitrate reductase [Bige	( 160)	180	49.9	0.001	gi 139953648 gb ECI60401.1	hypothetical protein G	( 63)	172	47.8	0.0017
gi 1762628 gb AAB39553.1	nitrate reductase	( 629)	187	51.9	0.001	gi 3038 emb CAA43600.1	nitrate reductase (NADPH)	( 982)	186	51.8	0.0017
gi 3169157 gb AAC23396.1	BC269730_1 [Homo sapiens	( 352)	184	51.0	0.001	gi 114187560 gb EAU29260.1	cytochrome b5 [Aspergi	( 463)	182	50.6	0.0017
gi 150414638 gb EDN10000.1	predicted protein [Aje	( 133)	179	49.6	0.001	gi 139852169 gb ECH91585.1	hypothetical protein G	( 260)	179	49.8	0.0017
gi 112053844 gb ABH96554.1	Sequence 31 from paten	( 439)	185	51.3	0.001	gi 29536222 emb CAD87611.1	unnamed protein produc	( 477)	182	50.6	0.0018
gi 170181205 gb ACB11556.1	putative delta-5 fatty	( 453)	185	51.3	0.0011	gi 23894018 emb CAD53323.1	delta 5 fatty acid des	( 477)	182	50.6	0.0018
gi 142358951 gb ECX50978.1	hypothetical protein G	( 253)	182	50.5	0.0011	gi 211590429 emb CAP96617.1	Pc21g17200 [Penicilli	( 1048)	186	51.8	0.0018
gi 213509833 emb CAS92466.1	unnamed protein produ	( 560)	186	51.6	0.0011	gi 167279701 gb ABZ32565.1	Sequence 6503 from pat	( 103)	174	48.4	0.0018
gi 136349935 gb EBN57019.1	hypothetical protein G	( 100)	177	49.1	0.0011	gi 85539725 emb CAJ58492.1	C. elegans protein D20	( 103)	174	48.4	0.0018
gi 164644646 gb EDR08895.1	fumarate reductase [La	( 584)	186	51.6	0.0011	gi 139318590 gb ECES1927.1	hypothetical protein G	( 185)	177	49.3	0.0018
gi 2385388 emb CAA04759.1	L-mandelate dehydrogena	( 491)	185	51.3	0.0011	gi 134838726 gb EBD76575.1	hypothetical protein G	( 274)	179	49.8	0.0018
gi 119713291 gb ABL97356.1	putative hydrocarbon o	( 333)	183	50.8	0.0011	gi 154691545 gb EDN91283.1	hypothetical protein S	( 497)	182	50.7	0.0018
gi 119403082 gb EAW13502.1	mitochondrial cytochro	( 500)	185	51.4	0.0011	gi 143290261 gb EDE14484.1	hypothetical protein G	( 337)	180	50.1	0.0018
gi 150857509 gb EDN32701.1	L-lactate ferricytochr	( 509)	185	51.4	0.0012	gi 17925 emb CAA38031.1	nitrate reductase (NADH)	( 898)	185	51.5	0.0018
gi 141337949 gb ECR14035.1	hypothetical protein G	( 237)	181	50.2	0.0012	gi 169241201 emb CAM62229.1	Putative linoleoyl-Co	( 414)	181	50.4	0.0019
gi 118170746 gb ABK71642.1	Fatty acid desaturase	( 363)	183	50.8	0.0012	gi 169990914 dbj BAG12906.1	nitrate reductase [Fu	( 904)	185	51.5	0.0019

gi 169990912 dbj BAG12905.1  nitrate reductase [Fu ( 904) 185 51.5 0.0019	gi 77799302 dbj BAE46746.1  nitrate reductase [Nic ( 904) 182 50.8 0.003
gi 1561580 emb CAA62232.1  nitrate reductase [Gibb ( 907) 185 51.5 0.0019	gi 19891 emb CAA32217.1  nitrate reductase [Nicoti ( 904) 182 50.8 0.003
gi 140162191 gb ECJ93962.1  hypothetical protein G ( 159) 176 49.0 0.0019	gi 53127692 emb CAG31175.1  hypothetical protein [ ( 130) 172 48.0 0.003
gi 56204621 emb CAI19905.1  cytochrome b5 reductas ( 109) 174 48.4 0.0019	gi 119404871 gb EAW15233.1  fumarate reductase Osm ( 629) 180 50.3 0.0031
gi 56203195 emb CAI22326.1  cytochrome b5 reductas ( 109) 174 48.4 0.0019	gi 134083573 emb CAL00488.1  unnamed protein produ ( 629) 180 50.3 0.0031
gi 142094407 gb ECV54250.1  hypothetical protein G ( 355) 180 50.1 0.0019	gi 119410250 gb EAW20197.1  fumarate reductase Osm ( 630) 180 50.3 0.0031
gi 145018780 gb EDK03059.1  hypothetical protein M ( 531) 182 50.7 0.0019	gi 158284105 gb EDP09855.1  fatty acid desaturase (1675) 185 51.7 0.0031
gi 3342268 gb AAC39508.1  delta 5 microsomal desat ( 446) 181 50.4 0.002	gi 157338493 emb CAO41844.1  unnamed protein produ ( 134) 172 48.0 0.0031
gi 929750 emb CAA29497.1  unnamed protein product ( 554) 182 50.7 0.002	gi 134984267 gb EBE73350.1  hypothetical protein G ( 114) 171 47.7 0.0032
gi 141151192 gb ECP98183.1  hypothetical protein G ( 142) 175 48.7 0.002	gi 685208 gb AAA96249.1  nitrate reductase ( 95) 170 47.5 0.0032
gi 118571949 gb ABL06700.1  linoleoyl-CoA desatura ( 377) 180 50.1 0.002	gi 685165 gb AAA96246.1  nitrate reductase ( 95) 170 47.5 0.0032
gi 146145929 gb EAR91939.2  Cytochrome b5-like Hem ( 215) 177 49.3 0.002	gi 1217984 emb CAA93814.1  NADPH-hemoprotein reduc ( 147) 172 48.0 0.0033
gi 158455068 gb AAI20116.2  CYB5B protein [Bos tau ( 146) 175 48.7 0.0021	gi 136618654 gb EBP32254.1  hypothetical protein G ( 321) 176 49.2 0.0033
gi 138664058 gb ECB14808.1  hypothetical protein G ( 329) 179 49.9 0.0021	gi 211584669 emb CAP74195.1  Pcl4g00540 [Penicilli ( 475) 178 49.7 0.0033
gi 169242596 emb CAM63624.1  Putative fatty acid d ( 407) 180 50.1 0.0021	gi 47028617 gb AAT09160.1  delta-5 fatty acid desa ( 475) 178 49.7 0.0033
gi 119415489 gb EAW25427.1  mitochondrial cytochro ( 495) 181 50.4 0.0021	gi 114197749 gb EAU39449.1  conserved hypothetical ( 477) 178 49.7 0.0034
gi 83770938 dbj BAE61071.1  unnamed protein produc ( 498) 181 50.4 0.0022	gi 930001 emb CAA31786.1  nitrate reductase NR1 (3 ( 393) 177 49.4 0.0034
gi 11119241 gb AAG30576.1 AF314093_1 nitrate reduc ( 914) 184 51.3 0.0022	gi 116056666 emb CAL52955.1  Fatty acid desaturase ( 491) 178 49.7 0.0034
gi 124390907 emb CAK56448.1  unnamed protein produ ( 513) 181 50.4 0.0022	gi 114193546 gb EAU35246.1  cytochrome b2, mitocho ( 500) 178 49.7 0.0035
gi 114190305 gb EAU32005.1  hypothetical protein A ( 626) 182 50.7 0.0022	gi 135714795 gb EBJ39076.1  hypothetical protein G ( 279) 175 48.9 0.0035
gi 1210064530 gb EEA18625.1  fumarate reductase Osm ( 627) 182 50.7 0.0022	gi 144576240 gb ABO94309.1  predicted protein [Ost ( 72) 168 46.9 0.0035
gi 119710111 gb ABL96296.1  delta-8 desaturase [Pa ( 427) 180 50.2 0.0022	gi 38567126 emb CAE76421.1  related to fumarate re ( 616) 179 50.0 0.0035
gi 41394542 gb AAS02413.1  hypothetical protein MA ( 110) 173 48.2 0.0022	gi 117663207 gb ABK55747.1  nitrate reductase [Cuc ( 130) 171 47.8 0.0035
gi 155288785 gb ABT44389.1  Sequence 131859 from p ( 93) 172 47.9 0.0023	gi 154704002 gb EDO03741.1  hypothetical protein S ( 629) 179 50.0 0.0036
gi 9951163 gb AAG08273.1 AE004902_1 acyl-CoA delta ( 370) 179 49.9 0.0023	gi 21900885 emb CAD42496.1  unnamed protein produc ( 519) 178 49.7 0.0036
gi 115588258 gb ABJ14273.1  putative fatty acid de ( 370) 179 49.9 0.0023	gi 160814779 emb CAP40234.1  unnamed protein produ ( 519) 178 49.7 0.0036
gi 126197595 gb EAE261658.1  conserved hypothetical ( 370) 179 49.9 0.0023	gi 20069125 gb AAM09688.1 AF489589_1 delta-4 fatty ( 519) 178 49.7 0.0036
gi 126170324 gb EAE255835.1  conserved hypothetical ( 370) 179 49.9 0.0023	gi 160830342 emb CAP40242.1  unnamed protein produ ( 519) 178 49.7 0.0036
gi 194150702 gb EDW66386.1  GJ16001 [Drosophila vi ( 117) 173 48.2 0.0024	gi 141255967 gb ECQ70414.1  hypothetical protein G ( 239) 174 48.6 0.0036
gi 140353702 gb ECL19512.1  hypothetical protein G ( 266) 177 49.3 0.0024	gi 34979829 gb AAQ83903.1  flavohemoprotein b5/b5R ( 435) 177 49.5 0.0037
gi 134060943 emb CAM37961.1  hypothetical protein, ( 219) 176 49.1 0.0024	gi 150960739 gb ABR82764.1  conserved hypothetical ( 362) 176 49.2 0.0037
gi 196192957 gb EDX87916.1  Fatty acid desaturase ( 399) 179 49.9 0.0025	gi 56679722 gb AAV96388.1  monooxygenase, putative ( 563) 178 49.8 0.0039
gi 76154600 gb AAX26053.2  SJCHGC05696 protein [Sc ( 223) 176 49.1 0.0025	gi 12007117 gb AAG45053.1 AF307840_1 hemoflavoprot ( 486) 177 49.5 0.004
gi 143334463 gb EDE39552.1  hypothetical protein G ( 400) 179 49.9 0.0025	gi 51330724 gb AAH80240.1  Cytochrome b5 reductase ( 486) 177 49.5 0.004
gi 134066684 emb CAM44486.1  delta8 fatty acid des ( 400) 179 49.9 0.0025	gi 34979827 gb AAQ83902.1  flavohemoprotein b5/b5R ( 486) 177 49.5 0.004
gi 46805324 dbj BAD16843.1  putative nitrate reduc ( 889) 183 51.0 0.0025	gi 1762630 gb AAB39554.1  nitrate reductase ( 487) 177 49.5 0.004
gi 215717065 dbj BAG95428.1  unnamed protein produ ( 889) 183 51.0 0.0025	gi 2731816 gb AAB93560.1  nitrate reductase [Glyci ( 875) 180 50.3 0.004
gi 113537784 dbj BAF10167.1  Os02g0770800 [Oryza s ( 889) 183 51.0 0.0025	gi 149018966 gb EDL77607.1  cytochrome b5 reductas ( 496) 177 49.5 0.0041
gi 135205268 gb EBG16172.1  hypothetical protein G ( 127) 173 48.2 0.0025	gi 4389417 gb AAD19790.1  nitrate reductase [Glyci ( 890) 180 50.3 0.0041
gi 2894356 emb CAA74005.1  nitrate reductase (NADP ( 891) 183 51.0 0.0025	gi 537627 gb AAA96813.1  inducible nitrate reducta ( 890) 180 50.3 0.0041
gi 3378500 emb CAA08857.1  nitrate reductase [Phae ( 891) 183 51.0 0.0025	gi 90303484 gb EAS33115.1  hypothetical protein CI ( 504) 177 49.5 0.0041
gi 211582852 emb CAP81055.1  Pcl2g14280 [Penicilli ( 497) 180 50.2 0.0025	gi 56759130 gb AAW27705.1  SJCHGC03671 protein [Sc ( 129) 170 47.5 0.0041
gi 197704680 gb EDY50492.1  delta fatty acid desat ( 338) 178 49.6 0.0025	gi 187985580 gb EDU51068.1  L-lactate dehydrogenas ( 509) 177 49.5 0.0042
gi 213509821 emb CAS92460.1  unnamed protein produ ( 502) 180 50.2 0.0025	gi 212512924 gb EEB15590.1  NADH-cytochrome b5 red ( 509) 177 49.5 0.0042
gi 19889 emb CAA32216.1  nitrate reductase [Nicoti ( 904) 183 51.0 0.0026	gi 14334876 gb AAK59616.1  putative nitrate reduct ( 917) 180 50.4 0.0042
gi 237969 gb AAB20155.1  nitrate reductase heme do ( 74) 170 47.4 0.0026	gi 140871229 gb ECO07207.1  hypothetical protein G ( 89) 168 47.0 0.0042
gi 81673810 gb AAI09570.1  Cytochrome b5 reductase ( 520) 180 50.2 0.0026	gi 116000309 emb CAL49989.1  delta-6 fatty acid de ( 237) 173 48.4 0.0042
gi 83765492 dbj BAE55635.1  unnamed protein produc ( 633) 181 50.5 0.0026	gi 60220808 emb CAI58903.1  unnamed protein produc ( 237) 173 48.4 0.0042
gi 164644197 gb EDR08447.1  acyl-CoA-dehydrogenase ( 522) 180 50.2 0.0026	gi 126633750 emb CAM55831.1  unnamed protein produ ( 237) 173 48.4 0.0042
gi 57229321 gb AAW45754.1  fumarate reductase (NAD ( 635) 181 50.5 0.0026	gi 76059308 emb CAJ30848.1  unnamed protein produc ( 237) 173 48.4 0.0042
gi 685155 gb AAA96242.1  nitrate reductase ( 91) 171 47.7 0.0026	gi 110565251 emb CAL23342.1  unnamed protein produ ( 237) 173 48.4 0.0042
gi 210122039 gb EEA69748.1  hypothetical protein B (2502) 188 52.5 0.0026	gi 149018965 gb EDL77606.1  cytochrome b5 reductas ( 520) 177 49.5 0.0042
gi 161162346 emb CAN93651.1  putative fatty acid d ( 366) 178 49.7 0.0027	gi 190579425 gb EDV19520.1  hypothetical protein T ( 75) 167 46.7 0.0043
gi 136562151 gb EBO96211.1  hypothetical protein G ( 119) 172 48.0 0.0028	gi 145573905 gb ABP83437.1  fatty acid desaturase ( 360) 175 49.0 0.0043
gi 134662566 gb EBC68085.1  hypothetical protein G ( 101) 171 47.7 0.0029	gi 118484348 gb ABK93619.1  unknown [Populus trich ( 136) 170 47.6 0.0043
gi 6759823 gb AAF28059.1 AF123281_1 nitrate reduct ( 870) 182 50.8 0.0029	gi 50844677 gb AAT84460.1  cytochrome B5 isoform C ( 136) 170 47.6 0.0043
gi 119407312 gb EAW17262.1  NADH-cytochrome B5 red ( 497) 179 50.0 0.003	gi 118485373 gb ABK94544.1  unknown [Populus trich ( 136) 170 47.6 0.0043
gi 109659810 dbj BAE96752.1  nitrate reductase 2 [ ( 904) 182 50.8 0.003	gi 119569038 gb EAW48653.1  hCG401131, isoform CRA ( 309) 174 48.7 0.0045

gi 49641322 emb CAH02583.1  KLLA0B14795p [Kluyvero ( 556) 177 49.5 0.0045	gi 74199582 dbj BAE41470.1  unnamed protein produc ( 536) 175 49.1 0.006
gi 143972813 gb EDH95743.1  hypothetical protein G ( 258) 173 48.4 0.0045	gi 139517562 gb ECF61542.1  hypothetical protein G ( 300) 172 48.2 0.006
gi 108879914 gb EAT744139.1  cytochrome b5, putativ ( 119) 169 47.3 0.0045	gi 685206 gb AAA96248.1  nitrate reductase ( 94) 166 46.5 0.006
gi 194032857 emb CAQ77148.1  nitrate reductase [Ar ( 845) 179 50.1 0.0046	gi 59750024 gb AAW98847.1  Sequence 16410 from pat ( 140) 168 47.1 0.0061
gi 210071681 gb EEA25770.1  cytochrome b5 reductas ( 472) 176 49.3 0.0046	gi 144976091 gb ABP3186.1  Sequence 8 from patent ( 172) 169 47.4 0.0061
gi 58014091 gb AAW63048.1  delta-6 fatty acid desa ( 153) 170 47.6 0.0047	gi 189860252 gb ACE35658.1  Sequence 2 from patent ( 383) 173 48.5 0.0062
gi 163776521 gb EDQ90140.1  predicted protein [Mon ( 599) 177 49.6 0.0048	gi 189846875 gb ACE26373.1  Sequence 128 from pate ( 383) 173 48.5 0.0062
gi 213509815 emb CAS92455.1  unnamed protein produ ( 497) 176 49.3 0.0048	gi 189704782 gb ACE16111.1  Sequence 128 from pate ( 383) 173 48.5 0.0062
gi 134081526 emb CAK41962.1  unnamed protein produ ( 500) 176 49.3 0.0048	gi 8886726 gb AAF80560.1 AF192486_1 omega-6 fatty ( 383) 173 48.5 0.0062
gi 139399268 gb ECE84652.1  hypothetical protein G ( 192) 171 47.9 0.0049	gi 59896214 gb AAX11454.1  microsomal oleic acid d ( 383) 173 48.5 0.0062
gi 145010236 gb EDJ94892.1  hypothetical protein M ( 509) 176 49.3 0.0049	gi 141474689 gb ECS01829.1  hypothetical protein G ( 214) 170 47.7 0.0063
gi 88181913 gb EAQ89381.1  hypothetical protein CH ( 509) 176 49.3 0.0049	gi 138070317 gb EBX57494.1  cytochrome b5, putativ ( 81) 165 46.3 0.0063
gi 207008942 emb CAR80385.1  unnamed protein produ ( 419) 175 49.0 0.0049	gi 138737529 gb ECB66494.1  hypothetical protein G ( 262) 171 48.0 0.0063
gi 136950397 gb EBR36166.1  hypothetical protein G ( 242) 172 48.2 0.005	gi 35210731 dbj BAC88112.1  gll10171 [Gloeobacter v ( 390) 173 48.5 0.0063
gi 148694572 gb EDL26519.1  mCG11884, isoform CRA_ ( 442) 175 49.0 0.0051	gi 158283021 gb EDP08772.1  flavohemoprotein b5/b5 ( 182) 169 47.4 0.0064
gi 145010043 gb EDJ94699.1  conserved hypothetical ( 540) 176 49.3 0.0051	gi 189053712 dbj BAG35964.1  unnamed protein produ ( 487) 174 48.8 0.0065
gi 685157 gb AAA96243.1  nitrate reductase ( 94) 167 46.8 0.0051	gi 155082042 gb ABS94877.1  Sequence 16 from paten ( 487) 174 48.8 0.0065
gi 34979825 gb AAQ83901.1  flavohemoprotein b5/b5R ( 451) 175 49.0 0.0052	gi 6166392 gb AAF04812.1 AF169803_1 flavohemoprote ( 487) 174 48.8 0.0065
gi 685159 gb AAA96250.1  nitrate reductase ( 95) 167 46.8 0.0052	gi 119569037 gb EAW48652.1  hCG401131, isoform CRA ( 487) 174 48.8 0.0065
gi 685163 gb AAA96245.1  nitrate reductase ( 95) 167 46.8 0.0052	gi 67588749 gb AAY73180.1  Sequence 16 from patent ( 487) 174 48.8 0.0065
gi 685167 gb AAA96247.1  nitrate reductase ( 95) 167 46.8 0.0052	gi 108868602 gb EBX57494.1  cytochrome b5, putativ ( 103) 166 46.6 0.0065
gi 685161 gb AAA96244.1  nitrate reductase ( 95) 167 46.8 0.0052	gi 134991760 gb EBE78443.1  hypothetical protein G ( 333) 172 48.2 0.0065
gi 134067939 emb CAM66221.1  cytochrome b5, putati ( 142) 169 47.3 0.0052	gi 44890326 gb AAH66748.1  Cytochrome b5 type B [D ( 153) 168 47.1 0.0065
gi 68124823 emb CAJ02657.1  cytochrome b5, putativ ( 142) 169 47.3 0.0052	gi 108873820 gb EAT38045.1  cytochrome B5 (cytb5) ( 104) 166 46.6 0.0066
gi 194160147 gb EDW75048.1  GK19965 [Drosophila wi ( 118) 168 47.1 0.0053	gi 24030478 gb AAN41389.1  putative nitrate reduct ( 917) 177 49.7 0.0067
gi 60392574 gb AAX19393.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053	gi 22757 emb CAA79494.1  nitrate reductase [Arabid ( 917) 177 49.7 0.0067
gi 60392576 gb AAX19394.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053	gi 15983499 gb AAL11617.1 AF424624_1 Atlg77760/T32 ( 917) 177 49.7 0.0067
gi 60392578 gb AAX19395.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053	gi 12323295 gb AAG51627.1 AC012193_9 nitrate reduct ( 917) 177 49.7 0.0067
gi 18418651 gb AAL68982.1 AF251843_1 delta-12 olea ( 383) 174 48.7 0.0053	gi 20259345 gb AAM13997.1  putative nitrate reduct ( 917) 177 49.7 0.0067
gi 60392572 gb AAX19392.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053	gi 142125111 gb ECV77356.1  hypothetical protein G ( 89) 165 46.3 0.0068
gi 60392580 gb AAX19396.1  delta-12 oleate desatur ( 383) 174 48.7 0.0053	gi 164640618 gb EDR04882.1  acyl-CoA-dehydrogenase ( 514) 174 48.8 0.0068
gi 134055511 emb CAK37158.1  unnamed protein produ ( 475) 175 49.0 0.0054	gi 148878755 emb CAD91715.2  C. elegans protein Y5 ( 516) 174 48.8 0.0068
gi 190408190 gb EDV11455.1  L-lactate cytochrome c ( 591) 176 49.3 0.0055	gi 14530946 gb AAK63186.1  probable acyl-CoA dehyd ( 520) 174 48.8 0.0068
gi 577142 emb CAA86721.1  cytochrome b2 precursor ( 591) 176 49.3 0.0055	gi 119569035 gb EAW48650.1  hCG401131, isoform CRA ( 521) 174 48.8 0.0068
gi 66968234 gb AAY59538.1  nitrate reductase [Cyli ( 873) 178 49.9 0.0055	gi 123246238 emb CAI19904.2  cytochrome b5 reducta ( 521) 174 48.8 0.0068
gi 90307490 gb EAS37121.1  hypothetical protein CI ( 492) 175 49.0 0.0056	gi 71052101 gb AAH25380.2  Cytochrome b5 reductase ( 521) 174 48.8 0.0068
gi 148694571 gb EDL26518.1  mCG11884, isoform CRA_ ( 493) 175 49.0 0.0056	gi 123231684 emb CAI22325.2  cytochrome b5 reducta ( 521) 174 48.8 0.0068
gi 12802901 gb AAK08116.1 AF338818_1 flavohemoprot ( 494) 175 49.0 0.0056	gi 167882814 gb ACA06109.1  cytochrome b5 reductas ( 521) 174 48.8 0.0068
gi 26354983 dbj BAC41118.1  unnamed protein produ ( 494) 175 49.0 0.0056	gi 89267449 emb CAJ83762.1  novel protein similar ( 523) 174 48.8 0.0069
gi 111069742 gb EAT90862.1  hypothetical protein S ( 496) 175 49.0 0.0056	gi 194162158 gb EDW77059.1  GK22167 [Drosophila wi ( 528) 174 48.8 0.0069
gi 159122277 gb EDP47399.1  mitochondrial cytochro ( 500) 175 49.0 0.0056	gi 116059990 emb CAL56049.1  Nia, nitrate reductas ( 952) 177 49.7 0.007
gi 34979823 gb AAQ83900.1  flavohemoprotein b5/b5R ( 502) 175 49.0 0.0057	gi 44984185 gb AAS33151.1  AFL223Wp [Ashbya gossyp ( 165) 168 47.1 0.007
gi 74178803 dbj BAE34044.1  unnamed protein produc ( 502) 175 49.0 0.0057	gi 39545945 gb AAR28035.1  delta-5 desaturase [Mor ( 446) 173 48.6 0.0071
gi 74186235 dbj BAE42908.1  unnamed protein produc ( 502) 175 49.0 0.0057	gi 137074039 gb EBS06013.1  hypothetical protein G ( 207) 169 47.4 0.0071
gi 19343569 gb AAH25438.1  Cyb5r4 protein [Mus mus ( 502) 175 49.0 0.0057	gi 148878754 emb CAJ83762.1  C. elegans protein Y5 ( 552) 174 48.8 0.0072
gi 144577191 gb ABO95258.1  predicted protein [Ost ( 417) 174 48.8 0.0057	gi 138028652 gb EBX35101.1  hypothetical protein G ( 258) 170 47.7 0.0073
gi 210093325 gb EEA41530.1  hypothetical protein B ( 283) 172 48.2 0.0057	gi 6118361 gb AAF04094.1 AF188264_1 delta-12 oleat ( 383) 172 48.3 0.0073
gi 136152096 gb EBM23834.1  hypothetical protein G ( 284) 172 48.2 0.0057	gi 6118359 gb AAF04093.1 AF188263_1 delta-12 oleat ( 383) 172 48.3 0.0073
gi 100811423 dbj BAE94683.1  cytochrome b5 [Physar ( 132) 168 47.1 0.0058	gi 136543878 gb EBO84500.1  hypothetical protein G ( 180) 168 47.2 0.0075
gi 148694573 gb EDL26520.1  mCG11884, isoform CRA_ ( 521) 175 49.1 0.0058	gi 49642320 emb CAH00282.1  KLLA0D02640p [Kluyvero ( 589) 174 48.9 0.0076
gi 148694570 gb EDL26517.1  mCG11884, isoform CRA_ ( 521) 175 49.1 0.0058	gi 213509825 emb CAS92462.1  unnamed protein produ ( 589) 174 48.9 0.0076
gi 50844679 gb AAT84461.1  cytochrome b5 isoform C ( 134) 168 47.1 0.0059	gi 1262166 gb AAA96727.1  nitrate reductase ( 886) 176 49.4 0.0077
gi 139956548 gb ECI62451.1  hypothetical protein G ( 111) 167 46.8 0.0059	gi 211592741 emb CAP99107.1  Pc22g18190 [Penicilli ( 494) 173 48.6 0.0077
gi 148694574 gb EDL26521.1  mCG11884, isoform CRA_ ( 530) 175 49.1 0.0059	gi 143689120 gb EDG29192.1  hypothetical protein G ( 337) 171 48.0 0.0077
gi 148694569 gb EDL26516.1  mCG11884, isoform CRA_ ( 536) 175 49.1 0.006	gi 1903346046 gb EDK38044.2  hypothetical protein P ( 156) 167 46.9 0.0078
	gi 136608109 gb EBP25642.1  hypothetical protein G ( 129) 166 46.6 0.0078
	gi 145011655 gb EDJ96311.1  hypothetical protein M ( 911) 176 49.4 0.0079
	gi 143292923 gb EDE15893.1  hypothetical protein G ( 284) 170 47.7 0.0079

gi 3264765 gb AAC24586.1	omega-6 fatty acid desat	( 346)	171	48.0	0.0079	gi 141175753 gb ECQ15498.1	hypothetical protein G	( 277)	168	47.3	0.011
gi 146450057 gb EDK44313.1	hypothetical protein L	( 160)	167	46.9	0.008	gi 210065776 gb EAA19870.1	mitochondrial cytochro	( 497)	171	48.1	0.011
gi 147818083 emb CAN78289.1	hypothetical protein	( 133)	166	46.6	0.008	gi 158596083 gb EDP34488.1	Cytochrome b5-like Hem	( 414)	170	47.8	0.011
gi 157353583 emb CAO46100.1	unnamed protein produ	( 133)	166	46.6	0.008	gi 88185681 gb EAQ93149.1	conserved hypothetical	( 615)	172	48.4	0.011
gi 124422313 emb CAK87150.1	unnamed protein produ	( 358)	171	48.0	0.0081	gi 30090027 gb AAO17707.1	cytochrome b5 [Sorghum	( 133)	164	46.2	0.011
gi 116782813 gb ABK22670.1	unknown [Picea sitchen	( 136)	166	46.6	0.0082	gi 190621368 gb EDV36892.1	GF13182 [Drosophila an	( 134)	164	46.2	0.011
gi 210124132 gb EEA71830.1	hypothetical protein B	(3128)	182	51.1	0.0083	gi 144998358 gb ABP16931.1	Sequence 25 from paten	( 446)	170	47.9	0.011
gi 135652066 gb EBJ00330.1	hypothetical protein G	( 304)	170	47.8	0.0083	gi 126633744 emb CAM55828.1	unnamed protein produ	( 446)	170	47.9	0.011
gi 154702325 gb EDO02064.1	hypothetical protein S	( 452)	172	48.3	0.0084	gi 27278517 gb AAN93255.1	Sequence 12 from patent	( 446)	170	47.9	0.011
gi 57228742 gb AAW45177.1	L-mandelate dehydrogena	( 555)	173	48.6	0.0085	gi 3859488 gb AAC72755.1	delta-5 fatty acid desat	( 446)	170	47.9	0.011
gi 190629074 gb EDV44491.1	GF20301 [Drosophila an	( 117)	165	46.4	0.0085	gi 145025094 gb ABP24251.1	Sequence 39 from paten	( 446)	170	47.9	0.011
gi 58013373 gb AAW63040.1	microsomal delta-12 ole	( 381)	171	48.1	0.0086	gi 157393820 emb CAP07471.1	unnamed protein produ	( 446)	170	47.9	0.011
gi 60392523 gb AAX19368.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 60220728 emb CAI58863.1	unnamed protein produc	( 446)	170	47.9	0.011
gi 60392517 gb AAX19365.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 42683654 gb AAS29215.1	Sequence 30 from patent	( 446)	170	47.9	0.011
gi 60392533 gb AAX19373.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 155070721 gb ABS91066.1	Sequence 51 from paten	( 446)	170	47.9	0.011
gi 60392535 gb AAX19374.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 75183352 gb ABA13323.1	Sequence 29 from patent	( 446)	170	47.9	0.011
gi 60392525 gb AAX19369.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 23310238 gb AAN18904.1	Sequence 23 from patent	( 446)	170	47.9	0.011
gi 60392521 gb AAX19367.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 76059228 emb CAJ30811.1	unnamed protein produc	( 446)	170	47.9	0.011
gi 60392519 gb AAX19366.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 112060964 gb ABH98583.1	Sequence 27 from paten	( 446)	170	47.9	0.011
gi 18418653 gb AAL68983.1	AF251844_1 delta-12 olea	( 382)	171	48.1	0.0086	gi 33757662 gb AAQ51235.1	Sequence 2 from patent	( 446)	170	47.9	0.011
gi 60392537 gb AAW63040.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 155707465 gb ABU33114.1	Sequence 4 from patent	( 446)	170	47.9	0.011
gi 60392531 gb AAX19372.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 12808264 gb AAE43484.1	Sequence 5 from patent	( 446)	170	47.9	0.011
gi 60392527 gb AAX19370.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 189868191 gb ACE40437.1	Sequence 30 from paten	( 446)	170	47.9	0.011
gi 60392529 gb AAX19371.1	delta-12 oleate desatur	( 382)	171	48.1	0.0086	gi 10056254 gb AAE33160.1	Sequence 2 from patent	( 446)	170	47.9	0.011
gi 215510977 gb EEC20430.1	cytochrome b5, putativ	( 145)	166	46.7	0.0086	gi 138183810 gb EBY26414.1	hypothetical protein G	( 205)	166	46.7	0.011
gi 194339835 gb EDX20801.1	delta fatty acid desat	( 100)	164	46.1	0.0087	gi 23329315 gb AAN26149.1	Sequence 46 from patent	( 447)	170	47.9	0.011
gi 53955894 gb AAV05891.1	Sequence 17848 from pat	( 219)	168	47.2	0.0088	gi 62774607 gb AAJ02000.1	Sequence 10 from patent	( 447)	170	47.9	0.011
gi 146451121 gb EDK45377.1	cytochrome b2, mitoch	( 582)	173	48.6	0.0088	gi 125603712 gb EAZ43037.1	hypothetical protein O	( 660)	172	48.4	0.011
gi 21019 emb CAA37672.1	nitrate reductase [Phaseo	( 881)	175	49.2	0.009	gi 57230918 gb AAW47227.1	cytoplasm protein, puta	( 305)	168	47.3	0.012
gi 59956948 dbj BAD89863.1	microsomal omega-6 fat	( 337)	170	47.8	0.0091	gi 136797655 gb EBQ47335.1	hypothetical protein G	( 140)	164	46.2	0.012
gi 211592111 emb CAP98435.1	Pc22g11470 [Penicilli	( 502)	172	48.4	0.0091	gi 61402002 gb AAH92017.1	MGC85036 protein [Xenop	( 141)	164	46.2	0.012
gi 194717283 gb ACF93242.1	nitrate reductase [Bra	( 910)	175	49.2	0.0092	gi 193907545 gb EDW06412.1	GI21528 [Drosophila mo	( 117)	163	45.9	0.012
gi 540485 dbj BAA07394.1	nitrate reductase [Brass	( 911)	175	49.2	0.0092	gi 77369196 gb ABA66944.1	Sequence 2586 from pate	( 261)	167	47.0	0.012
gi 145009796 gb EDJ94452.1	conserved hypothetical	( 619)	173	48.6	0.0093	gi 136436694 gb EBO15454.1	hypothetical protein G	( 99)	162	45.6	0.012
gi 59803125 gb AAX07713.1	FAD-dependent oxidoredu	( 619)	173	48.6	0.0093	gi 159128112 gb EDP53227.1	cytochrome b5 reductas	( 479)	170	47.9	0.012
gi 142958067 gb EDB79503.1	hypothetical protein G	( 348)	170	47.8	0.0093	gi 19065 emb CAA42739.1	nitrate reductase (NAD(P)	( 891)	173	48.7	0.012
gi 57230302 gb AAW46703.1	conserved hypothetical	( 514)	172	48.4	0.0093	gi 168517 gb AAA33483.1	nitrate reductase	( 501)	170	47.9	0.013
gi 164644433 gb EDR08683.1	acyl-CoA-dehydrogenase	( 519)	172	48.4	0.0094	gi 10834811 gb AAG23835.1	AF290427_1 cytochrome b5	( 131)	163	45.9	0.013
gi 126633798 emb CAM55855.1	unnamed protein produ	( 536)	172	48.4	0.0097	gi 158420737 gb ABW37749.1	cytochrome b5 [Drosoph	( 134)	163	45.9	0.013
gi 60220810 emb CAI58904.1	unnamed protein produc	( 536)	172	48.4	0.0097	gi 21645586 gb AAF59233.3	CG2140-PB, isoform B [D	( 134)	163	45.9	0.013
gi 76059310 emb CAJ30849.1	unnamed protein produc	( 536)	172	48.4	0.0097	gi 28557605 gb AAO45208.1	RE66521p [Drosophila me	( 134)	163	45.9	0.013
gi 116001279 emb CAL49891.1	unnamed protein produ	( 536)	172	48.4	0.0097	gi 51092023 gb AAT94425.1	RE73695p [Drosophila me	( 134)	163	45.9	0.013
gi 110565247 emb CAL23340.1	unnamed protein produ	( 536)	172	48.4	0.0097	gi 194124733 gb EDW46776.1	GM20961 [Drosophila se	( 134)	163	45.9	0.013
gi 125540509 gb EAY86904.1	hypothetical protein O	( 138)	165	46.4	0.0097	gi 194175589 gb EDW89200.1	GE19131 [Drosophila ya	( 134)	163	45.9	0.013
gi 125583074 gb EAE224005.1	hypothetical protein O	( 138)	165	46.4	0.0097	gi 194192455 gb EDX06031.1	GD10488 [Drosophila si	( 134)	163	45.9	0.013
gi 1133537116 dbj BAF09499.1	Os02g0649800 [Oryza s	( 138)	165	46.4	0.0097	gi 190662478 gb EDV59670.1	GG23285 [Drosophila er	( 134)	163	45.9	0.013
gi 49387865 dbj BAD26552.1	putative cytochrome b5	( 138)	165	46.4	0.0097	gi 193903202 gb EDW02069.1	GH20101 [Drosophila gr	( 134)	163	45.9	0.013
gi 215694965 dbj BAG90156.1	unnamed protein produ	( 138)	165	46.4	0.0097	gi 63102503 gb AAH95683.1	Zgc:112177 [Danio rerio	( 527)	170	47.9	0.013
gi 49388452 dbj BAD25582.1	putative cytochrome b5	( 138)	165	46.4	0.0097	gi 108464299 gb ABF89484.1	fatty acid desaturase	( 383)	168	47.4	0.014
gi 126091469 gb ABN66242.1	NADPH cytochrome B5 ox	( 139)	165	46.4	0.0098	gi 3646444 emb CAA20908.1	NADPH-hemoprotein reduc	( 145)	163	46.0	0.014
gi 2564237 emb CAA71199.1	omega-6 desaturase [Gos	( 383)	170	47.8	0.01	gi 22137120 gb AAM91405.1	Atlg60660/F8A5_18 [Arab	( 121)	162	45.7	0.014
gi 91125664 gb ABE12612.1	Sequence 6 from patent	( 383)	170	47.8	0.01	gi 15146312 gb AAK83639.1	Atlg60660/F8A5_18 [Arab	( 121)	162	45.7	0.014
gi 5994481 gb AAE19894.1	Sequence 4 from patent U	( 384)	170	47.8	0.01	gi 2462759 gb AAB71978.1	Putative Cytochrome B5 [	( 121)	162	45.7	0.014
gi 164661518 gb AAX51386.1	delta-5 fatty acid desa	( 476)	171	48.1	0.01	gi 90299640 gb EAS29271.1	hypothetical protein CI	( 1044)	173	48.8	0.014
gi 211962233 gb EEA97428.1	cytochrome b5-like hem	(1579)	177	49.8	0.011	gi 119594383 gb EAW73977.1	fatty acid desaturase	( 325)	167	47.1	0.014
gi 76573515 dbj BAE44599.1	hypothetical protein [	( 126)	164	46.2	0.011	gi 213509837 emb CAS92468.1	unnamed protein produ	( 585)	170	47.9	0.014
gi 49650093 emb CAG79819.1	YAL10E21307p [Yarrowia	( 493)	171	48.1	0.011	gi 5262950 emb CAB45871.1	cytochrome b2 [Kluyvero	( 585)	170	47.9	0.014
gi 213509829 emb CAS92464.1	unnamed protein produ	( 493)	171	48.1	0.011	gi 68130365 emb CAJ09677.1	delta8 fatty acid desa	( 400)	168	47.4	0.014

gi 210071626 gb EEA25715.1	nitrate reductase NiaD ( 883)	172	48.5	0.015	gi 111979069 gb ABH83312.1	Sequence 20 from paten ( 515)	168	47.4	0.018
gi 156219664 gb EDO40543.1	predicted protein [Nem ( 87)	160	45.1	0.015	gi 155082199 gb ABS94939.1	Sequence 19 from paten ( 515)	168	47.4	0.018
gi 136496996 gb EB054490.1	hypothetical protein G ( 231)	165	46.5	0.015	gi 155082221 gb ABS94961.1	Sequence 70 from paten ( 515)	168	47.4	0.018
gi 540487 dbj BAA07395.1	nitrate reductase [Brass ( 911)	172	48.5	0.015	gi 155095502 gb ABS99957.1	Sequence 21 from paten ( 515)	168	47.4	0.018
gi 113623975 dbj BAF23920.1	Os08g0468100 [Oryza s ( 916)	172	48.5	0.015	gi 155116364 gb ABT11290.1	Sequence 19 from paten ( 515)	168	47.4	0.018
gi 42407400 dbj BAD09558.1	nitrate reductase apoe ( 916)	172	48.5	0.015	gi 155116386 gb ABT11312.1	Sequence 70 from paten ( 515)	168	47.4	0.018
gi 113623978 dbj BAF23923.1	Os08g0468700 [Oryza s ( 916)	172	48.5	0.015	gi 60220756 emb CAI58877.1	unnamed protein produc ( 515)	168	47.4	0.018
gi 27527625 emb CAA33817.2	nitrate reductase apoe ( 916)	172	48.5	0.015	gi 160814787 emb CAP40238.1	unnamed protein produ ( 515)	168	47.4	0.018
gi 125603710 gb EAZ43035.1	hypothetical protein O ( 916)	172	48.5	0.015	gi 160830340 emb CAP40241.1	unnamed protein produ ( 515)	168	47.4	0.018
gi 42407404 dbj BAD09562.1	putative nitrate reduc ( 916)	172	48.5	0.015	gi 155095499 gb ABS99954.1	Sequence 18 from paten ( 515)	168	47.4	0.018
gi 150858368 gb EDN33560.1	hypothetical protein B ( 423)	168	47.4	0.015	gi 155116366 gb ABT11292.1	Sequence 21 from paten ( 515)	168	47.4	0.018
gi 140669635 gb ECM69837.1	hypothetical protein G ( 238)	165	46.5	0.015	gi 160814789 emb CAP40239.1	unnamed protein produ ( 515)	168	47.4	0.018
gi 2695711 emb CAA04703.1	cytochrome b5 [Olea euro ( 134)	162	45.7	0.015	gi 25956290 gb AAN75708.1	AF391544_1 delta 4-desat ( 515)	168	47.4	0.018
gi 158273950 gb EDO99735.1	cytochrome b5 protein ( 112)	161	45.4	0.015	gi 76059256 emb CAJ30825.1	unnamed protein produc ( 515)	168	47.4	0.018
gi 60220806 emb CAL23341.1	unnamed protein produc ( 201)	164	46.3	0.016	gi 155102609 gb ABT03232.1	Sequence 29 from paten ( 515)	168	47.4	0.018
gi 126633748 emb CAM55830.1	unnamed protein produ ( 201)	164	46.3	0.016	gi 155116365 gb ABT11291.1	Sequence 20 from paten ( 515)	168	47.4	0.018
gi 76059306 emb CAJ30847.1	unnamed protein produc ( 201)	164	46.3	0.016	gi 155095501 gb ABS99956.1	Sequence 20 from paten ( 515)	168	47.4	0.018
gi 110565249 emb CAL23341.1	unnamed protein produ ( 201)	164	46.3	0.016	gi 111979070 gb ABH83333.1	Sequence 21 from paten ( 515)	168	47.4	0.018
gi 156219508 gb EDO40389.1	predicted protein [Nem ( 361)	167	47.1	0.016	gi 111979090 gb ABH83333.1	Sequence 70 from paten ( 515)	168	47.4	0.018
gi 210095508 gb EEA43670.1	hypothetical protein B ( 361)	167	47.1	0.016	gi 155082201 gb ABS94941.1	Sequence 21 from paten ( 515)	168	47.4	0.018
gi 211582522 emb CAP80710.1	Pc12g10830 [Penicilli ( 137)	162	45.7	0.016	gi 155095500 gb ABS99955.1	Sequence 19 from paten ( 515)	168	47.4	0.018
gi 60220754 emb CAI58876.1	unnamed protein produc ( 541)	169	47.7	0.016	gi 25956288 gb AAN75707.1	AF391543_1 delta 4-desat ( 515)	168	47.4	0.018
gi 126633794 emb CAM55853.1	unnamed protein produ ( 541)	169	47.7	0.016	gi 111979067 gb ABH83330.1	Sequence 18 from paten ( 515)	168	47.4	0.018
gi 76059254 emb CAJ30824.1	unnamed protein produc ( 541)	169	47.7	0.016	gi 215506991 gb EEC16485.1	cytochrome B5, putativ ( 134)	161	45.5	0.018
gi 160814785 emb CAP40237.1	unnamed protein produ ( 541)	169	47.7	0.016	gi 51011616 gb AAT92217.1	cytochrome b5 [Ixodes p ( 134)	161	45.5	0.018
gi 33466346 gb AAQ19605.1	delta-4 fatty acid desa ( 541)	169	47.7	0.016	gi 34103762 gb AAQ60123.1	probable linoleoyl-CoA ( 357)	166	46.9	0.018
gi 116001283 emb CAL49893.1	unnamed protein produ ( 541)	169	47.7	0.016	gi 195652285 gb ACG45610.1	cytochrome b5 [Zea may ( 135)	161	45.5	0.018
gi 55467928 emb CAH69570.1	unnamed protein produc ( 541)	169	47.7	0.016	gi 195623138 gb ACG33399.1	cytochrome b5 [Zea may ( 135)	161	45.5	0.018
gi 141417734 gb ECR68442.1	hypothetical protein G ( 250)	165	46.6	0.016	gi 162667052 gb EDQ53691.1	predicted protein [Phy ( 77)	158	44.6	0.018
gi 140106319 gb ECJ57827.1	hypothetical protein G ( 78)	159	44.9	0.016	gi 146449222 gb EDK43478.1	conserved hypothetical ( 248)	164	46.3	0.018
gi 190650077 gb EDV47355.1	GG17685 [Drosophila er ( 117)	161	45.4	0.016	gi 199429801 emb CAG85354.2	DEHA2B09196p [Debaryo ( 170)	162	45.8	0.019
gi 23428547 gb AAL23676.1	delta-12 fatty acid des ( 382)	167	47.1	0.016	gi 141122012 gb ECP77867.1	hypothetical protein G ( 307)	165	46.6	0.019
gi 156227910 gb EDO48711.1	predicted protein [Nem ( 315)	166	46.9	0.016	gi 49645443 emb CAG99015.1	KLLA0F27577p [Kluyvero ( 172)	162	45.8	0.019
gi 76059404 emb CAJ30867.1	unnamed protein produc ( 383)	167	47.1	0.016	gi 134067698 emb CAM65978.1	cytochrome b5-like, p ( 117)	160	45.2	0.019
gi 13447102 gb AAK26633.1	AF343065_1 delta-12 fatt ( 383)	167	47.1	0.016	gi 136563461 gb EBO97051.1	hypothetical protein G ( 143)	161	45.5	0.019
gi 17382283 emb CAD13056.1	unnamed protein produc ( 383)	167	47.1	0.016	gi 167876111 gb AAW039494.1	cytochrome b5 [Culex q ( 121)	160	45.2	0.019
gi 83702515 gb ABC41578.1	endoplasmic reticulum 1 ( 388)	167	47.1	0.016	gi 198261777 gb EDY86063.1	linoleoyl-coa desatura ( 392)	166	46.9	0.019
gi 83775528 dbj BAE65648.1	unnamed protein produc ( 101)	160	45.2	0.017	gi 134900714 gb EBE17538.1	hypothetical protein G ( 150)	161	45.5	0.02
gi 138183035 gb EBY25878.1	hypothetical protein G ( 269)	165	46.6	0.017	gi 138148757 gb EBY01924.1	hypothetical protein G ( 187)	162	45.8	0.02
gi 156203103 gb EDO27494.1	predicted protein [Nem ( 327)	166	46.9	0.017	gi 140893949 gb ECO22325.1	hypothetical protein G ( 155)	161	45.5	0.02
gi 211582756 emb CAP80956.1	Pc12g13290 [Penicilli ( 488)	168	47.4	0.017	gi 111069636 gb EAT90756.1	hypothetical protein S ( 502)	167	47.2	0.02
gi 137712075 gb EBV59302.1	hypothetical protein G ( 332)	166	46.9	0.017	gi 29469883 gb AAO73962.1	cytochrome b5 [Candida ( 129)	160	45.2	0.02
gi 140226881 gb ECK38746.1	hypothetical protein G ( 186)	163	46.0	0.017	gi 29703119 gb AAO96611.1	Sequence 2 from patent ( 129)	160	45.2	0.02
gi 83769244 dbj BAE59381.1	unnamed protein produc ( 495)	168	47.4	0.017	gi 42677386 gb AAS26339.1	Sequence 5 from patent ( 129)	160	45.2	0.02
gi 676850 gb AAA62316.1	nitrate reductase ( 889)	171	48.3	0.017	gi 156611998 gb AAW04235.1	Sequence 5 from patent ( 129)	160	45.2	0.02
gi 144097145 gb ED184470.1	hypothetical protein G ( 277)	165	46.6	0.017	gi 150855546 gb EDN30738.1	hypothetical protein B ( 907)	170	48.0	0.02
gi 2342599 emb CAA04554.1	Nitrate reductase [Meta ( 892)	171	48.3	0.017	gi 6224515 emb CAB60010.1	nitrate reductase [Hebe ( 908)	170	48.0	0.02
gi 141122011 gb ECP77866.1	hypothetical protein G ( 280)	165	46.6	0.017	gi 154697219 gb EDN96957.1	hypothetical protein S ( 910)	170	48.0	0.021
gi 155095522 gb ABS99977.1	Sequence 70 from paten ( 515)	168	47.4	0.018	gi 5020385 gb AAD38068.1	AF153448_1 nitrate reduct ( 910)	170	48.0	0.021
gi 25956294 gb AAN75710.1	AF391546_1 delta 4-desat ( 515)	168	47.4	0.018	gi 138729976 gb ECB61117.1	hypothetical protein G ( 283)	164	46.4	0.021
gi 111979068 gb ABH83311.1	Sequence 19 from paten ( 515)	168	47.4	0.018	gi 138192263 gb EBY31848.1	hypothetical protein G ( 233)	163	46.1	0.021
gi 160814992 emb CAP40240.1	unnamed protein produ ( 515)	168	47.4	0.018	gi 19045 emb CAA40975.1	nitrate reductase [Hordeu ( 912)	170	48.0	0.021
gi 116001281 emb CAL49892.1	unnamed protein produ ( 515)	168	47.4	0.018	gi 18994 emb CAA40976.1	nitrate reductase [Hordeu ( 915)	170	48.0	0.021
gi 155082200 gb ABS94940.1	Sequence 20 from paten ( 515)	168	47.4	0.018	gi 118481960 gb ABK92912.1	unknown [Populus trich ( 134)	160	45.2	0.021
gi 25956292 gb AAN75709.1	AF391545_1 delta 4-desat ( 515)	168	47.4	0.018	gi 118483464 gb ABK93631.1	unknown [Populus trich ( 134)	160	45.2	0.021
gi 155116363 gb ABT11289.1	Sequence 18 from paten ( 515)	168	47.4	0.018	gi 118489280 gb ABK96445.1	unknown [Populus trich ( 134)	160	45.2	0.021
gi 155082198 gb ABS94938.1	Sequence 18 from paten ( 515)	168	47.4	0.018	gi 194112989 gb EDW35032.1	GL20014 [Drosophila pe ( 135)	160	45.2	0.021
gi 126633796 emb CAM55854.1	unnamed protein produ ( 515)	168	47.4	0.018	gi 198136706 gb EAL25975.2	GA15264 [Drosophila ps ( 135)	160	45.2	0.021

gi 194145667 gb EDW62063.1  GJ19962 [Drosophila vi ( 135) 160 45.2 0.021	gi 60392566 gb AA19389.1  delta-12 oleate desatur ( 378) 164 46.4 0.026
gi 195659495 gb ACG49215.1  cytochrome b5 [Zea may ( 135) 160 45.2 0.021	gi 69061718 gb AA199777.1  delta-12 oleate desatur ( 378) 164 46.4 0.026
gi 170944233 emb CAP70343.1  unnamed protein produ ( 952) 170 48.1 0.021	gi 60418974 gb AA19894.1  delta-12 oleate desatur ( 378) 164 46.4 0.026
gi 119408251 gb EAW18200.1  cytochrome b5, putativ ( 136) 160 45.3 0.021	gi 60392570 gb AA19391.1  delta-12 oleate desatur ( 378) 164 46.4 0.026
gi 194194233 gb EDX07809.1  GD11452 [Drosophila si ( 535) 167 47.2 0.021	gi 69061719 gb AA199778.1  delta-12 oleate desatur ( 378) 164 46.4 0.026
gi 194126550 gb EDW48593.1  GM21957 [Drosophila se ( 535) 167 47.2 0.021	gi 134284837 gb ABO69520.1  microsomal oleate desa ( 378) 164 46.4 0.026
gi 125550542 gb EAY96251.1  hypothetical protein O ( 137) 160 45.3 0.021	gi 60392568 gb AA19390.1  delta-12 oleate desatur ( 378) 164 46.4 0.026
gi 14719320 gb AAK73138.1 AC079022_11 cytochrome B ( 137) 160 45.3 0.021	gi 33766657 gb AAQ52860.1  Sequence 14 from patent ( 378) 164 46.4 0.026
gi 113577985 dbj BAF16348.1  Os05g0108800 [Oryza s ( 137) 160 45.3 0.021	gi 60418976 gb AA19895.1  delta-12 oleate desatur ( 378) 164 46.4 0.026
gi 125592545 gb EAZ32604.1  hypothetical protein O ( 137) 160 45.3 0.021	gi 2290404 gb AAB65146.1  delta-12 oleate desatura ( 378) 164 46.4 0.026
gi 215694024 dbj BAG89223.1  unnamed protein produ ( 137) 160 45.3 0.021	gi 18418649 gb AAL68981.1 AF251842_1 delta-12 olea ( 378) 164 46.4 0.026
gi 414705 emb CAA53366.1  cytochrome b5 [Oryza sat ( 137) 160 45.3 0.021	gi 209967428 gb ACJ02341.1  seed-specific oleoyl-p ( 378) 164 46.4 0.026
gi 52353573 gb AAU44139.1  cytochrome b5 [Oryza sa ( 137) 160 45.3 0.021	gi 60392564 gb AA19388.1  delta-12 oleate desatur ( 378) 164 46.4 0.026
gi 54635516 gb EAL24919.1  GAL0870 [Drosophila pse ( 536) 167 47.2 0.021	gi 134284835 gb ABO69519.1  microsomal oleate desa ( 378) 164 46.4 0.026
gi 194109647 gb EDW31690.1  GL10825 [Drosophila pe ( 536) 167 47.2 0.021	gi 155689134 gb ABU29144.1  Sequence 14 from paten ( 378) 164 46.4 0.026
gi 194144162 gb EDW60558.1  GJ20792 [Drosophila vi ( 539) 167 47.2 0.022	gi 145046502 gb ABP33181.1  nitrate reductase [Dek ( 379) 164 46.4 0.026
gi 296386 emb CAA50575.1  cytochrome b5 [Nicotiana ( 139) 160 45.3 0.022	gi 198146999 gb EAL32156.2  GAL17524 [Drosophila ps ( 118) 158 44.8 0.026
gi 28202143 gb AAO34680.1  reductase [Gibberella z ( 452) 166 46.9 0.022	gi 149038111 gb EDL92471.1  cytochrome b5 type B, ( 146) 159 45.0 0.027
gi 68124617 emb CAJ03111.1  cytochrome b5-like, pu ( 117) 159 45.0 0.022	gi 48735409 gb AAH72535.1  Cytochrome b5 type B [R ( 146) 159 45.0 0.027
gi 144976090 gb ABP13185.1  Sequence 6 from patent ( 173) 161 45.5 0.022	gi 2253161 emb CAA73117.1  cytochrome b5, mitochon ( 146) 159 45.0 0.027
gi 154423266 gb ABS81534.1  ortho-nitrophenol 2-mo ( 558) 167 47.2 0.022	gi 159129010 gb EDP54124.1  cytochrome b5, putativ ( 217) 161 45.6 0.027
gi 136615850 gb EBP30589.1  hypothetical protein G ( 258) 163 46.1 0.022	gi 89301602 gb EAR99590.1  Fatty acid desaturase f ( 399) 164 46.5 0.027
gi 134718411 gb EBD00780.1  hypothetical protein G ( 258) 163 46.1 0.022	gi 116061100 emb CAL56488.1  Linoleoyl-CoA desatur ( 487) 165 46.7 0.027
gi 5994480 gb AAE19893.1  Sequence 2 from patent U ( 382) 165 46.7 0.022	gi 134062959 emb CAM39407.1  hypothetical protein, ( 488) 165 46.7 0.027
gi 140396654 gb ECL49154.1  hypothetical protein G ( 259) 163 46.1 0.022	gi 156114680 gb EDO16188.1  hypothetical protein K ( 596) 166 47.0 0.027
gi 32451979 gb AAH54749.1  Cytochrome b5 type B [M ( 146) 160 45.3 0.023	gi 215508350 gb EEC17804.1  flavohemoprotein B5/b5 ( 492) 165 46.7 0.028
gi 148679454 gb EDL11401.1  cytochrome b5 type B [ ( 146) 160 45.3 0.023	gi 119610528 gb EAW90122.1  cytochrome b5 domain c ( 157) 159 45.1 0.028
gi 12841545 dbj BAB25251.1  unnamed protein produc ( 146) 160 45.3 0.023	gi 91131655 gb ABE15393.1  Sequence 2926 from pate ( 157) 159 45.1 0.028
gi 38566255 gb AAH62980.1  Cytochrome b5 type B [M ( 146) 160 45.3 0.023	gi 16552638 dbj BAB1357.1  unnamed protein produc ( 157) 159 45.1 0.028
gi 74225098 dbj BAE38245.1  unnamed protein produc ( 146) 160 45.3 0.023	gi 28850428 gb AAO53192.1  similar to Homo sapiens ( 158) 159 45.1 0.028
gi 37590501 gb AAH58812.1  Cytochrome b5 type B [M ( 146) 160 45.3 0.023	gi 76781148 gb ABA54489.1  cytochrome b5 type 06 [ ( 131) 158 44.8 0.028
gi 74214155 dbj BAE40334.1  unnamed protein produc ( 146) 160 45.3 0.023	gi 89296735 gb EAR94723.1  Cytochrome b5-like Heme ( 109) 157 44.5 0.029
gi 12859383 dbj BAB31635.1  unnamed protein produc ( 146) 160 45.3 0.023	gi 23197754 gb AAN15404.1  putative cytochrome b5 ( 134) 158 44.8 0.029
gi 12833936 dbj BAB22721.1  unnamed protein produc ( 146) 160 45.3 0.023	gi 22136052 gb AAM91608.1  putative cytochrome b5 ( 134) 158 44.8 0.029
gi 26354094 dbj BAC40677.1  unnamed protein produc ( 146) 160 45.3 0.023	gi 2914701 gb AAC04491.1  putative cytochrome b5 [ ( 134) 158 44.8 0.029
gi 26342999 dbj BAC35156.1  unnamed protein produc ( 146) 160 45.3 0.023	gi 110743053 dbj BAE99419.1  putative cytochrome b ( 134) 158 44.8 0.029
gi 12834709 dbj BAB23012.1  unnamed protein produc ( 146) 160 45.3 0.023	gi 194106690 gb EDW28733.1  GL18786 [Drosophila pe ( 440) 164 46.5 0.029
gi 141086034 gb ECP52629.1  hypothetical protein G ( 264) 163 46.1 0.023	gi 190657990 gb EDV55203.1  GG21968 [Drosophila er ( 535) 165 46.8 0.03
gi 119407800 gb EAW17749.1  nitrate reductase, put (1032) 170 48.1 0.023	gi 190659447 gb EDV56660.1  GG22772 [Drosophila er ( 441) 164 46.5 0.03
gi 4007804 emb CAA22444.1  cytochrome b5 (predicte ( 124) 159 45.0 0.023	gi 146451117 gb EDK45373.1  hypothetical protein L ( 655) 166 47.0 0.03
gi 164650801 gb EDR15041.1  predicted protein [Lac ( 485) 166 47.0 0.023	gi 16945429 emb CAB91687.2  probable cytochrome b5 ( 139) 158 44.8 0.03
gi 142471021 gb ECY31970.1  hypothetical protein G ( 333) 164 46.4 0.023	gi 135195289 gb EBG10299.1  hypothetical protein G ( 170) 159 45.1 0.03
gi 111062588 gb EAT83708.1  hypothetical protein S ( 498) 166 47.0 0.024	gi 27924030 gb AAO27755.1  reductase [Fusarium spo ( 452) 164 46.5 0.03
gi 170948370 emb CAP60534.1  unnamed protein produ ( 607) 167 47.3 0.024	gi 190584960 gb EDV25029.1  hypothetical protein T ( 551) 165 46.8 0.03
gi 168519 gb AAA03202.1  NADH:nitrate reductase ( 618) 167 47.3 0.024	gi 45446819 gb AAN09163.3  CG3566-PB, isoform B [D ( 117) 157 44.5 0.03
gi 45446820 gb AAS65265.1  CG3566-PC, isoform C [D ( 89) 157 44.4 0.024	gi 194115856 gb EDW37899.1  GL21352 [Drosophila pe ( 118) 157 44.5 0.031
gi 17946653 gb AAL49357.1  RH45308p [Drosophila me ( 89) 157 44.4 0.024	gi 146156749 gb ABQ07603.1  fatty acid desaturase ( 386) 163 46.2 0.031
gi 136515691 gb EBO06540.1  hypothetical protein G ( 132) 159 45.0 0.024	gi 162471891 gb ABX99726.1  Sequence 2 from patent ( 120) 157 44.5 0.031
gi 144579309 gb ABO97371.1  predicted protein [Ost ( 517) 166 47.0 0.024	gi 431762 gb AAA67468.1  cytochrome b5 [Saccharomy ( 120) 157 44.5 0.031
gi 139943757 gb ECI54134.1  hypothetical protein G ( 240) 162 45.9 0.025	gi 22316532 emb CAD44473.1  unnamed protein produc ( 216) 160 45.4 0.031
gi 50844675 gb AAT84459.1  cytochrome b5 isoform C ( 134) 159 45.0 0.025	gi 22316686 emb CAD44443.1  unnamed protein produc ( 216) 160 45.4 0.031
gi 139996105 gb ECI90046.1  hypothetical protein G ( 111) 158 44.7 0.025	gi 134925723 gb EBE34119.1  hypothetical protein G ( 324) 162 45.9 0.032
gi 76781150 gb ABA54490.1  cytochrome b5 type 11 [ ( 136) 159 45.0 0.025	gi 28828102 gb AAO50785.1  similar to cytochrome b ( 149) 158 44.8 0.032
gi 198138222 gb EDY70015.1  GA25795 [Drosophila ps ( 440) 165 46.7 0.025	gi 126095722 gb ABN65544.1  cytochrome b5 [Pichia ( 124) 157 44.5 0.03
gi 7302484 gb AAF57568.1  CG11257-PA [Drosophila m ( 535) 166 47.0 0.025	gi 136207959 gb EBM60653.1  hypothetical protein G ( 489) 164 46.5 0.032
gi 66771089 gb AA154856.1  IP11715p [Drosophila me ( 535) 166 47.0 0.025	gi 138293221 gb EBY83808.1  hypothetical protein G ( 127) 157 44.5 0.033
gi 190345236 gb EDK37091.2  hypothetical protein P ( 453) 165 46.7 0.026	gi 55733155 emb CAH93261.1  hypothetical protein [ ( 228) 160 45.4 0.033
gi 116787072 gb ABK24364.1  unknown [Picea sitchen ( 375) 164 46.4 0.026	gi 138408697 gb EBZ46713.1  hypothetical protein G ( 156) 158 44.8 0.033

gi 154702550 gb EDO02289.1	hypothetical protein S ( 509)	164	46.5	0.033	gi 155265493 gb ABT21097.1	Sequence 108567 from p ( 142)	156	44.3	0.042
gi 211581814 emb CAP79936.1	Pcl2g03090 [Penicilli ( 622)	165	46.8	0.033	gi 155324281 gb ABT79885.1	Sequence 167355 from p ( 142)	156	44.3	0.042
gi 2647949 emb CAA04702.1	cytochrome b5 [Olea eur ( 132)	157	44.6	0.034	gi 8980835 gb AAF82295.1	microsomal oleate desatu ( 379)	161	45.7	0.042
gi 51968520 dbj BAD42952.1	putative cytochrome b5 ( 132)	157	44.6	0.034	gi 8980833 gb AAF82294.1	microsomal oleate desatu ( 379)	161	45.7	0.042
gi 98961069 gb ABF59018.1	At2g46650 [Arabidopsis ( 132)	157	44.6	0.034	gi 67090583 gb AA67653.1	oleate desaturase [Arac ( 379)	161	45.7	0.042
gi 21593247 gb IAM65196.1	putative cytochrome b5 ( 132)	157	44.6	0.034	gi 211587273 emb CAP79467.1	Pc19g00510 [Penicilli ( 469)	162	46.0	0.043
gi 3831439 gb AAC69922.1	putative cytochrome b5 [ ( 132)	157	44.6	0.034	gi 83767338 dbj BAE57477.1	unnamed protein produc ( 573)	163	46.3	0.043
gi 20197779 gb AAM15242.1	putative cytochrome b5 ( 132)	157	44.6	0.034	gi 136648940 gb EBP50174.1	hypothetical protein G ( 320)	160	45.5	0.043
gi 2062405 gb AAC49701.1	cytochrome b5 [Borago of ( 132)	157	44.6	0.034	gi 139643374 gb ECG46848.1	hypothetical protein G ( 268)	159	45.2	0.044
gi 24899389 gb AAN64993.1	nitrate reductase [Tube ( 929)	167	47.4	0.034	gi 121905115 gb EAY10049.1	Cytochrome b5-like Hem ( 102)	154	43.8	0.044
gi 193808522 emb CAQ39225.1	Heme binding protein, ( 162)	158	44.8	0.034	gi 90299699 gb EAS29330.1	hypothetical protein CI ( 337)	160	45.5	0.045
gi 30090033 gb AAO86521.1	cytochrome B5 [Triticum ( 135)	157	44.6	0.034	gi 155265491 gb ABT21095.1	Sequence 108565 from p ( 158)	156	44.4	0.046
gi 195644840 gb ACG41888.1	cytochrome b5 [Zea may ( 135)	157	44.6	0.034	gi 155116369 gb ABT11295.1	Sequence 37 from paten ( 509)	162	46.1	0.046
gi 114192094 gb EAU33794.1	cytochrome b5 [Aspergi ( 137)	157	44.6	0.035	gi 155095505 gb ABS99960.1	Sequence 37 from paten ( 509)	162	46.1	0.046
gi 51969026 dbj BAD43205.1	putative cytochrome b5 ( 140)	157	44.6	0.035	gi 155082204 gb ABS94944.1	Sequence 37 from paten ( 509)	162	46.1	0.046
gi 134059770 emb CAM41893.1	cytochrome b5-like, p ( 117)	156	44.3	0.036	gi 111979073 gb ABH83316.1	Sequence 37 from paten ( 509)	162	46.1	0.046
gi 19853 emb CAA8240.1	cytochrome b5 [Nicotiana ( 97)	155	44.0	0.036	gi 68127215 emb CAJ05265.1	hypothetical protein, (1126)	166	47.2	0.046
gi 1054843 emb CAA63432.1	D12 oleate desaturase [ ( 383)	162	46.0	0.036	gi 140257004 gb ECK59579.1	hypothetical protein G ( 161)	156	44.4	0.046
gi 34600650 gb AAQ78507.1	Sequence 12 from patent ( 383)	162	46.0	0.036	gi 134070521 emb CAM68864.1	hypothetical protein, (1148)	166	47.2	0.047
gi 17225582 gb AAL37484.1	AF331163_1 delta-12 fatt ( 384)	162	46.0	0.036	gi 158594261 gb EDP32845.1	Cytochrome b5-like Hem ( 111)	154	43.8	0.047
gi 190409098 gb EDV12363.1	cytochrome b5 [Sacchar ( 120)	156	44.3	0.036	gi 170940958 emb CAP66608.1	unnamed protein produ ( 136)	155	44.1	0.047
gi 167275173 gb ABZ28037.1	Sequence 1975 from pat ( 120)	156	44.3	0.036	gi 157350710 emb CAO40801.1	unnamed protein produ ( 166)	156	44.4	0.048
gi 51013663 gb AAT93125.1	YNL111C [Saccharomyces ( 120)	156	44.3	0.036	gi 195608042 gb ACG25851.1	cytochrome b5 [Zea may ( 139)	155	44.1	0.048
gi 1302032 emb CAA95990.1	CYB5 [Saccharomyces cer ( 120)	156	44.3	0.036	gi 195608192 gb ACG25926.1	cytochrome b5 [Zea may ( 139)	155	44.1	0.048
gi 1183962 emb CAA93396.1	Cytochrome B5 [Saccharo ( 120)	156	44.3	0.036	gi 195615256 gb ACG29458.1	cytochrome b5 [Zea may ( 139)	155	44.1	0.048
gi 18478404 dbj BAB84515.1	nitrate reductase [Mon ( 873)	166	47.1	0.038	gi 194187409 gb EDX00993.1	GE16473 [Drosophila ya ( 117)	154	43.8	0.049
gi 138746826 gb ECB72846.1	hypothetical protein G ( 125)	156	44.3	0.038	gi 8980831 gb AAF82293.1	microsomal oleate desatu ( 379)	160	45.5	0.049
gi 144005727 gb EDI19070.1	hypothetical protein G ( 153)	157	44.6	0.038	gi 66734339 gb AAY53559.1	oleate desaturase [Arac ( 379)	160	45.5	0.049
gi 140913054 gb ECO34721.1	hypothetical protein G ( 153)	157	44.6	0.038	gi 121104181 gb ABM47430.1	delta-12 fatty acid de ( 379)	160	45.5	0.049
gi 146452690 gb EDK46946.1	cytochrome b5 [Loddero ( 127)	156	44.3	0.038	gi 121104183 gb ABM47431.1	delta-12 fatty acid de ( 379)	160	45.5	0.049
gi 38174502 gb AAH60779.1	Cytochrome b5 domain co ( 228)	159	45.2	0.038	gi 14572857 gb AAK67829.1	delta-12 fatty acid des ( 379)	160	45.5	0.049
gi 119610525 gb EAW90119.1	cytochrome b5 domain c ( 228)	159	45.2	0.038	gi 71064149 gb AAZ22543.1	oleate desaturase [Arac ( 379)	160	45.5	0.049
gi 119610527 gb EDK46946.1	cytochrome b5 domain c ( 228)	159	45.2	0.038	gi 49647598 emb CAG82041.1	YALI0C11627p [Yarrowia ( 257)	158	45.0	0.05
gi 158260063 dbj BAF82209.1	unnamed protein produ ( 228)	159	45.2	0.038	gi 126233687 gb ABN97087.1	fatty acid desaturase ( 380)	160	45.5	0.05
gi 136563033 gb EBO96777.1	hypothetical protein G ( 188)	158	44.9	0.038	gi 162694677 gb EDQ81024.1	predicted protein [Phy ( 144)	155	44.1	0.05
gi 187979816 gb EDU46442.1	L-lactate dehydrogenas ( 508)	163	46.3	0.039	gi 160703451 gb EAT80428.2	hypothetical protein S ( 471)	161	45.8	0.05
gi 163777626 gb EDQ91242.1	predicted protein [Mon ( 130)	156	44.3	0.039	gi 138092570 gb EBX70193.1	hypothetical protein G ( 147)	155	44.1	0.051
gi 66968448 gb AAY59603.1	fatty acid desaturase [ ( 159)	157	44.6	0.039	gi 190348933 gb EDK41487.2	hypothetical protein P ( 151)	155	44.1	0.052
gi 197713706 gb EDY57740.1	fatty acid desaturase ( 235)	159	45.2	0.039	gi 27868666 gb AAO24766.1	cytochrome b5 [Anophele ( 128)	154	43.9	0.053
gi 111979074 gb ABH83317.1	Sequence 46 from paten ( 513)	163	46.3	0.039	gi 119855481 gb ABM01874.1	cytochrome b5 [Anophel ( 128)	154	43.9	0.053
gi 155095506 gb ABS99961.1	Sequence 46 from paten ( 513)	163	46.3	0.039	gi 134076459 emb CAK45099.1	unnamed protein produ ( 901)	164	46.7	0.053
gi 155082205 gb ABS99495.1	Sequence 46 from paten ( 513)	163	46.3	0.039	gi 140473492 gb ECL94361.1	hypothetical protein G ( 72)	151	43.0	0.053
gi 155116370 gb ABT11296.1	Sequence 46 from paten ( 513)	163	46.3	0.039	gi 144118082 gb EDI99440.1	hypothetical protein G ( 344)	159	45.3	0.054
gi 134609363 gb EBC36463.1	hypothetical protein G ( 288)	160	45.4	0.039	gi 57997557 emb CAI46070.1	hypothetical protein [ ( 107)	153	43.6	0.054
gi 194157067 gb EDW1968.1	GK10686 [Drosophila wi ( 133)	156	44.3	0.04	gi 116060798 emb CAL57276.1	Cytochrome b5 (ISS) [ ( 921)	164	46.7	0.054
gi 53956025 gb AAV06022.1	Sequence 17979 from pat ( 241)	159	45.2	0.04	gi 139918077 gb ECI36068.1	hypothetical protein G ( 289)	158	45.0	0.055
gi 135410697 gb EBH45357.1	hypothetical protein G ( 356)	161	45.7	0.04	gi 9759195 dbj BAB09732.1	cytochrome b5 [Arabidop ( 134)	154	43.9	0.055
gi 53954683 gb AAV04680.1	Sequence 16637 from pat ( 434)	162	46.0	0.04	gi 21592682 gb AAM64631.1	cytochrome b5 (dbj BAA7 ( 134)	154	43.9	0.055
gi 193910639 gb EDW09506.1	GI18997 [Drosophila mo ( 135)	156	44.3	0.04	gi 4240120 dbj BAA74839.1	cytochrome b5 [Arabidop ( 134)	154	43.9	0.055
gi 450585 gb AAA62621.1	cytochrome b5 ( 135)	156	44.3	0.04	gi 21281008 gb AAM45093.1	putative cytochrome b5 ( 134)	154	43.9	0.055
gi 193911737 gb EDW10604.1	GI21190 [Drosophila mo ( 528)	163	46.3	0.04	gi 19423894 gb AAL87348.1	putative cytochrome b5 ( 134)	154	43.9	0.055
gi 194176616 gb EDW90227.1	GE12766 [Drosophila ya ( 441)	162	46.0	0.041	gi 138331574 gb EBZ01581.1	hypothetical protein G ( 243)	157	44.7	0.055
gi 134071272 emb CAM69957.1	nitrate reductase, pu ( 537)	163	46.3	0.041	gi 190620188 gb EDV35712.1	GF12339 [Drosophila an ( 534)	161	45.8	0.056
gi 194177892 gb EDW91503.1	GE12047 [Drosophila ya ( 537)	163	46.3	0.041	gi 136449013 gb EBO23435.1	hypothetical protein G ( 64)	150	42.7	0.057
gi 162678763 gb EDQ65218.1	predicted protein [Phy ( 138)	156	44.3	0.041	gi 118486433 gb ABK95056.1	unknown [Populus trich ( 140)	154	43.9	0.057
gi 167881581 gb EDS44964.1	conserved hypothetical ( 444)	162	46.0	0.041	gi 115879980 gb ABJ46912.1	Sequence 7651 from pat ( 79)	151	43.0	0.058
gi 114192719 gb EAU34419.1	hypothetical protein A ( 541)	163	46.3	0.041	gi 40046146 emb CAF01849.1	unnamed protein produc ( 79)	151	43.0	0.058
gi 193899317 gb EDV98183.1	GH22815 [Drosophila gr ( 547)	163	46.3	0.041	gi 77454024 gb ABA85719.1	Sequence 7651 from pate ( 79)	151	43.0	0.058

gi 60117056 gb AAX14399.1	oleate desaturase [Arac	( 379)	159	45.3	0.058	gi 192910754 gb ACF06485.1	cytochrome b5 [Elaeis	( 135)	152	43.4	0.076
gi 110623234 emb CAL24257.1	unnamed protein produ	( 387)	159	45.3	0.059	gi 136475405 gb EBO040494.1	hypothetical protein G	( 297)	156	44.5	0.077
gi 110623232 emb CAL24256.1	unnamed protein produ	( 387)	159	45.3	0.059	gi 83767336 dbj BAE57475.1	unnamed protein produc	( 137)	152	43.4	0.077
gi 134058839 emb CAM41406.1	cytochrome b-domain p	( 218)	156	44.4	0.06	gi 212513236 gb EEB15854.1	cytochrome B5, putativ	( 455)	158	45.1	0.079
gi 139086057 gb ECD31462.1	hypothetical protein G	( 83)	151	43.0	0.06	gi 213509827 emb CAS92463.1	unnamed protein produ	( 558)	159	45.4	0.08
gi 55726804 emb CAH90162.1	hypothetical protein [	( 150)	154	43.9	0.06	gi 114188382 gb EAU30082.1	conserved hypothetical	( 460)	158	45.1	0.08
gi 141266737 gb ECQ77935.1	hypothetical protein G	( 125)	153	43.6	0.061	gi 33766655 gb AAQ52858.1	Sequence 11 from patent	( 380)	157	44.8	0.08
gi 142121294 gb ECV74577.1	hypothetical protein G	( 333)	158	45.0	0.061	gi 45643653 gb AAS72902.1	trans-delta12 oleic aci	( 380)	157	44.8	0.08
gi 155095520 gb ABS99975.1	Sequence 68 from paten	( 335)	158	45.0	0.062	gi 155689132 gb ABU29142.1	Sequence 11 from paten	( 380)	157	44.8	0.08
gi 155082219 gb ABS94959.1	Sequence 68 from paten	( 335)	158	45.0	0.062	gi 155349158 gb ABU04763.1	Sequence 192232 from p	( 82)	149	42.6	0.082
gi 155116384 gb ABT11310.1	Sequence 68 from paten	( 335)	158	45.0	0.062	gi 56199450 gb AAV84214.1	cytochrome B5 [Culicoid	( 149)	152	43.4	0.083
gi 111979088 gb ABH83331.1	Sequence 68 from paten	( 335)	158	45.0	0.062	gi 134076460 emb CAK45100.1	unnamed protein produ	(1048)	162	46.2	0.083
gi 187981254 gb EDU47880.1	nitrate reductase [Pyr	( 605)	161	45.9	0.062	gi 142648604 gb ECZ57889.1	hypothetical protein G	( 331)	156	44.6	0.084
gi 134058564 emb CAK96451.1	unnamed protein produ	( 503)	160	45.6	0.062	gi 114187902 gb EAU29602.1	conserved hypothetical	( 490)	158	45.1	0.084
gi 167881026 gb EDS44409.1	cytochrome B5 [Culex q	( 129)	153	43.6	0.063	gi 140473491 gb ECL94360.1	hypothetical protein G	( 225)	154	44.0	0.084
gi 145386893 gb ABP65296.1	omega-6 fatty desatura	( 350)	158	45.0	0.064	gi 124402256 emb CAK67729.1	unnamed protein produ	( 279)	155	44.3	0.086
gi 5919159 gb AAD56233.1	cytochrome b558 [Ectothi	( 90)	151	43.1	0.064	gi 164648448 gb EDR12691.1	predicted protein [Lac	( 129)	151	43.2	0.086
gi 143054273 gb EDC47947.1	hypothetical protein G	( 242)	156	44.5	0.065	gi 199432414 emb CAG87560.2	DEHA2E00836p [Debaryo	( 615)	159	45.4	0.086
gi 187984054 gb EDU49542.1	microsomal cytochrome	( 135)	153	43.6	0.065	gi 57228635 gb AAW45070.1	cytochrome b5, putative	( 158)	152	43.4	0.087
gi 154698802 gb EDN98540.1	hypothetical protein S	( 137)	153	43.6	0.066	gi 11177032 dbj BAB17854.1	cytochrome b5 [Ciona s	( 132)	151	43.2	0.088
gi 125551501 gb AAM63789.1	cytochrome b5 (dbj BAA7	( 140)	153	43.6	0.067	gi 125545758 gb EAY91897.1	hypothetical protein O	( 196)	153	43.7	0.088
gi 4240122 dbj BAA74840.1	cytochrome b5 [Arabidop	( 140)	153	43.6	0.067	gi 125587957 gb EAZ28621.1	hypothetical protein O	( 196)	153	43.7	0.088
gi 17104717 gb AAL34247.1	putative cytochrome b5	( 140)	153	43.6	0.067	gi 195622790 gb ACG33225.1	cytochrome b5 [Zea may	( 133)	151	43.2	0.088
gi 9758880 dbj BAB09434.1	cytochrome b5 [Arabidop	( 140)	153	43.6	0.067	gi 195651237 gb ACG45086.1	cytochrome b5 [Zea may	( 133)	151	43.2	0.088
gi 13877987 gb AAK44071.1	AF370256_1 putative cyto	( 140)	153	43.6	0.067	gi 195627196 gb ACG35428.1	cytochrome b5 [Zea may	( 133)	151	43.2	0.088
gi 157337660 emb CAO22006.1	unnamed protein produ	( 376)	158	45.1	0.068	gi 13786468 gb AAK39593.1	AC025296_28 putative cyt	( 134)	151	43.2	0.089
gi 147858117 emb CAN79670.1	hypothetical protein	( 376)	158	45.1	0.068	gi 600524 gb AAA56985.1	cytochrome b5 [Musca dome	( 134)	151	43.2	0.089
gi 116057571 emb CAL53774.1	delta8 fatty acid des	( 461)	159	45.3	0.068	gi 31433081 gb AAP54641.1	Cytochrome b5, putative	( 134)	151	43.2	0.089
gi 168014138 gb ACA14460.1	oleate desaturase [Car	( 380)	158	45.1	0.068	gi 116785377 gb ABK23699.1	unknown [Picea sitchen	( 134)	151	43.2	0.089
gi 124400724 emb CAK66208.1	unnamed protein produ	( 259)	156	44.5	0.069	gi 194699934 gb ACF84051.1	unknown [Zea mays]	( 135)	151	43.2	0.089
gi 116057908 emb CAL54111.1	Cytochrome b5 (JSS) [	( 145)	153	43.7	0.069	gi 195605698 gb ACG24679.1	cytochrome b5 [Zea may	( 135)	151	43.2	0.089
gi 27261183 gb AAN87574.1	delta 12 fatty acid con	( 386)	158	45.1	0.069	gi 195627462 gb ACG35561.1	cytochrome b5 [Zea may	( 135)	151	43.2	0.089
gi 211589285 emb CAP95425.1	Pc21g05280 [Penicilli	( 469)	159	45.3	0.069	gi 190615928 gb EDV31452.1	GF15361 [Drosophila an	( 440)	157	44.9	0.09
gi 37514836 gb AAH14431.2	Cytochrome b5 type B (o	( 146)	153	43.7	0.069	gi 119415338 gb EAW25276.1	acyl-CoA dehydrogenase	( 541)	158	45.1	0.091
gi 13325120 gb AAH04373.1	Cytochrome b5 type B (o	( 146)	153	43.7	0.069	gi 159125110 gb EDP50227.1	acyl-CoA dehydrogenase	( 541)	158	45.1	0.091
gi 158256584 dbj BAF84265.1	unnamed protein produ	( 146)	153	43.7	0.069	gi 143580935 gb EDF74097.1	hypothetical protein G	( 305)	155	44.3	0.092
gi 2662291 dbj BAA23735.1	cytochrome b5 [Homo sap	( 146)	153	43.7	0.069	gi 124408857 emb CAK74210.1	unnamed protein produ	( 253)	154	44.0	0.093
gi 110623228 emb CAL24254.1	unnamed protein produ	( 387)	158	45.1	0.069	gi 150844218 gb EDN19411.1	acyl-CoA dehydrogenase	( 554)	158	45.2	0.093
gi 110623230 emb CAL24255.1	unnamed protein produ	( 387)	158	45.1	0.069	gi 162684231 gb EDQ70635.1	predicted protein [Phy	( 143)	151	43.2	0.094
gi 146391238 gb EDK39396.1	hypothetical protein P	( 122)	152	43.4	0.07	gi 53136458 emb CAG32558.1	hypothetical protein [	( 144)	151	43.2	0.094
gi 155278884 gb ABT34488.1	Sequence 121958 from p	( 123)	152	43.4	0.071	gi 157348500 emb CAO23392.1	unnamed protein produ	( 382)	156	44.6	0.094
gi 142213441 gb ECW44286.1	hypothetical protein G	( 123)	152	43.4	0.071	gi 51556906 gb AAT72296.2	microsomal omega-6-desa	( 383)	156	44.6	0.095
gi 90084591 dbj BAE91137.1	unnamed protein produc	( 150)	153	43.7	0.071	gi 76257461 gb ABA41034.1	delta12-fatty acid desa	( 383)	156	44.6	0.095
gi 119603681 gb EAW83275.1	cytochrome b5 type B (	( 150)	153	43.7	0.071	gi 124429694 emb CAK94485.1	unnamed protein produ	( 214)	153	43.8	0.095
gi 119603682 gb EAW83276.1	cytochrome b5 type B (	( 150)	153	43.7	0.071	gi 33358364 gb AAQ16653.1	delta-12 fatty acid des	( 384)	156	44.6	0.095
gi 142104369 gb ECV62134.1	hypothetical protein G	( 330)	157	44.8	0.071	gi 33358366 gb AAQ16654.1	delta-12 fatty acid des	( 384)	156	44.6	0.095
gi 156226481 gb EDO47290.1	predicted protein [Nem	( 333)	157	44.8	0.072	gi 159126666 gb EDP51782.1	nitrate reductase, put	(1026)	161	46.0	0.096
gi 139286247 gb ECE45492.1	hypothetical protein G	( 154)	153	43.7	0.072	gi 7331156 gb AAF60299.1	AF233640_1 cytochrome b5	( 149)	151	43.2	0.097
gi 137563224 gb EBU77215.1	hypothetical protein G	( 277)	156	44.5	0.072	gi 49645271 emb CAG98843.1	KLLAOF23672p [Kluyvero	( 123)	150	42.9	0.097
gi 5977400 gb AAE14810.1	Sequence 1 from patent U	( 155)	153	43.7	0.073	gi 155284665 gb ABT40269.1	Sequence 127739 from p	( 150)	151	43.2	0.097
gi 12813432 gb AAE44732.1	Sequence 1 from patent	( 155)	153	43.7	0.073	gi 140877332 gb ECO11367.1	hypothetical protein G	( 227)	153	43.8	0.099
gi 145365861 emb CAC42651.1	unnamed protein produc	( 105)	151	43.1	0.073	gi 142972052 gb EDB89098.1	hypothetical protein G	( 345)	155	44.3	0.1
gi 5748690 emb CAB53082.1	cytochrome b5 (predicte	( 129)	152	43.4	0.073	gi 138164275 gb EBY12800.1	hypothetical protein G	( 285)	154	44.1	0.1
gi 124422542 emb CAK87368.1	unnamed protein produ	( 417)	158	45.1	0.074	gi 89272063 emb CAJ82840.1	cytochrome b-5 [Xenopu	( 132)	150	42.9	0.1
gi 155280300 gb ABT35904.1	Sequence 123374 from p	( 134)	152	43.4	0.076	gi 163915979 gb AAI57168.1	Hypothetical protein L	( 132)	150	42.9	0.1
gi 167140 gb AAA32990.1	cytochrome b-5	( 134)	152	43.4	0.076	gi 118485108 gb ABK94417.1	unknown [Populus trich	( 134)	150	42.9	0.1
gi 25044825 gb AAM28288.1	cytochrome b5 [Ananas c	( 134)	152	43.4	0.076	gi 195609184 gb ACG26422.1	cytochrome b5 [Zea may	( 134)	150	42.9	0.1
gi 155280299 gb ABT35903.1	Sequence 123373 from p	( 134)	152	43.4	0.076	gi 195650059 gb ACG44497.1	cytochrome b5 [Zea may	( 134)	150	42.9	0.1

gi 195636578 gb ACG37757.1	cytochrome b5 [Zea may ( 134)	150	42.9	0.1	gi 145280641 gb ABP49577.1	oleate desaturase [Car ( 383)	154	44.1	0.13
gi 116784877 gb ABK23501.1	unknown [Picea sitchens ( 134)	150	42.9	0.1	gi 136362143 gb EBN65335.1	hypothetical protein G ( 121)	148	42.5	0.13
gi 195657733 gb ACG448334.1	cytochrome b5 [Zea may ( 134)	150	42.9	0.1	gi 145009425 gb EDJ94117.1	hypothetical protein M ( 480)	155	44.4	0.13
gi 155270908 gb ABT26512.1	Sequence 113982 from p ( 134)	150	42.9	0.1	gi 116059112 emb CAL54819.1	Medium-chain acyl-CoA (1048)	159	45.5	0.13
gi 195649129 gb ACG44032.1	cytochrome b5 [Zea may ( 134)	150	42.9	0.1	gi 143986234 gb EDIO4801.1	hypothetical protein G ( 273)	152	43.6	0.14
gi 157355224 emb CAO48600.1	unnamed protein produ ( 134)	150	42.9	0.1	gi 199431479 emb CAG86857.2	DEHA2D05720p [Debaryo ( 153)	149	42.7	0.14
gi 142611604 gb ECZ31808.1	hypothetical protein G ( 355)	155	44.3	0.1	gi 187975410 gb EDU42036.1	L-lactate dehydrogenas ( 500)	155	44.4	0.14
gi 137113171 gb EBS27626.1	hypothetical protein G ( 294)	154	44.1	0.1	gi 161162329 emb CAN93634.1	hypothetical protein ( 413)	154	44.2	0.14
gi 149391361 gb ABR25698.1	cytochrome b5 [Oryza s ( 135)	150	42.9	0.1	gi 167870179 gb EDS33562.1	conserved hypothetical ( 157)	149	42.8	0.14
gi 125573473 gb EAZ14988.1	hypothetical protein O ( 135)	150	42.9	0.1	gi 194697072 gb ACF82620.1	unknown [Zea mays] ( 135)	148	42.5	0.14
gi 510539 emb CAA56318.1	cytochrome b5 [Nicotiana ( 135)	150	42.9	0.1	gi 195621176 gb ACG32418.1	cytochrome b5 [Zea may ( 135)	148	42.5	0.14
gi 215767969 dbj BAH00198.1	unnamed protein produ ( 135)	150	42.9	0.1	gi 136753758 gb EBQ17986.1	hypothetical protein G ( 243)	151	43.3	0.14
gi 125529283 gb EAY77397.1	hypothetical protein O ( 135)	150	42.9	0.1	gi 119400878 gb EAW11302.1	cytochrome b5, putativ ( 136)	148	42.5	0.15
gi 15289978 dbj BAB63673.1	putative cytochrome b5 ( 135)	150	42.9	0.1	gi 114192897 gb EAU34597.1	hypothetical protein A ( 536)	155	44.5	0.15
gi 1133535065 dbj BAF07448.1	Os01g0971500 [Oryza s ( 135)	150	42.9	0.1	gi 210125472 gb EEA73163.1	hypothetical protein B ( 138)	148	42.5	0.15
gi 149392595 gb ABR26100.1	cytochrome b5 [Oryza s ( 135)	150	42.9	0.1	gi 124416107 emb CAK81155.1	unnamed protein produ ( 207)	150	43.1	0.15
gi 76781154 gb ABA54492.1	cytochrome b5 type 56 [ ( 136)	150	42.9	0.11	gi 116060159 emb CAL56218.1	Delta 6-fatty acid de ( 309)	152	43.6	0.15
gi 143350724 gb EDE49728.1	hypothetical protein G ( 244)	153	43.8	0.11	gi 83272395 gb ABC00771.1	delta-12 fatty acid des ( 377)	153	43.9	0.15
gi 210068794 gb EEA22885.1	heme/steroid binding p ( 297)	154	44.1	0.11	gi 84626279 gb ABC59684.1	delta-12 fatty acid ace ( 377)	153	43.9	0.15
gi 142149054 gb ECV95134.1	hypothetical protein G ( 137)	150	42.9	0.11	gi 146389168 gb EDK37326.1	hypothetical protein P ( 378)	153	43.9	0.15
gi 155298102 gb ABT53706.1	Sequence 141176 from p ( 138)	150	42.9	0.11	gi 60594769 gb AAZ29989.1	microsomal omega-6-desa ( 379)	153	43.9	0.15
gi 62484905 dbj BAD95486.1	delta5 fatty acid desa ( 446)	156	44.6	0.11	gi 21507257 gb AAM57793.1	Sequence 6 from patent ( 379)	153	43.9	0.15
gi 156207805 gb EDO29550.1	predicted protein [Nem ( 378)	155	44.4	0.11	gi 75205882 gb ABA17986.1	Sequence 6 from patent ( 379)	153	43.9	0.15
gi 2613051 gb AAB84262.1	omega-6 desaturase [Arac ( 379)	155	44.4	0.11	gi 62789094 gb AAY07977.1	Sequence 6 from patent ( 379)	153	43.9	0.15
gi 2501790 gb AAB80696.1	omega-6 fatty acid desat ( 382)	155	44.4	0.11	gi 115833234 gb ABJ40712.1	Sequence 6 from patent ( 379)	153	43.9	0.15
gi 49528253 emb CAG61910.1	unnamed protein produc ( 121)	149	42.7	0.11	gi 139750378 gb ECH20331.1	hypothetical protein G ( 314)	152	43.6	0.15
gi 136596108 gb EBP17865.1	hypothetical protein G ( 101)	148	42.4	0.11	gi 33766650 gb AAQ52853.1	Sequence 5 from patent ( 387)	153	43.9	0.15
gi 156114730 gb EDO16237.1	hypothetical protein K ( 123)	149	42.7	0.11	gi 34600651 gb AAQ78508.1	Sequence 13 from patent ( 387)	153	43.9	0.15
gi 49652236 emb CAG84528.1	DEHA2A05742p [Debaryom ( 123)	149	42.7	0.11	gi 155713301 gb ABU35457.1	Sequence 5 from patent ( 387)	153	43.9	0.15
gi 208498920 gb ACT129313.1	NADPH nitrate reductas ( 864)	159	45.5	0.11	gi 91125672 gb ABE12620.1	Sequence 33 from patent ( 387)	153	43.9	0.15
gi 30039221 gb AAP12556.1	nitrate reductase [Peni ( 864)	159	45.5	0.11	gi 904152 gb AAB00859.1	microsomal omega-6 desatu ( 387)	153	43.9	0.15
gi 134077192 emb CAK45533.1	nitrate reductase (NA ( 867)	159	45.5	0.11	gi 59956942 dbj BAD89860.1	microsomal omega-6 fat ( 387)	153	43.9	0.15
gi 141275093 gb ECQ83658.1	hypothetical protein G ( 222)	152	43.5	0.11	gi 5994482 gb AAE19895.1	Sequence 5 from patent U ( 387)	153	43.9	0.15
gi 195641908 gb ACG40422.1	cytochrome b5 [Zea may ( 185)	151	43.3	0.12	gi 155689127 gb ABU29137.1	Sequence 5 from patent ( 387)	153	43.9	0.15
gi 187979172 gb EDU45798.1	acyl-CoA dehydrogenase ( 511)	156	44.7	0.12	gi 155278641 gb ABT34245.1	Sequence 121715 from p ( 149)	148	42.5	0.16
gi 189016254 gb ACD70298.1	delta-6 fatty acid des ( 159)	150	43.0	0.12	gi 138540123 gb ECA29874.1	hypothetical protein G ( 270)	151	43.4	0.16
gi 189303970 gb ACD85900.1	nitrate reductase [Hyp ( 235)	152	43.5	0.12	gi 143250156 gb EDD89444.1	hypothetical protein G ( 273)	151	43.4	0.16
gi 99109681 gb ABF67509.1	cytochrome b5 [Haliotis ( 133)	149	42.7	0.12	gi 139505981 gb ECF53542.1	hypothetical protein G ( 86)	145	41.7	0.16
gi 118484567 gb ABK94157.1	unknown [Populus trich ( 134)	149	42.7	0.12	gi 134916704 gb EBE28096.1	hypothetical protein G ( 337)	152	43.6	0.16
gi 195655973 gb ACG47454.1	cytochrome b5 [Zea may ( 134)	149	42.7	0.12	gi 124403949 emb CAR69408.1	unnamed protein produ ( 280)	151	43.4	0.16
gi 143101975 gb EDC82888.1	hypothetical protein G ( 355)	154	44.1	0.12	gi 136137059 gb EBM15398.1	hypothetical protein G ( 159)	148	42.5	0.17
gi 11177030 dbj BAB17853.1	cytochrome b5 [Polyand ( 135)	149	42.7	0.12	gi 49527670 emb CAG61319.1	unnamed protein produc ( 194)	149	42.8	0.17
gi 215264539 emb CAS08906.1	predicted protein [Es ( 363)	154	44.1	0.12	gi 50416385 gb AAH77334.1	MGC80327 protein [Xenop ( 132)	147	42.2	0.17
gi 134064027 emb CAM40218.1	nitrate reductase, pu ( 537)	156	44.7	0.12	gi 138336124 gb EBZ03923.1	hypothetical protein G ( 74)	144	41.4	0.17
gi 119399890 gb EAW10316.1	acyl-CoA dehydrogenase ( 542)	156	44.7	0.13	gi 124423282 emb CAR88077.1	unnamed protein produ ( 358)	152	43.7	0.17
gi 57870222 gb AAH89049.1	LOC100036773 protein [X ( 140)	149	42.7	0.13	gi 199425292 emb CAG82239.2	YALI0C16797p [Yarrowi ( 530)	154	44.2	0.17
gi 160703651 gb EAT80311.2	hypothetical protein S ( 140)	149	42.7	0.13	gi 143330688 gb EDE37222.1	hypothetical protein G ( 296)	151	43.4	0.17
gi 55774572 gb AAV64871.1	cytochrome b5 [Xenopus ( 141)	149	42.7	0.13	gi 211587064 emb CAP94727.1	Pc18g05030 [Penicilli ( 361)	152	43.7	0.17
gi 77748376 gb AAI06221.1	Unknown (protein for MG ( 141)	149	42.7	0.13	gi 139049367 gb ECD05908.1	hypothetical protein G ( 93)	145	41.7	0.17
gi 197127610 gb ACH44108.1	putative cytochrome b5 ( 141)	149	42.7	0.13	gi 150851185 gb EDN26378.1	cytochrome b5 [Botryot ( 139)	147	42.3	0.17
gi 217071298 gb ACJ84009.1	unknown [Medicago trun ( 142)	149	42.7	0.13	gi 158274018 gb EDO99803.1	cytochrome b5 protein ( 139)	147	42.3	0.17
gi 217071624 gb ACJ84172.1	unknown [Medicago trun ( 142)	149	42.7	0.13	gi 14456133 emb CAC41650.1	putative nitrate reduc ( 983)	157	45.1	0.17
gi 189846878 gb ACE26376.1	Sequence 136 from pate ( 378)	154	44.1	0.13	gi 195657819 gb ACG48377.1	cytochrome b5 [Zea may ( 117)	146	42.0	0.18
gi 38564776 gb AAR23815.1	delta 12 fatty acid epo ( 378)	154	44.1	0.13	gi 31322135 gb AAO38032.1	delta12-fatty acid acet ( 377)	152	43.7	0.18
gi 189702340 gb ACE14957.1	Sequence 2 from patent ( 378)	154	44.1	0.13	gi 114190157 gb EAU31857.1	conserved hypothetical ( 999)	157	45.1	0.18
gi 193893371 gb EDV92237.1	GH24801 [Drosophila gr ( 118)	148	42.4	0.13	gi 3135020 emb CAA76157.1	delta 12 fatty acid des ( 379)	152	43.7	0.18
gi 49642276 emb CAH00238.1	KLLA0D01639p [Kluyvero ( 381)	154	44.1	0.13	gi 56759060 gb AAW27670.1	SJCHGC00480 protein [Sc ( 118)	146	42.0	0.18
gi 141194560 gb ECQ27436.1	hypothetical protein G ( 175)	150	43.0	0.13	gi 135612136 gb EBI75574.1	hypothetical protein G ( 314)	151	43.4	0.18

gi 438451 gb AAA32782.1  delta-12 desaturase ( 383) 152 43.7 0.18	gi 40737984 gb AAR89457.1  cytochrome B5 [Petunia ( 149) 146 42.0 0.22
gi 76007349 gb ABA38263.1  Sequence 6 from patent ( 383) 152 43.7 0.18	gi 10183662 emb CAC08830.1  unnamed protein produc ( 149) 146 42.0 0.22
gi 110623200 emb CAL24240.1  unnamed protein produ ( 383) 152 43.7 0.18	gi 194699154 gb ACF83661.1  unknown [Zea mays] ( 186) 147 42.3 0.22
gi 91125671 gb ABE12619.1  Sequence 32 from patent ( 383) 152 43.7 0.18	gi 119402848 gb EAW13269.1  cytochrome b5, putativ ( 105) 144 41.5 0.22
gi 56666937 gb AAW18476.1  Sequence 4 from patent ( 383) 152 43.7 0.18	gi 212003383 gb EEB09043.1  cytochrome b5 [Schizos ( 128) 145 41.8 0.22
gi 62789092 gb AAY07975.1  Sequence 2 from patent ( 383) 152 43.7 0.18	gi 89299416 gb EAR97404.1  Fatty acid desaturase f ( 413) 151 43.5 0.22
gi 14517474 gb AAK62627.1  AT3gl2120/T21B14_107 [A ( 383) 152 43.7 0.18	gi 138455028 gb EBZ79017.1  hypothetical protein G ( 280) 149 42.9 0.22
gi 75205880 gb ABA17984.1  Sequence 2 from patent ( 383) 152 43.7 0.18	gi 135549142 gb EBI35878.1  hypothetical protein G ( 344) 150 43.2 0.23
gi 17909752 gb AAE82559.1  Sequence 6 from patent ( 383) 152 43.7 0.18	gi 160705808 gb EAT76132.2  hypothetical protein S ( 619) 153 44.0 0.23
gi 34600647 gb AAQ78504.1  Sequence 9 from patent ( 383) 152 43.7 0.18	gi 154691737 gb EDN91475.1  hypothetical protein S ( 512) 152 43.7 0.23
gi 189846872 gb ACE26370.1  Sequence 125 from pate ( 383) 152 43.7 0.18	gi 136527749 gb EBO74245.1  hypothetical protein G ( 239) 148 42.6 0.23
gi 9294109 dbj BAB01960.1  omega-6 fatty acid desa ( 383) 152 43.7 0.18	gi 143299135 gb EDE19043.1  hypothetical protein G ( 198) 147 42.3 0.23
gi 17918535 gb AAE85969.1  Sequence 6 from patent ( 383) 152 43.7 0.18	gi 119404606 gb EAW14982.1  cytochrome b5-like Hem ( 163) 146 42.1 0.23
gi 189704779 gb ACE16108.1  Sequence 125 from pate ( 383) 152 43.7 0.18	gi 143089206 gb EDC73513.1  hypothetical protein G ( 297) 149 42.9 0.24
gi 68164987 gb AAY87459.1  omega-6 fatty acid desa ( 383) 152 43.7 0.18	gi 31419550 gb AAH53263.1  Cytochrome b5 type A (m ( 137) 145 41.8 0.24
gi 12322004 gb AAG51042.1 AC069473_4 omega-6 fatty ( 383) 152 43.7 0.18	gi 159156005 gb AAI54825.1  Cyb5a protein [Danio r ( 137) 145 41.8 0.24
gi 5955846 gb AAE07502.1  Sequence 41 from patent ( 383) 152 43.7 0.18	gi 134079114 emb CAR40669.1  unnamed protein produ ( 138) 145 41.8 0.24
gi 58013375 gb AAW63041.1  microsomal delta-12 ole ( 383) 152 43.7 0.18	gi 210125476 gb EEA73167.1  cytochrome b5 [Branchi ( 138) 145 41.8 0.24
gi 71057275 emb CAJ18799.1  unnamed protein produc ( 383) 152 43.7 0.18	gi 89294120 gb EAR92108.1  Cytochrome b5-like Heme ( 114) 144 41.5 0.24
gi 110623202 emb CAL24241.1  unnamed protein produ ( 383) 152 43.7 0.18	gi 135869837 gb EBK36254.1  hypothetical protein G ( 303) 149 42.9 0.24
gi 2492223 gb AAB80359.1 I66170 Sequence 41 from p ( 383) 152 43.7 0.18	gi 142975618 gb EDB91601.1  hypothetical protein G ( 251) 148 42.6 0.24
gi 22655458 gb AAM98321.1  At3gl2120/T21B14_107 [A ( 383) 152 43.7 0.18	gi 136600981 gb EBP20985.1  hypothetical protein G ( 307) 149 42.9 0.24
gi 21536781 gb AAM61113.1  omega-6 fatty acid desa ( 383) 152 43.7 0.18	gi 144578041 gb ABO96106.1  predicted protein [Ost ( 141) 145 41.8 0.24
gi 115833232 gb ABJ40710.1  Sequence 2 from patent ( 383) 152 43.7 0.18	gi 40644254 emb CAD22050.1  cytochrome b5 [Oryza s ( 143) 145 41.8 0.24
gi 21507255 gb AAM57791.1  Sequence 2 from patent ( 383) 152 43.7 0.18	gi 108878535 gb EAT42760.1  conserved hypothetical ( 462) 151 43.5 0.25
gi 150408849 gb EDN04305.1  hypothetical protein H ( 177) 148 42.6 0.18	gi 45272283 gb AAS57577.1  delta12-oleic acid desa ( 382) 150 43.2 0.25
gi 194153330 gb EDW68514.1  GJ12661 [Drosophila vi ( 120) 146 42.0 0.18	gi 113623677 dbj BAF23622.1  Os08g0386300 [Oryza s ( 119) 144 41.5 0.25
gi 28371827 gb AAO37754.1  delta-12 oleate desatur ( 387) 152 43.7 0.18	gi 40253472 dbj BAD05422.1  cytochrome b5-like [Or ( 119) 144 41.5 0.25
gi 160706885 gb EAT87086.2  hypothetical protein S ( 697) 155 44.5 0.18	gi 91125663 gb ABE12611.1  Sequence 4 from patent ( 385) 150 43.2 0.25
gi 135277729 gb EBG58802.1  hypothetical protein G ( 267) 150 43.1 0.18	gi 2578033 emb CAA65744.1  omega-6 desaturase [Gos ( 385) 150 43.2 0.25
gi 119395856 gb EAW06288.1  cytochrome b5, putativ ( 83) 144 41.4 0.18	gi 194700608 gb ACF84388.1  unknown [Zea mays] ( 216) 147 42.4 0.25
gi 149015873 gb EDL75180.1  cytochrome b-5, isofor ( 83) 144 41.4 0.18	gi 194708396 gb ACF88282.1  unknown [Zea mays] ( 216) 147 42.4 0.25
gi 142847889 gb EDB03384.1  hypothetical protein G ( 331) 151 43.4 0.19	gi 195619472 gb ACG31566.1  cytoplasm protein [Zea ( 216) 147 42.4 0.25
gi 124427005 emb CAK91785.1  unnamed protein produ ( 417) 152 43.7 0.19	gi 837345 gb AAB32285.1  peditoxin, pedin=cytochro ( 82) 142 41.0 0.25
gi 125536127 gb EAY82615.1  hypothetical protein O ( 159) 147 42.3 0.19	gi 139435639 gb ECF09823.1  hypothetical protein G ( 83) 142 41.0 0.25
gi 144104790 gb EDI89877.1  hypothetical protein G ( 353) 151 43.4 0.2	gi 211584179 emb CAP92210.1  nitrate reductase (NA ( 864) 154 44.3 0.25
gi 119400947 gb EAW11371.1  heme/steroid binding p ( 362) 151 43.4 0.2	gi 1431858 gb AAB03900.1  nitrate reductase ( 864) 154 44.3 0.25
gi 68127721 emb CAJ05968.1  nitrate reductase, put ( 536) 153 44.0 0.2	gi 140353714 gb ECL19515.1  hypothetical protein G ( 152) 145 41.8 0.26
gi 194374511 dbj BAG57151.1  unnamed protein produ ( 204) 148 42.6 0.2	gi 135411199 gb EBH45692.1  hypothetical protein G ( 337) 149 42.9 0.26
gi 170939457 emb CAP64685.1  unnamed protein produ ( 544) 153 44.0 0.2	gi 31322226 gb AAO63560.1  nitrate reductase [Vert ( 893) 154 44.4 0.26
gi 156531882 gb ABU76708.1  hypothetical protein E ( 369) 151 43.4 0.2	gi 155102616 gb ABT03239.1  Sequence 48 from paten ( 412) 150 43.2 0.26
gi 134058611 emb CAK38595.1  unnamed protein produ ( 545) 153 44.0 0.2	gi 136510696 gb EBO63349.1  hypothetical protein G ( 281) 148 42.7 0.26
gi 137947269 gb EBW91038.1  hypothetical protein G ( 78) 143 41.2 0.2	gi 134080434 emb CAK41183.1  unnamed protein produ ( 508) 151 43.5 0.27
gi 90300461 gb EAS30092.1  hypothetical protein CI ( 547) 153 44.0 0.2	gi 139123905 gb ECS57816.1  hypothetical protein G ( 130) 144 41.5 0.27
gi 189704778 gb ACE16103.1  Sequence 38 from paten ( 377) 151 43.4 0.21	gi 28950126 emb CAD70984.1  related to ACYL-COA DE ( 519) 151 43.5 0.27
gi 189846871 gb ACE26369.1  Sequence 42 from paten ( 377) 151 43.4 0.21	gi 708341224 gb EAN79626.1  cytochrome b5, putative ( 133) 144 41.6 0.27
gi 189704772 gb ACE16101.1  Sequence 36 from paten ( 377) 151 43.4 0.21	gi 139794221 gb ECH50961.1  hypothetical protein G ( 164) 145 41.8 0.27
gi 189704778 gb ACE16107.1  Sequence 42 from paten ( 377) 151 43.4 0.21	gi 119408175 gb EAW18124.1  heme/steroid binding p ( 358) 149 43.0 0.27
gi 189846865 gb ACE26363.1  Sequence 36 from paten ( 377) 151 43.4 0.21	gi 143665744 gb EDG15555.1  hypothetical protein G ( 296) 148 42.7 0.28
gi 189846867 gb ACE26365.1  Sequence 38 from paten ( 377) 151 43.4 0.21	gi 1483145 dbj BAA10888.1  Cytochrome b5 [Ascaris ( 112) 143 41.3 0.28
gi 124403690 emb CAK69152.1  unnamed protein produ ( 258) 149 42.9 0.21	gi 167275722 gb ABZ28586.1  Sequence 2524 from pat ( 201) 146 42.1 0.28
gi 137164908 gb EBS56599.1  hypothetical protein G ( 213) 148 42.6 0.21	gi 88177673 gb EAQ85141.1  cytochrome b5, putative ( 137) 144 41.6 0.28
gi 143332594 gb EDE38331.1  hypothetical protein G ( 259) 149 42.9 0.21	gi 186467605 gb ACC83406.1  fatty acid desaturase ( 366) 149 43.0 0.28
gi 159126631 gb EDP51747.1  cytochrome b5 reductas ( 471) 152 43.7 0.21	gi 25989476 gb AAL93620.1  fatty acid desaturase 2 ( 383) 149 43.0 0.29
gi 157335617 emb CAO61447.1  unnamed protein produ ( 147) 146 42.0 0.21	gi 55509203 gb AAV52834.1  delta-12 fatty acid des ( 383) 149 43.0 0.29
gi 147838440 emb CAN63256.1  hypothetical protein ( 147) 146 42.0 0.21	gi 181392 gb AAA52165.1  cytochrome b-5 ( 98) 142 41.0 0.29
gi 85700983 gb ABC74800.1  cytochrome B5 [Petunia ( 149) 146 42.0 0.22	gi 119586949 gb EAW66545.1  cytochrome b5 type A ( ( 98) 142 41.0 0.29
gi 4204575 gb AAD10774.1  cytochrome b5 DIF-F [Pet ( 149) 146 42.0 0.22	gi 135042934 gb EBF12759.1  hypothetical protein G ( 176) 145 41.9 0.29

gi 1212781 emb CAA62578.1	oleate desaturase [Bras	(384)	149	43.0	0.29	gi 71979795 dbj BAE17053.1	nitrate reductase [Phy	(892)	152	43.9	0.36
gi 34600648 gb AAQ78505.1	Sequence 10 from patent	(384)	149	43.0	0.29	gi 162683005 gb EDQ69419.1	predicted protein [Phy	(892)	152	43.9	0.36
gi 930010 emb CAA40090.1	nitrate reductase (NADH)	(318)	148	42.7	0.29	gi 73486691 dbj BAE19755.1	nitrate reductase [Phy	(892)	152	43.9	0.36
gi 119407840 gb EAW17789.1	cytochrome b5 reductas	(470)	150	43.3	0.29	gi 68532865 dbj BAE06057.1	pyridine nucleotide-de	(892)	152	43.9	0.36
gi 193918587 gb EDW17454.1	GI12677 [Drosophila m	(212)	143	41.3	0.29	gi 541566 gb AAA50579.1	nitrate reductase	(893)	152	43.9	0.36
gi 38175775 dbj BAC55856.2	flavoheomoprotein b5/b5	(121)	146	42.1	0.29	gi 217072516 gb ACJ84618.1	unknown [Medicago trun	(411)	148	42.8	0.36
gi 113610774 dbj BAF21152.1	Os07g0232200 [Oryza s	(218)	146	42.1	0.29	gi 211590769 emb CAP96968.1	Pc21g20710 [Penicilli	(513)	149	43.1	0.37
gi 195635929 gb ACG37433.1	omega-6 fatty acid des	(394)	149	43.0	0.3	gi 62088814 dbj BAD92854.1	cytochrome b-5 isoform	(132)	142	41.1	0.37
gi 119397119 gb EAW038550.1	nitrate reductase NiaD	(868)	153	44.1	0.3	gi 144581901 gb ABO99956.1	predicted protein [Ost	(74)	139	40.2	0.37
gi 154694855 gb EDN94593.1	hypothetical protein S	(124)	143	41.3	0.3	gi 23329307 gb AAN26141.1	Sequence 23 from patent	(133)	142	41.1	0.37
gi 135256356 gb EBG46227.1	hypothetical protein G	(271)	147	42.4	0.3	gi 62774618 gb AA02011.1	Sequence 22 from patent	(133)	142	41.1	0.37
gi 138277015 gb EBY75438.1	hypothetical protein G	(271)	147	42.4	0.3	gi 181227 gb AAA35729.1	cytochrome b5	(134)	142	41.1	0.37
gi 146150662 gb ABP97095.1	nitrate reductase [Chl	(877)	153	44.1	0.3	gi 15929506 gb AAH15182.1	Cytochrome b5 type A (m	(134)	142	41.1	0.37
gi 197701160 gb ABJ91208.4	nitrate reductase [Chl	(877)	153	44.1	0.3	gi 12822034 gb AAE48475.1	Sequence 1 from patent	(134)	142	41.1	0.37
gi 136567798 gb EBQ099802.1	hypothetical protein G	(334)	148	42.7	0.3	gi 48146097 emb CAG33271.1	CYB5 [Homo sapiens]	(134)	142	41.1	0.37
gi 144189797 gb EDJ52342.1	hypothetical protein G	(71)	140	40.5	0.31	gi 2642486 gb AAC48779.1	cytochrome b5 [Sus scrof	(134)	142	41.1	0.37
gi 145095505 gb EBF46310.1	hypothetical protein G	(71)	140	40.5	0.31	gi 119586948 gb EAW66544.1	cytochrome b5 type A (	(134)	142	41.1	0.37
gi 13530972 emb CAA03836.1	DELTA-12 DESATURASE [Co	(338)	148	42.7	0.31	gi 139669063 gb ECG64984.1	hypothetical protein G	(91)	140	40.5	0.38
gi 212508562 gb EEB12210.1	Cytochrome b5, putativ	(156)	144	41.6	0.31	gi 139179798 gb ECD95369.1	hypothetical protein G	(294)	146	42.2	0.38
gi 126633792 emb CAM55852.1	unnamed protein produ	(503)	150	43.3	0.31	gi 162471890 gb ABX99725.1	Sequence 1 from patent	(135)	142	41.1	0.38
gi 116001277 emb CAL49890.1	unnamed protein produ	(503)	150	43.3	0.31	gi 210074133 gb EEA28220.1	cytochrome b5, putativ	(135)	142	41.1	0.38
gi 60220818 emb CAI58908.1	unnamed protein produc	(503)	150	43.3	0.31	gi 194176547 gb EDW90158.1	GE13120 [Drosophila ya	(137)	142	41.1	0.38
gi 76059318 emb CAJ30853.1	unnamed protein produc	(503)	150	43.3	0.31	gi 138071748 gb EBX58336.1	hypothetical protein G	(113)	141	40.8	0.38
gi 83766286 dbj BAE56429.1	unnamed protein produc	(419)	149	43.0	0.31	gi 91685106 gb ABE41408.1	cytochrome b5 [Rhodopse	(115)	141	40.8	0.39
gi 145011783 gb EDJ96439.1	conserved hypothetical	(513)	150	43.3	0.31	gi 703083 gb AAA63169.1	cytochrome b5	(142)	142	41.1	0.39
gi 23505081 emb CAD51863.1	heme binding protein,	(162)	144	41.6	0.32	gi 12813433 gb AAE44733.1	Sequence 3 from patent	(142)	142	41.1	0.39
gi 136436696 gb EB015456.1	hypothetical protein G	(242)	146	42.2	0.32	gi 5977401 gb AAE14811.1	Sequence 3 from patent U	(142)	142	41.1	0.39
gi 159128931 gb EDP54045.1	heme/steroid binding p	(358)	148	42.7	0.32	gi 149053047 gb EDM04864.1	similar to novel prote	(97)	140	40.5	0.4
gi 190657614 gb EDV54827.1	GG21732 [Drosophila er	(137)	143	41.3	0.33	gi 195621540 gb ACG32600.1	cytochrome b5 [Zea may	(118)	141	40.8	0.4
gi 26107962 gb AAN80162.1	AE016760_21 Hypothetical	(363)	148	42.7	0.33	gi 197111724 gb ACH43026.1	omega-6 fatty acid des	(387)	147	42.5	0.4
gi 54645384 gb EAL34124.1	GA19919 [Drosophila pse	(138)	143	41.3	0.33	gi 59956944 dbj BAD89861.1	microsomal omega-6 fat	(387)	147	42.5	0.4
gi 194117726 gb EDW39769.1	GL15857 [Drosophila pe	(138)	143	41.3	0.33	gi 21507259 gb AAM57794.1	Sequence 8 from patent	(387)	147	42.5	0.4
gi 140367568 gb ECL28905.1	hypothetical protein G	(169)	144	41.6	0.33	gi 194688628 gb ACF78398.1	unknown [Zea mays]	(387)	147	42.5	0.4
gi 162471892 gb ABX99727.1	Sequence 5 from patent	(115)	142	41.1	0.33	gi 62789095 gb AA07978.1	Sequence 8 from patent	(387)	147	42.5	0.4
gi 160814783 emb CAP40236.1	unnamed protein produ	(550)	150	43.3	0.33	gi 115833235 gb ABJ40713.1	Sequence 8 from patent	(387)	147	42.5	0.4
gi 60173017 gb AA14506.1	soluble cytochrome b5	(550)	150	43.3	0.33	gi 75205883 gb ABA17987.1	Sequence 8 from patent	(387)	147	42.5	0.4
gi 115878494 gb ABJ45510.1	Sequence 6249 from pat	(116)	142	41.1	0.33	gi 70799836 gb AAZ10014.1	cytochrome b-domain pro	(218)	144	41.7	0.41
gi 40043342 emb CAF00447.1	unnamed protein produc	(116)	142	41.1	0.33	gi 70801860 gb AAZ11766.1	nitrate reductase, puta	(394)	147	42.5	0.41
gi 77452622 gb ABA84317.1	Sequence 6249 from pate	(116)	142	41.1	0.33	gi 62360424 gb AA080838.1	nitrate reductase, puta	(394)	147	42.5	0.41
gi 194346322 gb ACF49507.1	omega-6 desaturase [Li	(382)	148	42.7	0.34	gi 134380916 gb EBB02366.1	hypothetical protein G	(221)	144	41.7	0.41
gi 194702722 gb ACF85445.1	unknown [Zea mays]	(382)	148	42.7	0.34	gi 113648928 dbj BAF29440.1	Os12g0223300 [Oryza s	(150)	142	41.1	0.41
gi 4530970 emb CAA03835.1	DELTA-12 DESATURASE [Co	(382)	148	42.7	0.34	gi 215765640 dbj BAG87337.1	unnamed protein produ	(150)	142	41.1	0.41
gi 119655554 gb ABL86147.1	delta-12 oleic acid de	(383)	148	42.7	0.34	gi 77553981 gb ABA96777.1	Cytochrome b5-like Heme	(150)	142	41.1	0.41
gi 1372997 gb AAC14455.1	cytochrome b-5 [Bos tau	(98)	141	40.8	0.34	gi 77553982 gb ABA96778.1	Cytochrome b5-like Heme	(150)	142	41.1	0.41
gi 471150 dbj BAA01712.1	soluble cytochrome b5 [O	(98)	141	40.8	0.34	gi 159131406 gb EDP56519.1	hypothetical protein O	(150)	142	41.1	0.41
gi 14536614 emb CAC42665.1	unnamed protein produc	(469)	149	43.0	0.34	gi 119412643 gb EAW22584.1	nitrate reductase NiaD	(869)	151	43.7	0.41
gi 162667805 gb EDQ54426.1	predicted protein [Phy	(469)	149	43.0	0.34	gi 42820686 emb CAF31999.1	nitrate reductase, put	(869)	151	43.7	0.41
gi 197111722 gb ACH43025.1	omega-6 fatty acid des	(387)	148	42.8	0.34	gi 159131406 gb EDP56519.1	nitrate reductase NiaD	(869)	151	43.7	0.41
gi 155295235 gb ABT50839.1	Sequence 138309 from p	(387)	148	42.8	0.34	gi 162670060 gb EDQ56636.1	predicted protein [Phy	(124)	141	40.8	0.41
gi 150415386 gb EDN10739.1	hypothetical protein H	(1049)	153	44.2	0.35	gi 144578118 gb ABO96183.1	predicted protein [Ost	(485)	148	42.8	0.41
gi 19171683 gb AAL85636.1	AF336236_1 nitrate reduc	(869)	152	43.9	0.35	gi 111069428 gb EAT90548.1	hypothetical protein S	(1062)	152	43.9	0.41
gi 137453581 gb EBU18923.1	hypothetical protein G	(223)	145	41.9	0.35	gi 135719112 gb EBJ41763.1	hypothetical protein G	(272)	145	42.0	0.41
gi 168062 gb AAA33314.1	nitrate reductase	(873)	152	43.9	0.35	gi 139933428 gb ECI46694.1	hypothetical protein G	(272)	145	42.0	0.41
gi 164638088 gb EDR02368.1	nitrate reductase [Lac	(880)	152	43.9	0.36	gi 155325093 gb ABT80697.1	Sequence 168167 from p	(224)	144	41.7	0.41
gi 134956202 gb EBE54415.1	hypothetical protein G	(333)	147	42.5	0.36	gi 44982549 gb AAS51835.1	ADL085Cp [Ashbya gossyp	(273)	145	42.0	0.42
gi 108868763 gb EAT32988.1	conserved hypothetical	(154)	143	41.4	0.36	gi 90655562 gb ABD96399.1	fatty acid desaturase [	(185)	143	41.4	0.42
gi 108875378 gb EAT39603.1	conserved hypothetical	(154)	143	41.4	0.36	gi 145016037 gb EDK00527.1	hypothetical protein M	(1586)	154	44.5	0.42
gi 190589801 gb EDV29823.1	expressed hypothetical	(127)	142	41.1	0.36	gi 134922019 gb EBE31653.1	hypothetical protein G	(338)	146	42.3	0.42

gi 143513831 gb EDF39707.1	hypothetical protein G ( 344)	146	42.3	0.43	gi 152022930 gb ABS20700.1	fatty acid desaturase ( 360)	145	42.0	0.52
gi 210065986 gb EEA20079.1	acyl-CoA dehydrogenase ( 512)	148	42.8	0.43	gi 160705089 gb EAT77467.2	hypothetical protein S (1713)	153	44.3	0.52
gi 134055198 emb CAK43785.1	unnamed protein produ ( 350)	146	42.3	0.43	gi 145016063 gb EDK00553.1	hypothetical protein M ( 139)	140	40.6	0.53
gi 50844673 gb AAT84458.1	cytochrome b5 isoform C ( 133)	141	40.9	0.44	gi 162471893 gb ABX99728.1	Sequence 7 from patent ( 115)	139	40.4	0.53
gi 135224456 gb EBG27440.1	hypothetical protein G ( 353)	146	42.3	0.44	gi 52138991 gb AAH82722.1	Hypothetical LOC496418 ( 141)	140	40.6	0.54
gi 5977402 gb AAE14812.1	Sequence 4 from patent U ( 134)	141	40.9	0.44	gi 167278288 gb ABZ31152.1	Sequence 5090 from pat ( 141)	140	40.6	0.54
gi 146230092 gb ABQ12619.1	cytochrome b5 [Capra h ( 134)	141	40.9	0.44	gi 13384553 gb AAK21480.1	Hypothetical protein W0 ( 141)	140	40.6	0.54
gi 79160196 gb AAI08114.1	CYB5 protein [Bos tauru ( 134)	141	40.9	0.44	gi 136222416 gb EBM70431.1	hypothetical protein G ( 141)	140	40.6	0.54
gi 164785 gb AAB03878.1	cytochrome b-5 ( 134)	141	40.9	0.44	gi 155264893 gb ABT20497.1	Sequence 107967 from p ( 118)	139	40.4	0.55
gi 12813434 gb AAE44734.1	Sequence 4 from patent ( 134)	141	40.9	0.44	gi 212559737 gb ACJ32792.1	Fatty acid desaturase ( 380)	145	42.1	0.55
gi 298 emb CAA31949.1	unnamed protein product [Bo ( 134)	141	40.9	0.44	gi 139259149 gb ECE38644.1	hypothetical protein G ( 258)	143	41.5	0.55
gi 211707 gb AAA48740.1	cytochrome b5 ( 138)	141	40.9	0.45	gi 146141441 gb ABQ301458.1	oleate 12-hydroxylase ( 383)	145	42.1	0.55
gi 211693 gb AAA48733.1	cytochrome b5 ( 138)	141	40.9	0.45	gi 117957296 gb ABK59093.1	oleate desaturase [Ric ( 383)	145	42.1	0.55
gi 126633152 emb CAM55541.1	unnamed protein produ ( 446)	147	42.6	0.45	gi 27261181 gb AAN87573.1	delta 12 oleic acid des ( 383)	145	42.1	0.55
gi 138861632 gb ECC19277.1	hypothetical protein G ( 208)	143	41.4	0.46	gi 110623210 emb CAL24245.1	unnamed protein produ ( 383)	145	42.1	0.55
gi 89271352 emb CAJ83457.1	cyb5-m [Xenopus tropic ( 141)	141	40.9	0.46	gi 110623208 emb CAL24244.1	unnamed protein produ ( 383)	145	42.1	0.55
gi 140512248 gb ECM07288.1	hypothetical protein G ( 253)	144	41.7	0.46	gi 158307010 gb ABW28627.1	beta-carotene hydroxyl ( 316)	144	41.8	0.55
gi 135114892 gb EBF58711.1	hypothetical protein G ( 253)	144	41.7	0.46	gi 119402466 gb EAW19533.1	cytochrome b5 reductas ( 472)	146	42.3	0.56
gi 51968362 dbj BAD42873.1	unknown protein [Arabi ( 211)	143	41.4	0.46	gi 148677409 gb EDL09356.1	cytochrome b-5, isofor ( 122)	139	40.4	0.56
gi 34146794 gb AAQ62405.1	At5g09680 [Arabidopsis ( 211)	143	41.4	0.46	gi 18376390 emb CAD21279.1	probable cytochrome b5 ( 83)	137	39.8	0.56
gi 51969432 dbj BAD43408.1	unknown protein [Arabi ( 211)	143	41.4	0.46	gi 31322143 gb AAO38036.1	delta12-fatty acid acet ( 326)	144	41.8	0.56
gi 7671421 emb CAB89362.1	putative protein [Arabi ( 211)	143	41.4	0.46	gi 161611934 gb AAI55726.1	Zgc:112008 protein [Da ( 69)	136	39.5	0.57
gi 147776501 emb CAN71892.1	hypothetical protein ( 382)	146	42.3	0.47	gi 139014560 gb ECC81442.1	hypothetical protein G ( 270)	143	41.5	0.57
gi 33766658 gb AAQ52861.1	Sequence 15 from patent ( 383)	146	42.3	0.47	gi 155297801 gb ABT53405.1	Sequence 140875 from p ( 84)	137	39.8	0.57
gi 155689135 gb ABU29145.1	Sequence 15 from paten ( 383)	146	42.3	0.47	gi 156105864 gb ABU49297.1	cytochrome b5 domain-c ( 152)	140	40.7	0.57
gi 3417601 gb AAC31698.1	delta-12 fatty acid desa ( 383)	146	42.3	0.47	gi 156105858 gb ABU49294.1	cytochrome b5 domain-c ( 152)	140	40.7	0.57
gi 42541363 gb AAS19533.1	omega-6 fatty acid desa ( 383)	146	42.3	0.47	gi 156105860 gb ABU49295.1	cytochrome b5 domain-c ( 152)	140	40.7	0.57
gi 34600649 gb AAQ78506.1	Sequence 11 from patent ( 383)	146	42.3	0.47	gi 156105862 gb ABU49296.1	cytochrome b5 domain-c ( 152)	140	40.7	0.57
gi 904154 gb AAB00860.1	microsomal omega-6 desatu ( 383)	146	42.3	0.47	gi 156105856 gb ABU49293.1	cytochrome b5 domain-c ( 152)	140	40.7	0.57
gi 189846874 gb ACE26372.1	Sequence 127 from pate ( 383)	146	42.3	0.47	gi 134365592 gb EBA92006.1	hypothetical protein G ( 273)	143	41.5	0.57
gi 189704781 gb ACE16110.1	Sequence 127 from pate ( 383)	146	42.3	0.47	gi 135391117 gb EBH32165.1	hypothetical protein G ( 85)	137	39.8	0.57
gi 91125670 gb ABE12618.1	Sequence 31 from patent ( 383)	146	42.3	0.47	gi 143298767 gb EDE18862.1	hypothetical protein G ( 85)	137	39.8	0.57
gi 110623206 emb CAL24243.1	unnamed protein produ ( 387)	146	42.3	0.47	gi 78168019 gb ABB25116.1	fatty acid desaturase [ ( 333)	144	41.8	0.57
gi 923808791 dbj BAE93382.1	delta-12 fatty acid de ( 387)	146	42.3	0.47	gi 136112719 gb EBL99839.1	hypothetical protein G ( 333)	144	41.8	0.57
gi 29536061 emb CAD87608.1	unnamed protein produc ( 387)	146	42.3	0.47	gi 9758996 dbj BAB09523.1	unnamed protein product ( 275)	143	41.5	0.58
gi 94982471 gb ABF50053.1	FAD2 [Zea mays] ( 387)	146	42.3	0.47	gi 62358441 gb AAJ78904.1	fatty acid desaturase, ( 408)	145	42.1	0.58
gi 28564441 emb CAD24671.1	delta 12-acyl-lipid-de ( 387)	146	42.3	0.47	gi 34551088 gb AAQ74969.1	oleate desaturase [Tryp ( 408)	145	42.1	0.58
gi 110623204 emb CAL24242.1	unnamed protein produ ( 387)	146	42.3	0.47	gi 33348439 gb AAQ15765.1	fatty acid desaturase, ( 408)	145	42.1	0.58
gi 139863303 gb ECH99135.1	hypothetical protein G ( 216)	143	41.4	0.47	gi 115878493 gb ABJ45509.1	Sequence 6248 from pat ( 128)	139	40.4	0.58
gi 156113331 gb ED014908.1	hypothetical protein K ( 217)	143	41.4	0.47	gi 77452621 gb ABA84316.1	Sequence 6248 from pate ( 128)	139	40.4	0.58
gi 62774617 gb AAY02010.1	Sequence 21 from patent ( 179)	142	41.2	0.48	gi 40043340 emb CAF00446.1	unnamed protein produc ( 128)	139	40.4	0.58
gi 23329306 gb AAN26140.1	Sequence 22 from patent ( 179)	142	41.2	0.48	gi 143305952 gb EDE22864.1	hypothetical protein G ( 88)	137	39.8	0.59
gi 170941385 emb CAP67035.1	unnamed protein produ (1541)	153	44.3	0.48	gi 136345216 gb EBN53791.1	hypothetical protein G ( 193)	141	41.0	0.59
gi 119408444 gb EAW18393.1	cytochrome b5, putativ ( 84)	138	40.1	0.48	gi 136676011 gb EBP67037.1	hypothetical protein G ( 73)	136	39.6	0.59
gi 114190581 gb EAU32281.1	conserved hypothetical ( 84)	138	40.1	0.48	gi 114187625 gb EAU29325.1	hypothetical protein A ( 512)	146	42.4	0.59
gi 211583576 emb CAP91591.1	Pcl3g05220 [Penicilli ( 84)	138	40.1	0.48	gi 159124543 gb EDP49661.1	acyl-CoA dehydrogenase ( 512)	146	42.4	0.59
gi 1113863 gb AAC49460.1	nitrate reductase ( 877)	150	43.4	0.49	gi 119406364 gb EAW16315.1	acyl-CoA dehydrogenase ( 512)	146	42.4	0.59
gi 1113861 gb AAC49459.1	nitrate reductase ( 877)	150	43.4	0.49	gi 83773777 dbj BAE63902.1	unnamed protein produc ( 513)	146	42.4	0.59
gi 139082605 gb ECD29132.1	hypothetical protein G ( 273)	144	41.7	0.49	gi 135134683 gb EBF71466.1	hypothetical protein G ( 194)	141	41.0	0.6
gi 125583832 gb EAZ24763.1	hypothetical protein O ( 890)	150	43.4	0.49	gi 193810810 emb CAQ42708.1	heme/steroid binding ( 292)	143	41.5	0.61
gi 144160439 gb ADJ30569.1	hypothetical protein G ( 413)	146	42.3	0.5	gi 143300860 gb EDE19878.1	hypothetical protein G ( 169)	140	40.7	0.62
gi 124392166 emb CAK57700.1	unnamed protein produ ( 342)	145	42.0	0.5	gi 28371823 gb AAO37752.1	delta-12 oleate desatur ( 369)	144	41.8	0.62
gi 1197523 gb AAC02633.1	nitrate reductase [Botry ( 907)	150	43.4	0.5	gi 90302444 gb EAS32075.1	hypothetical protein CI ( 372)	144	41.8	0.63
gi 134532838 gb EBB90647.1	hypothetical protein G ( 282)	144	41.7	0.5	gi 116055625 emb CAL58293.1	P0434E03.7 gene produ ( 116)	138	40.1	0.63
gi 5478307 dbj BAA82441.1	cytochrome b5 [Mortiere ( 130)	140	40.6	0.5	gi 135130262 gb EBF68611.1	hypothetical protein G ( 211)	141	41.0	0.64
gi 5478287 dbj BAA82440.1	cytochrome b5 [Mortiere ( 130)	140	40.6	0.5	gi 144163625 gb EDJ32950.1	hypothetical protein G ( 211)	141	41.0	0.64
gi 170947135 emb CAP73940.1	unnamed protein produ ( 520)	147	42.6	0.51	gi 135084318 gb EBF39138.1	hypothetical protein G ( 211)	141	41.0	0.64
gi 190659446 gb EDV56659.1	GG20107 [Drosophila er ( 436)	146	42.3	0.52	gi 90655389 gb ABD96230.1	possible fatty acid des ( 379)	144	41.8	0.64



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190      200      210      220      230      240
del_6    240      250      260      270      280      290
DGVSRLFVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLWFP
gi|151   DGVSRLFVQYQHWTFFYPMCVARLNMLAQSFIMLFSSREVAQRVQGFGLAVFWVW
250      260      270      280      290      300

300      310      320      330      340      350
del_6    LSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVGNDWFKKQTAGTLNISC
gi|151   LSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVGNDWFKKQTAGTLNISC
310      320      330      340      350      360

360      370      380      390      400      410
del_6    PAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANVLTLE
gi|151   PAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANVLTLM
370      380      390      400      410      420

420      430      440
del_6    TLRNTAIEARDLSNPIPKNMVWEAVKNVG
gi|151   TLRNTAIEARDLSNPIPKNMVWEAVQTLG
430      440

>>gi|118627908|emb|CAL85354.1| unnamed protein product [ (453 aa)
initn: 2865 init1: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
188
Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
overlap (3-446:10-453)

10      20      30      40      50
del_6    MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
gi|118   MANKSPPNPKTYGITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
10      20      30      40      50      60

60      70      80      90      100     110
del_6    VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLKLLDSFHKMGFRARGHTAYA
gi|118   VTDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSSDYRKLKLLDNFHKHGLFRARGHTAYA
70      80      90      100     110     120

120     130     140     150     160     170
del_6    TFVIMILMLVSSVTGVLCSENPWWHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
gi|118   TFVFMIAMFLMSVTGVLCSDSAUVHLASGGAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
130     140     150     160     170     180

180     190     200     210     220     230
del_6    AQILSNCLQGIGISIGWKKWNHNAHIIACNSLEYDPLQYIPLLVVSPKFFNSLTSRFYDK
gi|118   AQILSNCLQGIGISIGWKKWNHNAHIIACNSLDYDPLQYIPLLVVSPKFFNSLTSRFYDK
190     200     210     220     230     240

240     250     260     270     280     290
del_6    KLNFDGVSRLFVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW

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gi|118   KLNFDGVSRLFVQYQHWTFFYPMCVARLNMLAQSFITLFSRREVCVHRAQEVFGLAVFWW
250     260     270     280     290     300

300     310     320     330     340     350
del_6    FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVGNDWFKKQTAGTL
gi|118   FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVGNDWFKKQTAGTL
310     320     330     340     350     360

360     370     380     390     400     410
del_6    NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANV
gi|118   NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANV
370     380     390     400     410     420

420     430     440
del_6    LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
gi|118   FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
430     440     450

>>gi|126633766|emb|CAM55839.1| unnamed protein product [ (453 aa)
initn: 2865 init1: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
188
Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
overlap (3-446:10-453)

10      20      30      40      50
del_6    MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
gi|126   MANKSPPNPKTYGITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
10      20      30      40      50      60

60      70      80      90      100     110
del_6    VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLKLLDSFHKMGFRARGHTAYA
gi|126   VTDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSSDYRKLKLLDNFHKHGLFRARGHTAYA
70      80      90      100     110     120

120     130     140     150     160     170
del_6    TFVIMILMLVSSVTGVLCSENPWWHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
gi|126   TFVFMIAMFLMSVTGVLCSDSAUVHLASGGAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
130     140     150     160     170     180

180     190     200     210     220     230
del_6    AQILSNCLQGIGISIGWKKWNHNAHIIACNSLEYDPLQYIPLLVVSPKFFNSLTSRFYDK
gi|126   AQILSNCLQGIGISIGWKKWNHNAHIIACNSLDYDPLQYIPLLVVSPKFFNSLTSRFYDK
190     200     210     220     230     240

240     250     260     270     280     290
del_6    KLNFDGVSRLFVQYQHWSFYPMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
gi|126   KLNFDGVSRLFVQYQHWTFFYPMCVARLNMLAQSFITLFSRREVCVHRAQEVFGLAVFWW
250     260     270     280     290     300

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      300      310      320      330      340      350
del_6  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPPVGNDFWFKKQTAGTL
      .....
gi |126  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPPVGNDFWFKKQTAGTL
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTYNIASF TKANV
      .....
gi |126  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTYNIASF TKANV
      370      380      390      400      410      420

      420      430      440
del_6  LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi |126  FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
      430      440      450

>>gi|39750753|emb|CAE84827.1| unnamed protein product [P (453 aa)
  initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
  188
  Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
  overlap (3-446:10-453)

      10      20      30      40      50
del_6  MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: .....
gi |397  MANKSPPNPKTGYITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10      20      30      40      50      60

      60      70      80      90      100      110
del_6  VTDAFLAYHPPSTARLLPPLSTNLLLEKHSVSETSSDYRKLKLDSPHKMGMFRRAGHTAYA
      .....
gi |397  VTDAFLAYHPPSTARLLPPLSTNLLLQNHVSPTSSDYRKLKLDNFHKHGLFRAGHTAYA
      70      80      90      100      110      120

      120      130      140      150      160      170
del_6  TFVIMILMLVSSVTGVLCSSENFWVHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
      .....
gi |397  TFVFMIAMFLMSVTGVLCSDSAWVHLASGGAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
      130      140      150      160      170      180

      180      190      200      210      220      230
del_6  AQILSSNCLQGIGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSVPKFFNSLTSRFYDK
      .....
gi |397  AQILSTNCLQGIGISIGWKKWNHNAHHIACNSLDYDPLQYIPLLVSVPKFFNSLTSRFYDK
      190      200      210      220      230      240

      240      250      260      270      280      290
del_6  KLNFDGVSRLFVQYQHSFYPMCVARLNMLAQSFILLFSRREVANRVQEIILGLAVFWLW
      .....
gi |397  KLNFDGVSRLFVQYQHSFYPMCVARLNMLAQSFITLFSREVCHRAQEVFGLAVFWVW
      250      260      270      280      290      300

      300      310      320      330      340      350
del_6  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPPVGNDFWFKKQTAGTL
      .....
gi |397  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPPVGNDFWFKKQTAGTL

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      310      320      330      340      350      360
      360      370      380      390      400      410
del_6  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTYNIASF TKANV
      .....
gi |397  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTYNIASF TKANV
      370      380      390      400      410      420

      420      430      440
del_6  LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi |397  FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
      430      440      450

>>gi|60220786|emb|CAI58892.1| unnamed protein product [P (453 aa)
  initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
  188
  Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
  overlap (3-446:10-453)

      10      20      30      40      50
del_6  MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: .....
gi |602  MANKSPPNPKTGYITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10      20      30      40      50      60

      60      70      80      90      100      110
del_6  VTDAFLAYHPPSTARLLPPLSTNLLLEKHSVSETSSDYRKLKLDSPHKMGMFRRAGHTAYA
      .....
gi |602  VTDAFLAYHPPSTARLLPPLSTNLLLQNHVSPTSSDYRKLKLDNFHKHGLFRAGHTAYA
      70      80      90      100      110      120

      120      130      140      150      160      170
del_6  TFVIMILMLVSSVTGVLCSSENFWVHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
      .....
gi |602  TFVFMIAMFLMSVTGVLCSDSAWVHLASGGAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
      130      140      150      160      170      180

      180      190      200      210      220      230
del_6  AQILSSNCLQGIGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSVPKFFNSLTSRFYDK
      .....
gi |602  AQILSTNCLQGIGISIGWKKWNHNAHHIACNSLDYDPLQYIPLLVSVPKFFNSLTSRFYDK
      190      200      210      220      230      240

      240      250      260      270      280      290
del_6  KLNFDGVSRLFVQYQHSFYPMCVARLNMLAQSFILLFSRREVANRVQEIILGLAVFWLW
      .....
gi |602  KLNFDGVSRLFVQYQHSFYPMCVARLNMLAQSFITLFSREVCHRAQEVFGLAVFWVW
      250      260      270      280      290      300

      300      310      320      330      340      350
del_6  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPPVGNDFWFKKQTAGTL
      .....
gi |602  FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPPVGNDFWFKKQTAGTL
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6  NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTYNIASF TKANV

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.....
gi|602 NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTPYNIASFYTKANV
      370      380      390      400      410      420

      420      430      440
del_6 LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|602 FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
      430      440      450

>>gi|30350277|gb|AAP23034.1| fatty acid delta-6 desaturase (453 aa)
  initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
  188
Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
overlap (3-446:10-453)

      10      20      30      40      50
del_6 MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: .....
gi|303 MANKSPPNPKTYITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10      20      30      40      50      60

      60      70      80      90      100      110
del_6 VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLKLDSPHKMGFRARGHTAYA
      .....
gi|303 VTDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSSDYRKLKLDNPHKHLFRARGHTAYA
      70      80      90      100      110      120

      120      130      140      150      160      170
del_6 TFVIMILMLVSSVTGVLCSNPVHVLVCGAAMGFAWIQCGWIGHDSGHYRIMDRKWNRF
      .....
gi|303 TFVFMIAMFLMSVTGVLCSNDSAWVHLASGGAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
      130      140      150      160      170      180

      180      190      200      210      220      230
del_6 AQILSSNCLQGIGISGWKWNHNAHIIACNSLEYDPLQYIPLLVVSPKFFNSLTSRFYDK
      .....
gi|303 AQILSTNCLQGIGISGWKWNHNAHIIACNSLDYDPLQYIPLLVVSPKFFNSLTSRFYDK
      190      200      210      220      230      240

      240      250      260      270      280      290
del_6 KLNFDGVSRLFVQYQHWFSFYPVMCVARLNMLAQSFILLFSRREANRVQEIILGLAVFWLW
      .....
gi|303 KLNFDGVSRLFVQYQHWTFYPVMCVARLNMLAQSFITLFSREVCCHRAQEVFGLAVFWVW
      250      260      270      280      290      300

      300      310      320      330      340      350
del_6 FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVPGNDWFKKQTAGTL
      .....
gi|303 FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVPGNDWFKKQTAGTL
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6 NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTPYNIASFYTKANV
      .....
gi|303 NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTPYNIASFYTKANV
      370      380      390      400      410      420

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      420      430      440
del_6 LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|303 FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG
      430      440      450

>>gi|76059286|emb|CAJ30837.1| unnamed protein product [P (453 aa)
  initn: 2865 initl: 2836 opt: 2836 Z-score: 3532.6 bits: 662.8 E(): 8.6e-
  188
Smith-Waterman score: 2836; 89.414% identity (96.622% similar) in 444 aa
overlap (3-446:10-453)

      10      20      30      40      50
del_6 MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
      :: .....
gi|760 MANKSPPNPKTYITSSDLKSHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10      20      30      40      50      60

      60      70      80      90      100      110
del_6 VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLKLDSPHKMGFRARGHTAYA
      .....
gi|760 VTDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSSDYRKLKLDNPHKHLFRARGHTAYA
      70      80      90      100      110      120

      120      130      140      150      160      170
del_6 TFVIMILMLVSSVTGVLCSNPVHVLVCGAAMGFAWIQCGWIGHDSGHYRIMDRKWNRF
      .....
gi|760 TFVFMIAMFLMSVTGVLCSNDSAWVHLASGGAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
      130      140      150      160      170      180

      180      190      200      210      220      230
del_6 AQILSSNCLQGIGISGWKWNHNAHIIACNSLEYDPLQYIPLLVVSPKFFNSLTSRFYDK
      .....
gi|760 AQILSTNCLQGIGISGWKWNHNAHIIACNSLDYDPLQYIPLLVVSPKFFNSLTSRFYDK
      190      200      210      220      230      240

      240      250      260      270      280      290
del_6 KLNFDGVSRLFVQYQHWFSFYPVMCVARLNMLAQSFILLFSRREANRVQEIILGLAVFWLW
      .....
gi|760 KLNFDGVSRLFVQYQHWTFYPVMCVARLNMLAQSFITLFSREVCCHRAQEVFGLAVFWVW
      250      260      270      280      290      300

      300      310      320      330      340      350
del_6 FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVPGNDWFKKQTAGTL
      .....
gi|760 FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVPGNDWFKKQTAGTL
      310      320      330      340      350      360

      360      370      380      390      400      410
del_6 NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTPYNIASFYTKANV
      .....
gi|760 NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVDRDLCKKHNLTPYNIASFYTKANV
      370      380      390      400      410      420

      420      430      440
del_6 LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|760 FTLKTLRNTAIEARDLSNPLPKNMVWEALKTLG

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430 440 450  
>>gi|118627910|emb|CAL85355.1| unnamed protein product [ (453 aa)  
initn: 2853 initl: 2821 opt: 2821 Z-score: 3513.9 bits: 659.4 E(): 9.5e-187  
Smith-Waterman score: 2821; 89.189% identity (96.622% similar) in 444 aa overlap (3-446:10-453)

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del_6      10      20      30      40      50
           MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
           :: ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|118     MANKSPNPNGTGYITSSDLKGHNKAGDLWISIHGEVYDVSSWAGLHPGGIAPLLALAGHD
           10      20      30      40      50      60
del_6      60      70      80      90      100     110
           VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLKLLDSFHKMGFRARGHTAYA
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|118     VTDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSDDYRKLKLLHNFHKIGMFRARGHTAYA
           70      80      90      100     110     120
del_6      120     130     140     150     160     170
           TFVIMILMLVSSVTGVLCSNPVWHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|118     TFVIMIVMFLTSVTGVLCSNDSAWVHLASGAAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
           130     140     150     160     170     180
del_6      180     190     200     210     220     230
           AQILSNCLQGIGISIGWKKWNHNAHIIACNSLEYDPLQYIPLLVSPPKFFNSLTSRFYDK
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|118     AQVLTNCLQGIGISIGWKKWNHNAHIIACNSLDYDPLQYIPLLVSPPKFFNSLTSRFYDK
           190     200     210     220     230     240
del_6      240     250     260     270     280     290
           KLNFDGVSRLFVQYQHSFYFVCMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|118     KLNFDGVSRLFVQYQHSFYFVCMCVARLNMLAQSFITLFSRREVGHRAEIIFGLAVFWVW
           250     260     270     280     290     300
del_6      300     310     320     330     340     350
           FPILLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTL
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|118     FPILLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTL
           310     320     330     340     350     360
del_6      360     370     380     390     400     410
           NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRLDCKKHNLTYNIASFTKANV
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|118     NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRLDCKKHNLTYNIASFTKANV
           370     380     390     400     410     420
del_6      420     430     440
           LTLETLRNTAIEARDLSNP IPKNMVWEAVKNVG
           ::::: . . . . . ::::: . . . . .
gi|118     LTLKTLRNTAIEARDLSNP TPKNMVWEAVHTHG
           430     440     450
```

>>gi|39750755|emb|CAE84828.1| unnamed protein product [P (453 aa)

initn: 2853 initl: 2821 opt: 2821 Z-score: 3513.9 bits: 659.4 E(): 9.5e-187  
Smith-Waterman score: 2821; 89.189% identity (96.622% similar) in 444 aa overlap (3-446:10-453)

```
del_6      10      20      30      40      50
           MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
           :: ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|397     MANKSPNPNGTGYITSSDLKGHNKAGDLWISIHGEVYDVSSWAGLHPGGIAPLLALAGHD
           10      20      30      40      50      60
del_6      60      70      80      90      100     110
           VTDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLKLLDSFHKMGFRARGHTAYA
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|397     VTDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSDDYRKLKLLHNFHKIGMFRARGHTAYA
           70      80      90      100     110     120
del_6      120     130     140     150     160     170
           TFVIMILMLVSSVTGVLCSNPVWHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRF
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|397     TFVIMIVMFLTSVTGVLCSNDSAWVHLASGAAMGFAWIQCGWIGHDSGHYRIMSDRKWNWF
           130     140     150     160     170     180
del_6      180     190     200     210     220     230
           AQILSNCLQGIGISIGWKKWNHNAHIIACNSLEYDPLQYIPLLVSPPKFFNSLTSRFYDK
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|397     AQVLTNCLQGIGISIGWKKWNHNAHIIACNSLDYDPLQYIPLLVSPPKFFNSLTSRFYDK
           190     200     210     220     230     240
del_6      240     250     260     270     280     290
           KLNFDGVSRLFVQYQHSFYFVCMCVARLNMLAQSFILLFSRREVANRVQEILGLAVFWLW
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|397     KLNFDGVSRLFVQYQHSFYFVCMCVARLNMLAQSFITLFSRREVGHRAEIIFGLAVFWVW
           250     260     270     280     290     300
del_6      300     310     320     330     340     350
           FPILLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTL
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|397     FPILLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGPVGNDFWFKKQTAGTL
           310     320     330     340     350     360
del_6      360     370     380     390     400     410
           NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRLDCKKHNLTYNIASFTKANV
           ::::: . . . . . ::::: . . . . . ::::: . . . . .
gi|397     NISCPAWMDWFHGGGLQFQVEHHLFPRMPRGQFRKISPFVRLDCKKHNLTYNIASFTKANV
           370     380     390     400     410     420
del_6      420     430     440
           LTLETLRNTAIEARDLSNP IPKNMVWEAVKNVG
           ::::: . . . . . ::::: . . . . .
gi|397     LTLKTLRNTAIEARDLSNP TPKNMVWEAVHTHG
           430     440     450
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>>gi|126633768|emb|CAM55840.1| unnamed protein product [ (453 aa)  
initn: 2845 initl: 2813 opt: 2813 Z-score: 3503.9 bits: 657.5 E(): 3.4e-186  
Smith-Waterman score: 2813; 88.964% identity (96.622% similar) in 444 aa overlap (3-446:10-453)



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del_6 VTDAFLAYHPPSTARLLPPFSTNLLLEKHSVSETSSDYRKLKLLDSFHKMGMFRRAGHTAYA
gi | 602 VTDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSDDYRKLHNFHFKIGMFRRAGHTAYA
      70          80          90          100         110         120

del_6   120     130     140     150     160     170
TFVIMILMLVSSVTGVLCSENPWVHLVCGAAMGFAWIQCQGWIGHDSGHYRIMTDRKWNRF
gi | 602 TFVIMIVMFLTSVTGVLCSDSA WVHLASGAAMGFAWIQCQGWIGHDSGHYRIMSDRKNWF
      130     140     150     160     170     180

del_6   180     190     200     210     220     230
AQILSSNCLQGIGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPPKFFNSLTSRFYDK
gi | 602 AQVLSNCLQGIGISIGWKKWNHNAHHIACNSLDYDPLQYIPLLVSPPKFFNSLTSRFYDK
      190     200     210     220     230     240

del_6   240     250     260     270     280     290
KLNFDGVSRLFVQYQHWSEFYPVMCVARLNMLAQSFILLFSRREVANRVQEIILGLAVFWLW
gi | 602 KLNFDGVSRLFVQYQHWSEFYPVMCVARLNMLAQSFITLFSRREVGHRQEIIFGLAVFWVW
      250     260     270     280     290     300

del_6   300     310     320     330     340     350
FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVGNDWFKKQTAGTL
gi | 602 FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVANDWFKKQTAGTL
      310     320     330     340     350     360

del_6   360     370     380     390     400     410
NISCPAWMDWFHGGQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANV
gi | 602 NISCPAWMDWFHGGQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLPYNIASFTKANV
      370     380     390     400     410     420

del_6   420     430     440
LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
gi | 602 LTLKTLRNTAIEARDLSNPTPKNMVWEAVHTHG
      430     440     450

>>gi|76059288|emb|CAJ30838.1| unnamed protein product [P (453 aa)
  initn: 2845 initl: 2813 opt: 2813 Z-score: 3503.9 bits: 657.5 E(): 3.4e-
  186
  Smith-Waterman score: 2813; 88.964% identity (96.622% similar) in 444 aa
  overlap (3-446:10-453)

del_6   10     20     30     40     50
MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
gi | 760 MANKSPPNPKTGYITSSDLKGNKAGDLWISIHGEVYDVSSWAGLHPGGSAPLMALAGHD
      10     20     30     40     50     60

del_6   60     70     80     90     100    110
VTDAFLAYHPPSTARLLPPFSTNLLLEKHSVSETSSDYRKLKLLDSFHKMGMFRRAGHTAYA
gi | 760 VTDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSDDYRKLHNFHFKIGMFRRAGHTAYA
      70     80     90     100    110    120

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del_6   120     130     140     150     160     170
TFVIMILMLVSSVTGVLCSENPWVHLVCGAAMGFAWIQCQGWIGHDSGHYRIMTDRKWNRF
gi | 760 TFVIMIVMFLTSVTGVLCSDSA WVHLASGAAMGFAWIQCQGWIGHDSGHYRIMSDRKNWF
      130     140     150     160     170     180

del_6   180     190     200     210     220     230
AQILSSNCLQGIGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPPKFFNSLTSRFYDK
gi | 760 AQVLSNCLQGIGISIGWKKWNHNAHHIACNSLDYDPLQYIPLLVSPPKFFNSLTSRFYDK
      190     200     210     220     230     240

del_6   240     250     260     270     280     290
KLNFDGVSRLFVQYQHWSEFYPVMCVARLNMLAQSFILLFSRREVANRVQEIILGLAVFWLW
gi | 760 KLNFDGVSRLFVQYQHWSEFYPVMCVARLNMLAQSFITLFSRREVGHRQEIIFGLAVFWVW
      250     260     270     280     290     300

del_6   300     310     320     330     340     350
FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVGNDWFKKQTAGTL
gi | 760 FPLLSSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPVANDWFKKQTAGTL
      310     320     330     340     350     360

del_6   360     370     380     390     400     410
NISCPAWMDWFHGGQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLTYNIASFTKANV
gi | 760 NISCPAWMDWFHGGQFQVEHHLFPRMPRGQFRKISPFVRDLCKKHNLPYNIASFTKANV
      370     380     390     400     410     420

del_6   420     430     440
LTLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
gi | 760 LTLKTLRNTAIEARDLSNPTPKNMVWEAVHTHG
      430     440     450

>>gi|30350275|gb|AAP23033.1| sphingolipid delta-8 desatu (452 aa)
  initn: 2532 initl: 2504 opt: 2504 Z-score: 3118.7 bits: 586.3 E(): 9.8e-
  165
  Smith-Waterman score: 2504; 76.351% identity (93.468% similar) in 444 aa
  overlap (3-446:9-452)

del_6   10     20     30     40     50
MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHD
gi | 303 MADPPPNPKTGYITSSDLKAHNKAGDLWISIHGQVYDVSSWAALHPGGTAPLMALAGHD
      10     20     30     40     50     60

del_6   60     70     80     90     100    110
TDAFLAYHPPSTARLLPPFSTNLLLEKHSVSETSSDYRKLKLLDSFHKMGMFRRAGHTAYAT
gi | 303 TDAFLAYHPPSTARLLPPLSANLLEHYSVSPTSDDYRKLHNFHFKLDLQTKSHTTCFT
      70     80     90     100    110    120

del_6   120     130     140     150     160     170
FVIMILMLVSSVTGVLCSENPWVHLVCGAAMGFAWIQCQGWIGHDSGHYRIMTDRKWNRF

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gi|303 FVAMVVLFFLSLLGVFCSdstwvhlASGGVMGVAWIQSGWLGHDShGYQIMSSRKTNRFA
      130      140      150      160      170      180
del_6      180      190      200      210      220      230
del_6 QILSSNCLQGIGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPKFFNSLTSRFYDKK
      .....
gi|303 QVLSGNCLAGISIAWKKWNHNAHHLACNSLDYDPLQHMPPFVSVSKFFNSLTSRFYDRK
      190      200      210      220      230      240
del_6      240      250      260      270      280      290
del_6 LNFDGVSRLFVQYQHWSFYVMCVARLNMLAQSFILLFSRREVANRVQEIILGLAVFWLWF
      .....
gi|303 LNFDGVSRLFVSYQHWSFYVMCLARINLFAQSFMLLFSSRKPDRVQEIFGIGVFWVWY
      250      260      270      280      290      300
del_6      300      310      320      330      340      350
del_6 PLLLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSDDVYVGGPVGNDWFKKQTAGTLN
      .....
gi|303 PLLVSCLPNWERIMFVVASFSVTGIQHVQFCLNHFSAEYVLGPPPEGNDWFEKQTAGTLN
      310      320      330      340      350      360
del_6      360      370      380      390      400      410
del_6 ISCPAWMDWFHGGQFQVEHHLFPRMQRGFRKISPFVRDLCKKHNLTYNIASFTKANVL
      .....
gi|303 ISCHSMDWFHGGQFQIEHHLFPRLRQLRQVSPFVRDLCKKHNLPYNVTSFTMANVL
      370      380      390      400      410      420
del_6      420      430      440
del_6 TLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|303 TLKTLRNAAIQARDLSNPTPKNLVWEAVNTHG
      430      440      450

>>gi|30350279|gb|AAP23035.1| sphingolipid delta-8 desatu (452 aa)
  initn: 2514 init1: 2486 opt: 2486 Z-score: 3096.3 bits: 582.1 E(): 1.7e-
  163
  Smith-Waterman score: 2486; 75.676% identity (93.468% similar) in 444 aa
  overlap (3-446:9-452)

del_6      10      20      30      40      50
del_6 MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDV
      .....
gi|303 MADPPNPKTSYITSSDLKGNKAGNLWISIHGEVYDVSSWAGLHPGGSAPLMALAGHDV
      10      20      30      40      50      60
del_6      60      70      80      90      100      110
del_6 TDAFLAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLDSFHKMGFRARGHTAYAT
      .....
gi|303 TDAFLAYHPPSTARLLPPLSTNLLQNHVSPTSDDYRKLHNFHFKIQLGFQKSHHTTCVT
      70      80      90      100      110      120
del_6      120      130      140      150      160      170
del_6 FVIMILMVSSVTGVLCSNPWVHLVCGAAMGFAWICQGWIGHDSGHYRIMTDRKWNRF
      .....
gi|303 FVAMVALFFLSLYGVFCSdSAWVHLASGGVMGVAWIQSGWLGHDShGYQIMSSRKTNRFA
      130      140      150      160      170      180
del_6      180      190      200      210      220      230

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del_6 QILSSNCLQGIGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPKFFNSLTSRFYDKK
      .....
gi|303 QVLSGNCLAGISIAWKKWNHNAHHLACNSLDYDPLQHMPPFVSVSKFFNSLTSRFYDRK
      190      200      210      220      230      240
del_6      240      250      260      270      280      290
del_6 LNFDGVSRLFVQYQHWSFYVMCVARLNMLAQSFILLFSRREVANRVQEIILGLAVFWLWF
      .....
gi|303 LRFDSVSRFLVSYQHWSFYVMCLARINLFAQSFMLLFSSRKPDRVQEIFGIGVFWVWY
      250      260      270      280      290      300
del_6      300      310      320      330      340      350
del_6 PLLLSCLPNWGERIMFLLASYSVTGIQHVQFSLNHFSDDVYVGGPVGNDWFKKQTAGTLN
      .....
gi|303 PLLVSCLPNWERIMFVVASFSVTGIQHVQFCLNHFSAEYVLGPPPEGNDWFEKQTAGTLN
      310      320      330      340      350      360
del_6      360      370      380      390      400      410
del_6 ISCPAWMDWFHGGQFQVEHHLFPRMQRGFRKISPFVRDLCKKHNLTYNIASFTKANVL
      .....
gi|303 ISCPAWMDWFHGGQFQIEHHLFPRLRQLRQVSPFVRDLCKKHNLTYNIASFTMANVL
      370      380      390      400      410      420
del_6      420      430      440
del_6 TLETLRNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|303 TLKTLRNAAIQARDLSNPTPKNLVWEAVNTHG
      430      440      450

>>gi|129593742|gb|ABO31111.1| sphingolipid delta-8 desat (447 aa)
  initn: 2215 init1: 2189 opt: 2189 Z-score: 2726.1 bits: 513.6 E(): 7.2e-
  143
  Smith-Waterman score: 2189; 65.760% identity (88.435% similar) in 441 aa
  overlap (6-446:7-447)

del_6      10      20      30      40      50
del_6 MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVDAFL
      .....
gi|129 MADSRKYITSEELKHNKPGDLWISIQGKVDVSDWIKHHPGGDFPLLNLQAGQDVDAFL
      10      20      30      40      50      60
del_6      60      70      80      90      100      110
del_6 AYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLDSFHKMGFRARGHTAYATFVIMI
      .....
gi|129 AYHPATAWQYLDKFNQVYLDKYSASEVSKDYRRLVSEFTKGLFEEKKGVCFYTMCSIA
      70      80      90      100      110      120
del_6      120      130      140      150      160      170
del_6 LMLVSVTGVLCSNPWVHLVCGAAMGFAWICQGWIGHDSGHYRIMTDRKWNRFQILSS
      .....
gi|129 MLFAVSVYGMCSSEVLVHLSGGLMGFLWISQGWIGHDSGHYQVMSRTRGNRFQVLTG
      130      140      150      160      170      180
del_6      180      190      200      210      220      230
del_6 NCLQGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPKFFNSLTSRFYDKKLNFDG
      .....
gi|129 NCLAGISIAWKKWNHNAHIAVNSLEYDPLQHMPPFVSVSKFFNSLTSYFYDRKMTFDS
      190      200      210      220      230      240

```

```

240      250      260      270      280      290
del_6 VSRFLVQYQHWSFYPMCVARLNMLAQSFIILLFSRREVANRVQEIILGLAVFWLWFPPLLS
      .....
gi|129 FTRFLVSNQHWTFYPMCLARINLFAQSFIILLSSKKNVYRQVQLLGGVVAFWIWIYPLLVS
      250      260      270      280      290      300

300      310      320      330      340      350
del_6 CLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPPVGNDFWFKKQTAGTLNISCPA
      .....
gi|129 CLPNWGERIMFVLAFTVTGIQHVQFCLNHFSSDIYVAPPKGNDWFEKQTGGSLDISCPS
      310      320      330      340      350      360

360      370      380      390      400      410
del_6 WMDWFHGGGLQFQVEHHLFPRMFRGQFRKISPFVRDLCKKHNLTYNIASFYMANALVTLETL
      .....
gi|129 WMDWFYGGGLQFQIEHHLFPRMFRGQFRKISPFVRDLCKKHNLTYNIASFYMANALVTLETL
      370      380      390      400      410      420

420      430      440
del_6 RNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|129 RTAALQARDLTKPVKPNLVWEAVNTHG
      430      440

>>gi|144583293|gb|ABP01349.1| D8-sphingolipid desaturase (447 aa)
  initn: 2175 initl: 2175 opt: 2175 Z-score: 2708.6 bits: 510.4 E(): 6.8e-
  142
Smith-Waterman score: 2175; 65.760% identity (87.528% similar) in 441 aa
overlap (6-446:7-447)

10      20      30      40      50
del_6 MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTD AFL
      .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 MADSKKYISEEELKHKTKSGDLWISIQGKVYNVTGWTKDHPGGELPLLHLGSDQVTD AFV
      10      20      30      40      50      60

60      70      80      90      100      110
del_6 AYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLKLDSEFHKMGFRARGHTAYATFVIMI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 AYHPPGTAWQYLDKFFTGYYLKDHSVSEVSKDYRKLKLAETKMGLEFKKGGHVTLVLCVVA
      70      80      90      100      110      120

120      130      140      150      160      170
del_6 LMLVSSVTGVLCSENPWVHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRFQILSS
      . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 MLLSFSIYGILCSDSTWVHLLSGGLIGFLWISQGWIGHDSGHYQVMTSPKINRLVQILTG
      130      140      150      160      170      180

180      190      200      210      220      230
del_6 NCLQGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPKFFNSLTSRFDYDKKLNFDG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 NCLAGISIAWKKWNHNAHHIACNSLEFDPLQHMPPFAVSSKLFSSLSYFYERKMNFDS
      190      200      210      220      230      240

240      250      260      270      280      290
del_6 VSRFLVQYQHWSFYPMCVARLNMLAQSFIILLFSRREVANRVQEIILGLAVFWLWFPPLLS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

gi|144 VCRFLVSYQHWTFFYPMCFARLNMLFAQSFIILLSSKRRVVPNRGQEIILGVLVFWIWIYPLLVS
      250      260      270      280      290      300

300      310      320      330      340      350
del_6 CLPNWGERIMFLLASYSVTGIQHVQFSLNHFSSDVYVGGPPVGNDFWFKKQTAGTLNISCPA
      .....
gi|144 CLPNWGERVMFVLAFAVTGIQHVQFCLNHFSSNVYVGLPSGNDWFEKQTKGTLNINCS
      310      320      330      340      350      360

360      370      380      390      400      410
del_6 WMDWFHGGGLQFQVEHHLFPRMFRGQFRKISPFVRDLCKKHNLTYNIASFYMANALVTLETL
      .....
gi|144 WMDWFHGGGLQFQIEHHLFPRMFRGQFRKISPFVRDLCKKHNLTYNIASFYMANALVTLETL
      370      380      390      400      410      420

420      430      440
del_6 RNTAIEARDLSNPIPKNMVWEAVKNVG
      .....
gi|144 SAAALQARDLANPVKPNLVWEAVNTHG
      430      440

>>gi|157339279|emb|CA043820.1| unnamed protein product [ (447 aa)
  initn: 2191 initl: 2166 opt: 2166 Z-score: 2697.4 bits: 508.3 E(): 2.9e-
  141
Smith-Waterman score: 2166; 65.986% identity (87.302% similar) in 441 aa
overlap (6-446:7-447)

10      20      30      40      50
del_6 MTKTIYITSSSELEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTD AFL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|157 MAETKRYISKEELKTHSRDGLWISIQGKVYNVSDWAKVHPGGSAPELLS LAGQDATDAFV
      10      20      30      40      50      60

60      70      80      90      100      110
del_6 AYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKLKLDSEFHKMGFRARGHTAYATFVIMI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|157 AYHPPGVLWRLDDFFTFHLEDYAVSEASRDYRRLVYEFKMGLEFKKGGHVTLVLCAMA
      70      80      90      100      110      120

120      130      140      150      160      170
del_6 LMLVSSVTGVLCSENPWVHLVCGAAMGFAWIQCGWIGHDSGHYRIMTDRKWNRFQILSS
      . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|157 VMFSACIYGVLSGSDNTWVHLASGALMGLFWISQGWIGHDSGHYQVMMNRRLNRFVQVLSG
      130      140      150      160      170      180

180      190      200      210      220      230
del_6 NCLQGISIGWKKWNHNAHHIACNSLEYDPLQYIPLLVSPKFFNSLTSRFDYDKKLNFDG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|157 NCLAGISIAWKKWNHNAHHIACNSLEFDPLQHMPPFAVSSKLFSSLSYFYERKMNFDC
      190      200      210      220      230      240

240      250      260      270      280      290
del_6 VSRFLVQYQHWSFYPMCVARLNMLAQSFIILLFSRREVANRVQEIILGLAVFWLWFPPLLS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|157 VARFLVSYQHWTFFYPMCVARLNMLFAQSFIILLSSKRRVRYRAQEIILGVLVFWIWIYPLLVS
      250      260      270      280      290      300

300      310      320      330      340      350

```





>>gi|70795233|gb|AAZ08559.1| delta-6 desaturase [Echium (448 aa)  
initn: 2120 initl: 2120 opt: 2120 Z-score: 2640.0 bits: 497.7 E(): 4.5e-138  
Smith-Waterman score: 2120; 65.079% identity (87.982% similar) in 441 aa  
overlap (6-446:8-448)

```
del_6      10      20      30      40      50
           MTKTIYITSSLEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTD
           ::::::::::::::::::::::::::::
gi|707     MANAIKKYITAEELKKHKAGDLWISIQGKIYDVS
           10      20      30      40      50      60
del_6      60      70      80      90      100     110
           LAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYRKL
           .:. .: .: .: .: .: .: .: .: .: .: .: .:
gi|707     VAFHSGTGWKLLKFFTYGYYLKDYSVSEVSKDYR
           70      80      90      100     110     120
del_6      120     130     140     150     160     170
           ILMVSSVTGVLCSNPVWHLVCGAAMGFAWIQCGW
           . . . : : : : . : : : : : : : : : : .
gi|707     AMLFGMSVYGVLFCEGVLVHLLAGGLMGFVWI
           130     140     150     160     170     180
del_6      180     190     200     210     220     230
           SNCLQGISIGWKKWNHNAHIIACNSLEYD
           .: .: .: .: .: .: .: .: .: .: .: .:
gi|707     ANCLSGISIGWKKWNHNAHIIACNSLDYD
           190     200     210     220     230     240
del_6      240     250     260     270     280     290
           GVSRLFVQYQHSFYVPMCVARLNMLAQSFILL
           .: .: .: .: .: .: .: .: .: .: .: .:
gi|707     SLSRFFVSHQHWTFYPVCMARVNMVQSLIM
           250     260     270     280     290     300
del_6      300     310     320     330     340     350
           SCLPNWGERIMFLLASYSVTGIQHVQFSLN
           : : : : : : : : : : : : : : : : :
gi|707     SCLPNWGERVMFVVASLVTGMQQVQFSLN
           310     320     330     340     350     360
del_6      360     370     380     390     400     410
           AWMDWFHGGQLQFQVEHHLFPRMPRGQFRK
           .: .: .: .: .: .: .: .: .: .: .: .:
gi|707     SWMDWFHGGQLQFQVEHHLFPKLPRCHLRK
           370     380     390     400     410     420
del_6      420     430     440
           LRNTAIEARDLSNPIPKNMVWEAVKNVG
           : : : : : : : : : : : : : : : :
gi|707     LRDTALQARDLTKPLPKNLVWEALNTHG
           430     440
```

>>gi|76059232|emb|CAJ30813.1| unnamed protein product [B (448 aa)  
initn: 2147 initl: 2120 opt: 2120 Z-score: 2640.0 bits: 497.7 E(): 4.5e-138

Smith-Waterman score: 2120; 65.306% identity (87.075% similar) in 441 aa  
overlap (6-446:8-448)

```
del_6      10      20      30      40      50
           MTKTIYITSSLEKHNKPGDLWISIHGQVYDVSSWAALHPGGIAPLLALAGHDVTD
           ::::::::::::::::::::::::::::::::::::
gi|760     MAAQIKKYITSDELKHNKPGDLWISIQGKAYDVS
           10      20      30      40      50      60
del_6      60      70      80      90      100     110
           LAYHPPSTSRLLPPFSTNLLLEKHSVSETSSDYR
           .: .: .: .: .: .: .: .: .: .: .: .:
gi|760     VAFHPASTWKNLKDFFTYGYYLKDYSVSEVSKDYR
           70      80      90      100     110     120
del_6      120     130     140     150     160     170
           ILMVSSVTGVLCSNPVWHLVCGAAMGFAWIQCGW
           . . . : : : : . : : : : : : : : : .
gi|760     AMLFAMSVMYGVLFCEGVLVHLLAGGLMGFVWI
           130     140     150     160     170     180
del_6      180     190     200     210     220     230
           SNCLQGISIGWKKWNHNAHIIACNSLEYD
           .: .: .: .: .: .: .: .: .: .: .: .:
gi|760     ANCLSGISIGWKKWNHNAHIIACNSLEYD
           190     200     210     220     230     240
del_6      240     250     260     270     280     290
           GVSRLFVQYQHSFYVPMCVARLNMLAQSFILL
           .: .: .: .: .: .: .: .: .: .: .: .:
gi|760     SLSRFFVSYQHWTFFYPIMCAARLNMYVQSLIM
           250     260     270     280     290     300
del_6      300     310     320     330     340     350
           SCLPNWGERIMFLLASYSVTGIQHVQFSLN
           : : : : : : : : : : : : : : : :
gi|760     SCLPNWGERIMFVIAVSLVTGMQQVQFSLN
           310     320     330     340     350     360
del_6      360     370     380     390     400     410
           AWMDWFHGGQLQFQVEHHLFPRMPRGQFRK
           .: .: .: .: .: .: .: .: .: .: .: .:
gi|760     PWMDWFHGGQLQFQIEHHLFPMKPRCNLRK
           370     380     390     400     410     420
del_6      420     430     440
           LRNTAIEARDLSNPIPKNMVWEAVKNVG
           : : : : : : : : : : : : : : : :
gi|760     LRNTALQARDITKPLPKNLVWEALNTHG
           430     440
```

>>gi|156141045|gb|ABU51607.1| delta 6-desaturase [Borago (448 aa)  
initn: 2147 initl: 2120 opt: 2120 Z-score: 2640.0 bits: 497.7 E(): 4.5e-138  
Smith-Waterman score: 2120; 65.306% identity (87.075% similar) in 441 aa  
overlap (6-446:8-448)

```
10      20      30      40      50
```





427 residues in 1 query sequences  
 307888 residues in 1386 library sequences  
 Scomplib [34t26]  
 start: Tue Oct 20 14:41:31 2009 done: Tue Oct 20 14:41:31 2009  
 Total Scan time: 0.160 Total Display time: 0.010

Function used was FASTA [version 3.4t26 July 7, 2006]

---

```
# fasta34 del_15.pep /home/andre/db/TOX_2009 -Q -E 1 -O del_15.pep_tx.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,
2006
```

Please cite:

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

del\_15, 427 aa  
 vs /home/andre/db/TOX\_2009 library

```

opt      E()
< 20    59    0:=====
22      0     0:                one = represents 12 library sequences
24      0     0:
26      1    0:=
28      18    2:*=
30      12    11:*
32      27    41:====*
34     105   110:=====*
36     247   227:=====*=
38     342   375:===== *
40     602   523:=====*=
42     555   639:===== *
44     551   705:===== *
46     711   718:=====*=
48     539   688:===== *
50     709   627:=====*=
52     669   552:=====*=
54     417   471:===== *
56     328   394:===== *
58     297   323:===== *
60     307   262:=====*=
62     111   210:===== *
64      92   167:===== *
66     123   132:=====*
68     134   104:=====*=
70     156   81:=====*=
72     108   64:=====*=
74      35   50:===== *
76      83   39:=====*=
78      22   30:=====*
80     185   23:=====*=
82      14   18:=====*
84      35   14:=====*=

```

```

86     14   11:=====
88     15   8:===== inset = represents 1 library sequences
90      8   7:=====
92      5   5:=====
94      7   4:=====
96      2   3:=====
98      0   2:=====
100     0   2:=====
102     0   1:=====
104     0   1:=====
106     0   1:=====
108     0   1:=====
110     0   1:=====
112     0   0:=====
114      1   0:======
116     0   0:=====
118     0   0:=====
>120    0   0:=====

```

1891534 residues in 7651 sequences  
 Expectation\_n fit: rho(ln(x))= 5.43590.000716; mu= 7.4762 0.036  
 mean\_var=58.033113.609, 0's: 59 Z-trim: 59 B-trim: 768 in 2/60  
 Lambda= 0.168359  
 Kolmogorov-Smirnov statistic: 0.0544 (N=29) at 66

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2  
 join: 37, opt: 25, open/ext: -10/-2, width: 16  
 !! No sequences with E() < 1.000000

427 residues in 1 query sequences  
 1891534 residues in 7651 library sequences  
 Scomplib [34t26]  
 start: Tue Oct 20 14:41:33 2009 done: Tue Oct 20 14:41:34 2009  
 Total Scan time: 0.700 Total Display time: 0.000

Function used was FASTA [version 3.4t26 July 7, 2006]

---

```
# fasta34 del_15.pep /home/andre/db/PRT_2009 -Q -E 1 -O del_15.pep_prt.fasta
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7,
2006
```

Please cite:

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

del\_15, 427 aa  
 vs /home/andre/db/PRT\_2009 library

```

opt      E()
< 20 221653 0:=====
22   126    0:=                one = represents 22582 library sequences
24   426   14:*
26   985  309:*
28  3808 3336:*
30 18208 20267:*
32 67668 78364:=====
34 179719 212513:===== *
36 379640 436452:===== *

```

```

38 663309 721292:===== *
40 948566 1006139:===== *
42 1158604 1229883:===== *
44 1308167
1356675:===== *
46 1354903
1381807:===== *
48 1328241
1322921:===== *
50 1191316 1207171:===== *
52 1076496 1061305:===== *
54 899846 906540:===== *
56 772898 757239:===== *
58 635312 621679:===== *
60 505671 503596:===== *
62 413251 403735:===== *
64 331577 321088:===== *
66 268151 253778:===== *
68 214438 199617:===== *
70 165894 156431:===== *
72 137283 122236:===== *
74 108787 95303:===== *
76 80277 74177:===== *
78 63324 57657:===== *
80 49705 44769:===== *
82 37718 34248:===== *
84 29315 27128:===== *
86 22297 20991:===== *
88 16817 16241:===== *
90 13286 12567:===== *
92 10447 9723:===== *
94 7631 7523:===== *
96 5880 5821:===== *
98 4384 4504:===== *
100 3359 3485:===== *
102 2937 2697:===== *
104 1997 2086:===== *
106 1495 1614:===== *
108 1196 1249:===== *
110 934 967:===== *
112 835 748:===== *
114 657 579:===== *
116 463 448:===== *
118 385 346:===== *
>120 4136 268:===== *
3787527556 residues in 14717352 library sequences
statistics sampled from 60000 to 14710445 sequences
Expectation_n fit: rho(ln(x))= 5.27860.000191; mu= 9.7049 0.010
mean_var=65.615013.206, 0's: 854 Z-trim: 868 B-trim: 0 in 0/62
Lambda= 0.158333
Kolmogorov-Smirnov statistic: 0.0258 (N=29) at 50

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 3rv, opt: 25, open/ext: -10/-2, width: 16
The best scores are:
E(14717352)
gi|88181398|gb|EQAQ88866.1| hypothetical protein CH ( 400) 1886 439.6 1.2e-120
gi|170940419|emb|CAP65646.1| unnamed protein produ ( 399) 1884 439.1 1.6e-120
gi|167276960|gb|ABZ29824.1| Sequence 3762 from pat ( 429) 1871 436.2 1.3e-119
gi|145012308|gb|EDJ96964.1| hypothetical protein M ( 394) 1674 391.2 4.4e-106
gi|158467921|gb|ABW45178.1| Sequence 58 from paten ( 402) 1658 387.5 5.6e-105
gi|217312880|gb|ACK35371.1| Sequence 94 from paten ( 402) 1658 387.5 5.6e-105
gi|82658705|gb|ABB88516.1| bifunctional D12/D15 fa ( 402) 1658 387.5 5.6e-105
gi|114188648|gb|EAU30348.1| conserved hypothetical ( 394) 1369 321.5 4.1e-85
gi|134082006|emb|CAK46691.1| unnamed protein produ ( 398) 1349 316.9 9.9e-84
gi|83776412|dbj|BAE66531.1| unnamed protein produc ( 392) 1337 314.2 6.5e-83
gi|119405648|gb|EAW15599.1| oleate delta-12 desatu ( 395) 1321 310.5 8.3e-82
gi|159122555|gb|EDP47676.1| oleate delta-12 desatu ( 396) 1318 309.8 1.3e-81
gi|211593378|emb|CAP99761.1| Pc22g24730 [Penicilli ( 395) 1306 307.1 8.9e-81
gi|119398366|gb|EAW08796.1| oleate delta-12 desatu ( 391) 1305 306.9 1e-80
gi|160707460|gb|EAT91011.2| hypothetical protein S ( 979) 1238 291.8 9e-76
gi|150408460|gb|EDN04001.1| hypothetical protein H ( 472) 1174 277.0 1.2e-71
gi|90301761|gb|EAS31392.1| hypothetical protein CI ( 445) 1165 274.9 4.9e-71
gi|159131376|gb|EDP56489.1| oleate delta-12 desatu ( 469) 1143 269.9 1.7e-69
gi|145025092|gb|ABP24249.1| Sequence 34 from paten ( 477) 1141 269.5 2.3e-69
gi|82658703|gb|ABB88515.1| delta-12 fatty acid des ( 477) 1141 269.5 2.3e-69
gi|144998356|gb|ABP16929.1| Sequence 20 from paten ( 477) 1141 269.5 2.3e-69
gi|158475488|gb|ABW48564.1| Sequence 27 from paten ( 477) 1141 269.5 2.3e-69
gi|155080899|gb|ABS94493.1| Sequence 69 from paten ( 477) 1141 269.5 2.3e-69
gi|155070719|gb|ABS91064.1| Sequence 46 from paten ( 477) 1141 269.5 2.3e-69
gi|119412672|gb|EAW22613.1| oleate delta-12 desatu ( 469) 1140 269.2 2.7e-69
gi|151935301|gb|ABS18716.1| delta12 fatty acid des ( 476) 1132 267.4 9.6e-69
gi|41581329|emb|CAE47978.1| oleate delta-12 desatu ( 424) 1131 267.1 1e-68
gi|145012848|gb|EDJ97489.1| hypothetical protein M ( 487) 1131 267.2 1.1e-68
gi|211584351|emb|CAP92386.1| Pc13g13170 [Penicilli ( 468) 1129 266.7 1.5e-68
gi|167277069|gb|ABZ29933.1| Sequence 3871 from pat ( 413) 1116 263.7 1.1e-67
gi|210071661|gb|EEA25750.1| oleate delta-12 desatu ( 470) 1112 262.8 2.3e-67
gi|30385622|gb|AAP23194.1| oleate delta-12 desatur ( 466) 1108 261.9 4.2e-67
gi|114197390|gb|EAU39090.1| hypothetical protein A ( 467) 1108 261.9 4.2e-67
gi|30721845|gb|AAP33789.1| oleate delta-12 desatur ( 466) 1106 261.4 5.8e-67
gi|83766627|dbj|BAE56767.1| unnamed protein produc ( 466) 1106 261.4 5.8e-67
gi|194400325|gb|ACF61036.1| delta-12 desaturase is ( 483) 1104 261.0 8.2e-67
gi|151935303|gb|ABS18717.1| fatty acid desaturase ( 477) 1101 260.3 1.3e-66
gi|194477488|gb|ACF74838.1| putative delta-12 desa ( 483) 1101 260.3 1.3e-66
gi|39652599|dbj|BAD04850.1| oleate delta12 desatur ( 466) 1098 259.6 2.1e-66
gi|134077147|emb|CAK45488.1| unnamed protein produ ( 466) 1097 259.4 2.4e-66
gi|187979836|gb|EDU46462.1| delta(12) fatty acid d ( 447) 1096 259.2 2.7e-66
gi|159906226|gb|ABI96224.2| putative delta-12 desa ( 480) 1094 258.7 4e-66
gi|119397150|gb|EAW07581.1| oleate delta-12 desatu ( 469) 1093 258.5 4.6e-66
gi|11527199|gb|AAG36933.1| AF262955_1 oleate delta- ( 420) 1088 257.3 9.2e-66
gi|111070000|gb|EAT91120.1| hypothetical protein S ( 494) 1088 257.4 1.1e-65
gi|194271138|gb|ACF37070.1| fatty acid hydroxylase ( 477) 1081 255.7 3.1e-65
gi|167286028|gb|ABZ38892.1| Sequence 12830 from pa ( 419) 1080 255.3 3.2e-65
gi|150845063|gb|EDN20256.1| hypothetical protein B ( 481) 1071 253.5 1.5e-64
gi|154699086|gb|EDN98824.1| hypothetical protein S ( 481) 1069 253.0 2.1e-64
gi|211999443|gb|EEB05103.1| Delta(12) fatty acid d ( 449) 1062 251.4 6e-64
gi|211581853|emb|CAP79976.1| Pc12g03490 [Penicilli ( 453) 943 224.2 9.1e-56
gi|23313402|gb|AAN19960.1| Sequence 4 from patent ( 399) 935 222.4 2.9e-55
gi|12808263|gb|AAE43483.1| Sequence 4 from patent ( 399) 935 222.4 2.9e-55
gi|14477723|gb|AAE61286.1| Sequence 4 from patent ( 399) 935 222.4 2.9e-55
gi|6448794|gb|AAF08684.1| AF110509_1 delta-12 fatty ( 399) 935 222.4 2.9e-55
gi|27278519|gb|EAB93257.1| Sequence 20 from patent ( 399) 935 222.4 2.9e-55
gi|10055431|gb|AAE32337.1| Sequence 4 from patent ( 399) 935 222.4 2.9e-55
gi|5257239|dbj|BAA81754.1| delta-12 fatty acid des ( 400) 931 221.4 5.5e-55
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gi|16033621|gb|AAL13301.1| AF417245_1 delta 12 fatt ( 400) 929 221.0 7.6e-55

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gi 145025099 gb ABP24256.1	Sequence 54 from paten	( 400)	929	221.0	7.6e-55	gi 15823622 dbj BAB69056.1	delta-12 fatty acid de	( 396)	518	127.1	1.4e-26
gi 157677395 emb CAL69821.1	delta12 fatty acid de	( 354)	848	202.5	2.5e-49	gi 68124764 emb CAJ03117.1	fatty acid desaturase,	( 394)	513	126.0	3e-26
gi 45861536 gb AAS78627.1	delta-12 fatty acid des	( 446)	827	197.7	8.5e-48	gi 68124625 emb CAJ02312.1	fatty acid desaturase,	( 394)	513	126.0	3e-26
gi 51873230 gb AAU12575.1	delta-12 fatty acid des	( 446)	827	197.7	8.5e-48	gi 134059778 emb CAM37203.1	fatty acid desaturase	( 394)	511	125.5	4.1e-26
gi 3724332 dbj BAA33772.1	fatty acid desaturase [	( 193)	800	191.3	3e-46	gi 17402593 dbj BAB78716.1	delta12 fatty acid des	( 376)	510	125.3	4.7e-26
gi 88175663 gb EAQ83131.1	hypothetical protein CH	( 348)	799	191.3	5.8e-46	gi 68129162 emb CAJ06920.1	fatty acid desaturase,	( 394)	510	125.3	4.8e-26
gi 62084356 dbj BAD91495.1	omega3 desaturase [Mor	( 403)	779	186.7	1.6e-44	gi 134059919 emb CAM37348.1	fatty acid desaturase	( 394)	509	125.0	5.7e-26
gi 57226459 gb AAW42919.1	Delta-12 fatty acid des	( 448)	775	185.8	3.2e-44	gi 154702189 gb EDO01928.1	hypothetical protein S	( 337)	507	124.5	6.8e-26
gi 57226460 gb AAW42920.1	Delta-12 fatty acid des	( 448)	775	185.8	3.2e-44	gi 160812279 emb CAP40201.1	unnamed protein produ	( 384)	506	124.3	8.9e-26
gi 155322974 gb ABT78578.1	Sequence 166048 from p	( 282)	768	184.1	6.6e-44	gi 162771694 emb CAP58838.1	unnamed protein produ	( 384)	506	124.3	8.9e-26
gi 167286479 gb ABZ39343.1	Sequence 13281 from pa	( 251)	765	183.4	9.7e-44	gi 134072754 emb CAM71471.1	fatty acid desaturase	( 394)	503	123.7	1.5e-25
gi 22316679 emb CAD44412.1	unnamed protein produc	( 436)	765	183.5	1.5e-43	gi 134067875 emb CAM66157.1	fatty acid desaturase	( 394)	502	123.4	1.7e-25
gi 22316525 emb CAD44412.1	unnamed protein produc	( 436)	765	183.5	1.5e-43	gi 157361224 gb ABV44669.1	fatty acid desaturase-	( 390)	501	123.2	2e-25
gi 27883909 gb AAO23564.1	delta 12 fatty acid des	( 436)	765	183.5	1.5e-43	gi 102230628 gb ABF70295.1	delta-12 desaturase [B	( 261)	498	122.4	2.3e-25
gi 209582989 gb AC165609.1	delta 12 fatty acid de	( 436)	765	183.5	1.5e-43	gi 102230633 gb ABF70297.1	delta-12 desaturase [B	( 261)	498	122.4	2.3e-25
gi 76059324 emb CAJ30856.1	unnamed protein produc	( 434)	746	179.2	3.1e-42	gi 102230621 gb ABF70292.1	delta-12 desaturase [B	( 261)	498	122.4	2.3e-25
gi 126633858 emb CAM55885.1	unnamed protein produ	( 434)	746	179.2	3.1e-42	gi 102230625 gb ABF70294.1	delta-12 desaturase [B	( 261)	498	122.4	2.3e-25
gi 60220824 emb CAI58911.1	unnamed protein produc	( 434)	746	179.2	3.1e-42	gi 102230639 gb ABF70299.1	delta-12 desaturase [B	( 261)	498	122.4	2.3e-25
gi 170939665 emb CAP64892.1	unnamed protein produ	( 343)	687	165.7	2.9e-38	gi 102230631 gb ABF70296.1	delta-12 desaturase [B	( 261)	498	122.4	2.3e-25
gi 190347297 gb EDK39542.2	hypothetical protein P	( 417)	665	160.7	1.1e-36	gi 102230623 gb ABF70293.1	delta-12 desaturase [B	( 261)	498	122.4	2.3e-25
gi 49655606 emb CAG8811.1	DEHA2E14542p [Debaryom	( 435)	648	156.8	1.7e-35	gi 46399191 gb AAS92240.1	delta-12 oleate desatur	( 384)	500	123.0	2.3e-25
gi 146447730 gb EDK42118.1	hypothetical protein L	( 432)	641	155.2	5.1e-35	gi 1212781 emb CAA62578.1	oleate desaturase [Bras	( 384)	500	123.0	2.3e-25
gi 22316519 emb CAD44409.1	unnamed protein produc	( 495)	638	154.6	9.2e-35	gi 34600648 gb AAQ78505.1	Sequence 10 from patent	( 384)	500	123.0	2.3e-25
gi 22316673 emb CAD44439.1	unnamed protein produc	( 495)	638	154.6	9.2e-35	gi 102230701 gb ABF70327.1	delta-12 desaturase [R	( 261)	497	122.2	2.7e-25
gi 27883911 gb AAO23565.1	delta 12 fatty acid des	( 495)	638	154.6	9.2e-35	gi 160812277 emb CAP40200.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 52546174 dbj BAD51484.1	delta 12-fatty acid de	( 435)	635	153.8	1.3e-34	gi 5997736 gb AAE21283.1	Sequence 2 from patent U	( 384)	499	122.7	2.7e-25
gi 41529188 dbj BAD08375.1	delta 12-fatty acid de	( 416)	627	152.0	4.6e-34	gi 46518253 emb CAG26981.1	fatty acid desaturase	( 384)	499	122.7	2.7e-25
gi 146452188 gb EDK46444.1	hypothetical protein L	( 428)	620	150.4	1.4e-33	gi 40193151 gb AAR78123.1	Sequence 8 from patent	( 384)	499	122.7	2.7e-25
gi 164649561 gb EDR13803.1	delta-12 fatty acid de	( 440)	618	150.0	2e-33	gi 20230154 gb AAE91297.1	Sequence 6 from patent	( 384)	499	122.7	2.7e-25
gi 49644538 emb CAG98110.1	KLLA0F07095p [Kluyvero	( 410)	601	146.1	2.8e-32	gi 210028785 emb CAR94993.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 134056016 emb CAK37451.1	unnamed protein produ	( 393)	598	145.4	4.3e-32	gi 83349266 gb ABC14919.1	Sequence 14 from patent	( 384)	499	122.7	2.7e-25
gi 49657448 emb CAG90237.1	DEHA2G05346p [Debaryom	( 416)	589	143.3	1.9e-31	gi 189846873 gb ACE26371.1	Sequence 126 from pate	( 384)	499	122.7	2.7e-25
gi 126091907 gb ABN66656.1	oleate delta-12 desatu	( 418)	586	142.6	3e-31	gi 20230159 gb AAE91302.1	Sequence 16 from patent	( 384)	499	122.7	2.7e-25
gi 150856710 gb EDN31902.1	hypothetical protein B	( 389)	577	140.6	1.2e-30	gi 210028783 emb CAR94992.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 60459908 gb AAX20125.1	delta 12-fatty acid des	( 420)	576	140.4	1.5e-30	gi 213508651 emb CAS91773.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 190346683 gb EDK38830.2	hypothetical protein P	( 417)	571	139.2	3.2e-30	gi 83349268 gb ABC14921.1	Sequence 18 from patent	( 384)	499	122.7	2.7e-25
gi 49646573 emb CAG82952.1	YALI0B10153p [Yarrowia	( 419)	569	138.8	4.5e-30	gi 21507256 gb AAM57792.1	Sequence 4 from patent	( 384)	499	122.7	2.7e-25
gi 53952284 gb AAV02281.1	Sequence 14238 from pat	( 441)	569	138.8	4.7e-30	gi 83349263 gb ABC14916.1	Sequence 8 from patent	( 384)	499	122.7	2.7e-25
gi 150843820 gb EDN19013.1	hypothetical protein B	( 221)	558	136.1	1.5e-29	gi 33749919 gb AAQ46759.1	Sequence 6 from patent	( 384)	499	122.7	2.7e-25
gi 145025098 gb ABP24255.1	Sequence 51 from paten	( 419)	560	136.7	1.9e-29	gi 40193152 gb AAR78124.1	Sequence 10 from patent	( 384)	499	122.7	2.7e-25
gi 158475490 gb ABW48566.1	Sequence 49 from paten	( 419)	560	136.7	1.9e-29	gi 162771688 emb CAP58835.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 89254947 emb CAJ81209.1	unnamed protein produc	( 419)	560	136.7	1.9e-29	gi 40193155 gb AAR78127.1	Sequence 16 from patent	( 384)	499	122.7	2.7e-25
gi 155070723 gb ABS91068.1	Sequence 59 from paten	( 419)	560	136.7	1.9e-29	gi 20520624 emb CAD30827.1	fatty acid desaturase	( 384)	499	122.7	2.7e-25
gi 158457287 gb ABW41481.1	Sequence 147 from pate	( 419)	560	136.7	1.9e-29	gi 115833233 gb ABJ40711.1	Sequence 4 from patent	( 384)	499	122.7	2.7e-25
gi 144998360 gb ABP16933.1	Sequence 33 from paten	( 419)	560	136.7	1.9e-29	gi 160812273 emb CAP40198.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 148915386 emb CAO00418.1	unnamed protein produ	( 419)	560	136.7	1.9e-29	gi 210028787 emb CAR94994.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 55469813 gb AAV52631.1	delta-12-fatty acid des	( 389)	559	136.5	2e-29	gi 62789093 gb AAQ07976.1	Sequence 4 from patent	( 384)	499	122.7	2.7e-25
gi 44885796 dbj BAD11952.1	omega-3 fatty acid des	( 419)	557	136.0	3e-29	gi 20230160 gb AAE91303.1	Sequence 18 from patent	( 384)	499	122.7	2.7e-25
gi 48994801 gb AAT48093.1	delta-12 fatty acid des	( 389)	555	135.5	3.9e-29	gi 189704780 gb ACE16109.1	Sequence 126 from pate	( 384)	499	122.7	2.7e-25
gi 49246463 gb AAT58363.1	delta-12-fatty acid des	( 389)	555	135.5	3.9e-29	gi 87055229 gb AAF78778.1	delta-12 oleate desatura	( 384)	499	122.7	2.7e-25
gi 49640683 emb CAH01944.1	KLLA0B00473p [Kluyvero	( 415)	551	134.6	7.7e-29	gi 20230158 gb AAE91301.1	Sequence 14 from patent	( 384)	499	122.7	2.7e-25
gi 119352252 gb ABL63813.1	delta 15-fatty acid de	( 415)	548	134.0	1.2e-28	gi 40193156 gb AAR78128.1	Sequence 18 from patent	( 384)	499	122.7	2.7e-25
gi 44985182 gb AAS53960.1	AFR589Cp [Ashbya gossyp	( 413)	545	133.3	2e-28	gi 20230156 gb AAE91299.1	Sequence 10 from patent	( 384)	499	122.7	2.7e-25
gi 123720728 dbj BAF45335.1	fatty acid desaturase	( 441)	540	132.1	4.6e-28	gi 213508653 emb CAS91774.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 24298827 dbj BAC22091.1	delta-12 desaturase [S	( 382)	528	129.4	2.7e-27	gi 75205881 gb ABA17985.1	Sequence 4 from patent	( 384)	499	122.7	2.7e-25
gi 134065453 emb CAM40887.1	fatty acid desaturase	( 394)	524	128.5	5.3e-27	gi 162771692 emb CAP58837.1	unnamed protein produ	( 384)	499	122.7	2.7e-25
gi 125599973 gb EAZ239549.1	hypothetical protein O	( 362)	521	127.8	7.9e-27	gi 83349262 gb ABC14915.1	Sequence 6 from patent	( 384)	499	122.7	2.7e-25
gi 125558094 gb EAO203630.1	hypothetical protein O	( 390)	518	127.1	1.4e-26	gi 158473902 gb ABW47802.1	Sequence 8 from patent	( 384)	499	122.7	2.7e-25

gi 210028775 emb CAR94988.1  unnamed protein produ	(384)	499	122.7	2.7e-25	gi 118901300 gb ABL51015.1  Sequence 2 from patent	(384)	489	120.5	1.3e-24
gi 83349264 gb ABC14917.1  Sequence 10 from patent	(384)	499	122.7	2.7e-25	gi 102230697 gb ABF70326.1  delta-12 desaturase [R	(260)	486	119.7	1.5e-24
gi 210028773 emb CAR94987.1  unnamed protein produ	(384)	499	122.7	2.7e-25	gi 102230655 gb ABF70307.1  delta-12 desaturase [E	(260)	486	119.7	1.5e-24
gi 118901302 gb ABL51017.1  Sequence 6 from patent	(384)	499	122.7	2.7e-25	gi 102230658 gb ABF70308.1  delta-12 desaturase [E	(260)	486	119.7	1.5e-24
gi 118901303 gb ABL51018.1  Sequence 8 from patent	(384)	499	122.7	2.7e-25	gi 56666937 gb AAW18476.1  Sequence 4 from patent	(383)	488	120.2	1.5e-24
gi 6778901 emb CAB70436.1  unnamed protein product	(384)	499	122.7	2.7e-25	gi 17909752 gb AAE82559.1  Sequence 6 from patent	(383)	488	120.2	1.5e-24
gi 40193150 gb AAR78122.1  Sequence 6 from patent	(384)	499	122.7	2.7e-25	gi 12322004 gb AAG51042.1 AC069473_4 omega-6 fatty	(383)	488	120.2	1.5e-24
gi 217272163 gb ACK28081.1  Sequence 2 from patent	(384)	499	122.7	2.7e-25	gi 14517474 gb AAK62627.1  AT3g12120/T21B14_107 [A	(383)	488	120.2	1.5e-24
gi 23334555 gb AAN27913.1  Sequence 6 from patent	(384)	499	122.7	2.7e-25	gi 21536781 gb AAM61113.1  omega-6 fatty acid desa	(383)	488	120.2	1.5e-24
gi 20230155 gb AAE91298.1  Sequence 8 from patent	(384)	499	122.7	2.7e-25	gi 5955846 gb AAE07502.1  Sequence 41 from patent	(383)	488	120.2	1.5e-24
gi 40193154 gb AAR78126.1  Sequence 14 from patent	(384)	499	122.7	2.7e-25	gi 22655458 gb AAM98321.1  At3g12120/T21B14_107 [A	(383)	488	120.2	1.5e-24
gi 158473901 gb ABW47801.1  Sequence 6 from patent	(384)	499	122.7	2.7e-25	gi 189704779 gb ACE16108.1  Sequence 125 from pate	(383)	488	120.2	1.5e-24
gi 83349267 gb ABC14920.1  Sequence 16 from patent	(384)	499	122.7	2.7e-25	gi 189846872 gb ACE26370.1  Sequence 125 from pate	(383)	488	120.2	1.5e-24
gi 91148810 gb ABE23044.1  Sequence 3 from patent	(392)	499	122.8	2.7e-25	gi 115833232 gb ABJ40710.1  Sequence 2 from patent	(383)	488	120.2	1.5e-24
gi 102230616 gb ABF70290.1  delta-12 desaturase [B	(260)	496	122.0	3.1e-25	gi 34600647 gb AAQ78504.1  Sequence 9 from patent	(383)	488	120.2	1.5e-24
gi 102230614 gb ABF70289.1  delta-12 desaturase [B	(261)	496	122.0	3.1e-25	gi 438451 gb AAA32782.1  delta-12 desaturase	(383)	488	120.2	1.5e-24
gi 149395006 gb ABR27357.1  fatty acid desaturase	(384)	498	122.5	3.2e-25	gi 110623202 emb CAL24241.1  unnamed protein produ	(383)	488	120.2	1.5e-24
gi 115833235 gb ABJ40713.1  Sequence 8 from patent	(387)	498	122.5	3.2e-25	gi 62789092 gb AAJ07975.1  Sequence 2 from patent	(383)	488	120.2	1.5e-24
gi 194688628 gb ACF78398.1  unknown [Zea mays]	(387)	498	122.5	3.2e-25	gi 2492223 gb AAB80359.1 I66170 Sequence 41 from p	(383)	488	120.2	1.5e-24
gi 21507259 gb AAM57794.1  Sequence 8 from patent	(387)	498	122.5	3.2e-25	gi 21507255 gb AAM57791.1  Sequence 2 from patent	(383)	488	120.2	1.5e-24
gi 62789095 gb AAJ07978.1  Sequence 8 from patent	(387)	498	122.5	3.2e-25	gi 75205880 gb ABA17984.1  Sequence 2 from patent	(383)	488	120.2	1.5e-24
gi 75205883 gb ABA17987.1  Sequence 8 from patent	(387)	498	122.5	3.2e-25	gi 110623200 emb CAL24240.1  unnamed protein produ	(383)	488	120.2	1.5e-24
gi 126633152 emb CAM55541.1  unnamed protein produ	(446)	499	122.6	3.6e-25	gi 9294109 dbj BAB01960.1  omega-6 fatty acid desa	(383)	488	120.2	1.5e-24
gi 4378875 gb AAD19742.1  delta-12 desaturase [Bra	(384)	497	122.3	3.7e-25	gi 17918535 gb AAE85969.1  Sequence 6 from patent	(383)	488	120.2	1.5e-24
gi 46849977 gb AAT02411.1  delta-12 oleate desatur	(384)	497	122.3	3.7e-25	gi 91125671 gb ABE12619.1  Sequence 32 from patent	(383)	488	120.2	1.5e-24
gi 102230693 gb ABF70324.1  delta-12 desaturase [O	(260)	494	121.5	4.3e-25	gi 71057275 emb CAJ18799.1  unnamed protein produc	(383)	488	120.2	1.5e-24
gi 195631540 gb ACG36665.1  omega-6 fatty acid des	(392)	495	121.8	5.2e-25	gi 76007349 gb ABA38263.1  Sequence 6 from patent	(383)	488	120.2	1.5e-24
gi 110623218 emb CAL24249.1  unnamed protein produ	(392)	495	121.8	5.2e-25	gi 125661169 gb ABN49520.1  fatty acid desaturase	(385)	488	120.2	1.5e-24
gi 195624882 gb ACG34271.1  omega-6 fatty acid des	(392)	495	121.8	5.2e-25	gi 92380879 dbj BAE93382.1  delta-12 fatty acid de	(387)	488	120.2	1.6e-24
gi 110623216 emb CAL24248.1  unnamed protein produ	(392)	495	121.8	5.2e-25	gi 94982471 gb ABF50053.1  FAD2 [Zea mays]	(387)	488	120.2	1.6e-24
gi 126633352 emb CAM55641.1  unnamed protein produ	(452)	495	121.9	5.8e-25	gi 195635929 gb ACG37433.1  omega-6 fatty acid des	(394)	488	120.2	1.6e-24
gi 102230612 gb ABF70288.1  delta-12 desaturase [B	(261)	492	121.1	5.9e-25	gi 102230682 gb ABF70319.1  delta-12 desaturase [I	(260)	485	119.5	1.8e-24
gi 40193153 gb AAR78125.1  Sequence 12 from patent	(384)	494	121.6	6e-25	gi 102230669 gb ABF70313.1  delta-12 desaturase [C	(260)	485	119.5	1.8e-24
gi 20230157 gb AAE91300.1  Sequence 12 from patent	(384)	494	121.6	6e-25	gi 5997738 gb AAE21285.1  Sequence 6 from patent U	(384)	487	120.0	1.8e-24
gi 83349265 gb ABC14918.1  Sequence 12 from patent	(384)	494	121.6	6e-25	gi 168805244 gb ACA28704.1  fatty acid desaturase	(387)	487	120.0	1.8e-24
gi 217272164 gb ACK28082.1  Sequence 4 from patent	(384)	494	121.6	6e-25	gi 102230703 gb ABF70328.1  delta-12 desaturase [S	(262)	483	119.0	2.5e-24
gi 102230671 gb ABF70314.1  delta-12 desaturase [C	(261)	491	120.8	6.9e-25	gi 189846864 gb ACE26362.1  Sequence 35 from paten	(383)	485	119.6	2.5e-24
gi 210028777 emb CAR94989.1  unnamed protein produ	(384)	492	121.1	8.2e-25	gi 189704771 gb ACE16100.1  Sequence 35 from paten	(383)	485	119.6	2.5e-24
gi 102230695 gb ABF70325.1  delta-12 desaturase [R	(260)	489	120.4	9.5e-25	gi 189704767 gb ACE16096.1  Sequence 22 from paten	(384)	485	119.6	2.5e-24
gi 217272165 gb ACK28083.1  Sequence 6 from patent	(384)	491	120.9	9.6e-25	gi 189846860 gb ACE26358.1  Sequence 22 from paten	(384)	485	119.6	2.5e-24
gi 217272166 gb ACK28084.1  Sequence 8 from patent	(384)	491	120.9	9.6e-25	gi 3135020 emb CAA76157.1  delta 12 fatty acid des	(379)	484	119.3	2.9e-24
gi 102230665 gb ABF70311.1  delta-12 desaturase [C	(260)	488	120.1	1.1e-24	gi 102230641 gb ABF70300.1  delta-12 desaturase [B	(260)	482	118.8	2.9e-24
gi 102230684 gb ABF70320.1  delta-12 desaturase [I	(260)	488	120.1	1.1e-24	gi 102230649 gb ABF70304.1  delta-12 desaturase [C	(260)	482	118.8	2.9e-24
gi 102230667 gb ABF70312.1  delta-12 desaturase [C	(260)	488	120.1	1.1e-24	gi 102230647 gb ABF70303.1  delta-12 desaturase [C	(260)	482	118.8	2.9e-24
gi 102230686 gb ABF70321.1  delta-12 desaturase [I	(260)	488	120.1	1.1e-24	gi 102230643 gb ABF70301.1  delta-12 desaturase [B	(260)	482	118.8	2.9e-24
gi 102230610 gb ABF70287.1  delta-12 desaturase [A	(260)	488	120.1	1.1e-24	gi 33749918 gb AAQ46758.1  Sequence 4 from patent	(384)	484	119.3	2.9e-24
gi 102230660 gb ABF70309.1  delta-12 desaturase [C	(261)	488	120.1	1.1e-24	gi 83349261 gb ABC14914.1  Sequence 4 from patent	(384)	484	119.3	2.9e-24
gi 189704761 gb ACE16090.1  Sequence 16 from paten	(384)	490	120.7	1.1e-24	gi 23334554 gb AAN27912.1  Sequence 4 from patent	(384)	484	119.3	2.9e-24
gi 189846854 gb ACE26352.1  Sequence 16 from paten	(384)	490	120.7	1.1e-24	gi 158473900 gb ABW47800.1  Sequence 4 from patent	(384)	484	119.3	2.9e-24
gi 17909753 gb AAE82560.1  Sequence 7 from patent	(383)	489	120.5	1.3e-24	gi 40193149 gb AAR78121.1  Sequence 4 from patent	(384)	484	119.3	2.9e-24
gi 20230152 gb AAE91295.1  Sequence 2 from patent	(384)	489	120.5	1.3e-24	gi 118901301 gb ABL51016.1  Sequence 4 from patent	(384)	484	119.3	2.9e-24
gi 158473899 gb ABW47799.1  Sequence 2 from patent	(384)	489	120.5	1.3e-24	gi 20230153 gb AAE91296.1  Sequence 4 from patent	(384)	484	119.3	2.9e-24
gi 23334553 gb AAN27911.1  Sequence 2 from patent	(384)	489	120.5	1.3e-24	gi 217072516 gb ACJ84618.1  unknown [Medicago trun	(411)	484	119.3	3.1e-24
gi 40193148 gb AAR78120.1  Sequence 2 from patent	(384)	489	120.5	1.3e-24	gi 102230688 gb ABF70322.1  delta-12 desaturase [P	(259)	480	118.3	3.9e-24
gi 83349260 gb ABC14913.1  Sequence 2 from patent	(384)	489	120.5	1.3e-24	gi 102230677 gb ABF70317.1  delta-12 desaturase [E	(260)	480	118.3	3.9e-24
gi 17918536 gb AAE85970.1  Sequence 7 from patent	(384)	489	120.5	1.3e-24	gi 102230645 gb ABF70302.1  delta-12 desaturase [C	(260)	480	118.3	3.9e-24
gi 33749917 gb AAQ46757.1  Sequence 2 from patent	(384)	489	120.5	1.3e-24	gi 102230635 gb ABF70298.1  delta-12 desaturase [B	(261)	480	118.3	4e-24
gi 76007350 gb ABA38264.1  Sequence 7 from patent	(384)	489	120.5	1.3e-24	gi 5997737 gb AAE21284.1  Sequence 4 from patent U	(384)	482	118.9	4e-24

gi 102230662 gb ABF70310.1  delta-12 desaturase [C ( 260) 479 118.1 4.6e-24	gi 28371827 gb AAO37754.1  delta-12 oleate desatur ( 387) 467 115.4 4.3e-23
gi 23428547 gb AAL23676.1  delta-12 fatty acid des ( 382) 480 118.4 5.4e-24	gi 110623226 emb CAL24253.1  unnamed protein produ ( 341) 466 115.2 4.5e-23
gi 102230705 gb ABF70329.1  delta-12 desaturase [T ( 260) 477 117.6 6.3e-24	gi 110623224 emb CAL24252.1  unnamed protein produ ( 341) 466 115.2 4.5e-23
gi 6118361 gb AAF04094.1 AF188264_1 delta-12 oleat ( 383) 479 118.2 6.4e-24	gi 60392519 gb AAX19366.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 102230651 gb ABF70305.1  delta-12 desaturase [C ( 260) 476 117.4 7.4e-24	gi 60392517 gb AAX19365.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 102230653 gb ABF70306.1  delta-12 desaturase [C ( 260) 476 117.4 7.4e-24	gi 18418653 gb AAL68983.1 AF251844_1 delta-12 olea ( 382) 464 114.8 6.9e-23
gi 147776501 emb CAN71892.1  hypothetical protein ( 382) 478 118.0 7.5e-24	gi 60392525 gb AAX19369.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 157348500 emb CAO23392.1  unnamed protein produ ( 382) 478 118.0 7.5e-24	gi 60392531 gb AAX19372.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 17918533 gb AAE85967.1  Sequence 4 from patent ( 384) 478 118.0 7.5e-24	gi 60392523 gb AAX19368.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 17909750 gb AAE82557.1  Sequence 4 from patent ( 384) 478 118.0 7.5e-24	gi 60392527 gb AAX19370.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 3452129 gb AAC32755.1  bifunctional oleate 12-h ( 384) 478 118.0 7.5e-24	gi 60392529 gb AAX19371.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 76007347 gb ABA38261.1  Sequence 4 from patent ( 384) 478 118.0 7.5e-24	gi 60392537 gb AAX19375.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 193290416 gb ACF17571.1  mutant bifunctional ol ( 355) 476 117.5 9.7e-24	gi 60392533 gb AAX19373.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 189704759 gb ACE16088.1  Sequence 14 from paten ( 384) 476 117.5 1e-23	gi 60392535 gb AAX19374.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 189846852 gb ACE26350.1  Sequence 14 from paten ( 384) 476 117.5 1e-23	gi 60392521 gb AAX19367.1  delta-12 oleate desatur ( 382) 464 114.8 6.9e-23
gi 154813798 gb ABS86964.1  delta-12 fatty acid de ( 383) 475 117.3 1.2e-23	gi 140421522 gb ECL64495.1  hypothetical protein G ( 284) 462 114.2 7.3e-23
gi 189860252 gb ACE35658.1  Sequence 2 from patent ( 383) 474 117.0 1.4e-23	gi 60392578 gb AAX19395.1  delta-12 oleate desatur ( 383) 463 114.5 8.1e-23
gi 8886726 gb AAF80560.1 AF192486_1 omega-6 fatty ( 383) 474 117.0 1.4e-23	gi 18418651 gb AAL68982.1 AF251843_1 delta-12 olea ( 383) 463 114.5 8.1e-23
gi 189704782 gb ACE16111.1  Sequence 128 from pate ( 383) 474 117.0 1.4e-23	gi 60392580 gb AAX19396.1  delta-12 oleate desatur ( 383) 463 114.5 8.1e-23
gi 189846875 gb ACE26373.1  Sequence 128 from pate ( 383) 474 117.0 1.4e-23	gi 60392574 gb AAX19393.1  delta-12 oleate desatur ( 383) 463 114.5 8.1e-23
gi 59896214 gb AAX11454.1  microsomal oleic acid d ( 383) 474 117.0 1.4e-23	gi 60392572 gb AAX19392.1  delta-12 oleate desatur ( 383) 463 114.5 8.1e-23
gi 189846855 gb ACE26353.1  Sequence 17 from paten ( 384) 474 117.0 1.4e-23	gi 60392576 gb AAX19394.1  delta-12 oleate desatur ( 383) 463 114.5 8.1e-23
gi 189704776 gb ACE16105.1  Sequence 40 from paten ( 384) 474 117.0 1.4e-23	gi 29536061 emb CAD87608.1  unnamed protein produc ( 387) 463 114.5 8.1e-23
gi 189846869 gb ACE26367.1  Sequence 40 from paten ( 384) 474 117.0 1.4e-23	gi 28564441 emb CAD24671.1  delta 12-acyl-lipid-de ( 387) 463 114.5 8.1e-23
gi 189704762 gb ACE16091.1  Sequence 17 from paten ( 384) 474 117.0 1.4e-23	gi 116001287 emb CAL49895.1  unnamed protein produ ( 398) 463 114.5 8.3e-23
gi 189846880 gb ACE26378.1  Sequence 138 from pate ( 384) 474 117.0 1.4e-23	gi 77920892 gb ABB05230.1  delta 12 desaturase [Li ( 378) 462 114.3 9.3e-23
gi 2501790 gb AAB80696.1  omega-6 fatty acid desat ( 382) 473 116.8 1.6e-23	gi 42541363 gb AAS19533.1  omega-6 fatty acid desa ( 383) 462 114.3 9.4e-23
gi 76059404 emb CAJ30867.1  unnamed protein produc ( 383) 473 116.8 1.7e-23	gi 194346324 gb ACF49508.1  omega-6 desaturase [Li ( 378) 461 114.1 1.1e-22
gi 2501792 gb AAB80697.1  fungal elicitor-induced ( 383) 473 116.8 1.7e-23	gi 33358366 gb AAQ16654.1  delta-12 fatty acid des ( 384) 461 114.1 1.1e-22
gi 6118359 gb AAF04093.1 AF188263_1 delta-12 oleat ( 383) 473 116.8 1.7e-23	gi 33358364 gb AAQ16653.1  delta-12 fatty acid des ( 384) 461 114.1 1.1e-22
gi 17382283 emb CAD13056.1  unnamed protein produc ( 383) 473 116.8 1.7e-23	gi 189846870 gb ACE26368.1  Sequence 41 from paten ( 374) 460 113.8 1.3e-22
gi 13447102 gb AAK26633.1 AF343065_1 delta-12 fatt ( 383) 473 116.8 1.7e-23	gi 189704777 gb ACE16106.1  Sequence 41 from paten ( 374) 460 113.8 1.3e-22
gi 189846877 gb ACE26375.1  Sequence 135 from pate ( 374) 472 116.6 1.9e-23	gi 84626279 gb ABC59684.1  delta-12 fatty acid ace ( 377) 460 113.8 1.3e-22
gi 102230675 gb ABF70316.1  delta-12 desaturase [C ( 260) 470 116.0 1.9e-23	gi 102230691 gb ABF70323.1  delta-12 desaturase [L ( 260) 458 113.3 1.3e-22
gi 58013373 gb AAW63040.1  microsomal delta-12 ole ( 381) 471 116.4 2.3e-23	gi 17225582 gb AAL37484.1 AF331163_1 delta-12 fatt ( 384) 460 113.8 1.3e-22
gi 189704766 gb ACE16095.1  Sequence 21 from paten ( 383) 471 116.4 2.3e-23	gi 31322135 gb AAO38032.1  delta12-fatty acid acet ( 377) 459 113.6 1.5e-22
gi 189846859 gb ACE26357.1  Sequence 21 from paten ( 383) 471 116.4 2.3e-23	gi 102230673 gb ABF70315.1  delta-12 desaturase [C ( 260) 457 113.1 1.5e-22
gi 102230679 gb ABF70318.1  delta-12 desaturase [E ( 260) 468 115.6 2.6e-23	gi 10863190 gb AAG23929.1 AF239833_1 ELI7.8 [Petro ( 382) 459 113.6 1.5e-22
gi 189846862 gb ACE26360.1  Sequence 24 from paten ( 380) 470 116.1 2.6e-23	gi 58013375 gb AAW63041.1  microsomal delta-12 ole ( 383) 459 113.6 1.5e-22
gi 189704769 gb ACE16098.1  Sequence 24 from paten ( 380) 470 116.1 2.6e-23	gi 68146846 emb CAI48076.2  omega-6 desaturase [Ca ( 306) 457 113.1 1.7e-22
gi 146141441 gb ABQ01458.1  oleate 12-hydroxylase ( 383) 470 116.1 2.7e-23	gi 22532409 gb AAM97924.1  delta-12 desaturase [Mu ( 396) 458 113.4 1.8e-22
gi 59956946 dbj BAD98862.1  microsomal omega-6 fat ( 383) 470 116.1 2.7e-23	gi 3264765 gb AAC24586.1  omega-6 fatty acid desat ( 346) 457 113.1 1.9e-22
gi 110623210 emb CAL24245.1  unnamed protein produ ( 383) 470 116.1 2.7e-23	gi 145280641 gb ABP49577.1  oleate desaturase [Car ( 383) 457 113.2 2.1e-22
gi 76257461 gb ABA41034.1  delta12-fatty acid desa ( 383) 470 116.1 2.7e-23	gi 10863182 gb AAG23925.1 AF239829_1 ELI7.4 [Petro ( 384) 457 113.2 2.1e-22
gi 107785184 gb ABF84063.1  microsomal oleate desa ( 383) 470 116.1 2.7e-23	gi 102230619 gb ABF70291.1  delta-12 desaturase [B ( 265) 455 112.6 2.1e-22
gi 110623208 emb CAL24244.1  unnamed protein produ ( 383) 470 116.1 2.7e-23	gi 5917670 gb AAD55982.1  delta-12 desaturase [Muc ( 396) 457 113.2 2.1e-22
gi 10278514 emb CAC09644.1  unnamed protein produc ( 374) 469 115.9 3.1e-23	gi 17909756 gb AAE82563.1  Sequence 10 from patent ( 371) 456 112.9 2.4e-22
gi 3135018 emb CAA76156.1  delta 12 fatty acid epo ( 374) 469 115.9 3.1e-23	gi 17918539 gb AAE85973.1  Sequence 10 from patent ( 372) 456 112.9 2.4e-22
gi 34600643 gb AAQ78500.1  Sequence 2 from patent ( 374) 469 115.9 3.1e-23	gi 76007353 gb ABA38267.1  Sequence 10 from patent ( 372) 456 112.9 2.4e-22
gi 189846853 gb ACE26351.1  Sequence 15 from paten ( 383) 469 115.9 3.1e-23	gi 189704763 gb ACE16092.1  Sequence 18 from paten ( 374) 456 112.9 2.4e-22
gi 189704760 gb ACE16089.1  Sequence 15 from paten ( 383) 469 115.9 3.1e-23	gi 189846856 gb ACE26354.1  Sequence 18 from paten ( 374) 456 112.9 2.4e-22
gi 189704765 gb ACE16094.1  Sequence 20 from paten ( 384) 469 115.9 3.1e-23	gi 13560785 gb AAK30206.1 AF349965_1 fatty acid de ( 383) 456 112.9 2.4e-22
gi 189846858 gb ACE26356.1  Sequence 20 from paten ( 384) 469 115.9 3.1e-23	gi 25989476 gb AAL93620.1  fatty acid desaturase 2 ( 383) 456 112.9 2.4e-22
gi 189846879 gb ACE26377.1  Sequence 137 from pate ( 374) 468 115.7 3.6e-23	gi 1161568 emb CAA64414.1  lipid desaturase-like p ( 333) 455 112.7 2.5e-22
gi 194346322 gb ACF49507.1  omega-6 desaturase [Li ( 382) 467 115.4 4.3e-23	gi 904154 gb AAB00860.1  microsomal omega-6 desatu ( 383) 455 112.7 2.9e-22
gi 117957296 gb ABK59093.1  oleate desaturase [Ric ( 383) 467 115.4 4.3e-23	gi 189704781 gb ACE16110.1  Sequence 127 from pate ( 383) 455 112.7 2.9e-22
gi 189846861 gb ACE26359.1  Sequence 23 from paten ( 384) 467 115.4 4.3e-23	gi 68164987 gb AAY87459.1  omega-6 fatty acid desa ( 383) 455 112.7 2.9e-22
gi 189704768 gb ACE16097.1  Sequence 23 from paten ( 384) 467 115.4 4.3e-23	gi 10863178 gb AAG23923.1 AF239827_1 ELI7.1 [Petro ( 383) 455 112.7 2.9e-22

gi 91125670 gb ABE12618.1  Sequence 31 from patent ( 383)	455	112.7	2.9e-22	gi 2564237 emb CAA71199.1  omega-6 desaturase [Gos ( 383)	444	110.2	1.6e-21
gi 34600649 gb AAQ78506.1  Sequence 11 from patent ( 383)	455	112.7	2.9e-22	gi 155713304 gb ABU35460.1  Sequence 24 from patent ( 387)	444	110.2	1.6e-21
gi 189846874 gb ACE26372.1  Sequence 127 from pate ( 383)	455	112.7	2.9e-22	gi 165882019 gb ABY71269.1  delta-12 fatty acid de ( 234)	441	109.4	1.7e-21
gi 10863188 gb AAG23928.1 AF239832_1 ELI7.7 [Petro ( 384)	455	112.7	2.9e-22	gi 33766648 gb AAQ52851.1  Sequence 2 from patent ( 374)	443	110.0	1.9e-21
gi 10863186 gb AAG23927.1 AF239831_1 ELI7.6 [Petro ( 384)	455	112.7	2.9e-22	gi 17382281 emb CAD13055.1  unnamed protein produc ( 374)	443	110.0	1.9e-21
gi 154701225 gb ED000964.1  hypothetical protein S ( 221)	452	111.9	2.9e-22	gi 155689125 gb ABU29135.1  Sequence 2 from patent ( 374)	443	110.0	1.9e-21
gi 10863180 gb AAG23924.1 AF239828_1 ELI7.2 [Petro ( 383)	454	112.5	3.3e-22	gi 11991241 gb AAG42259.1 AF310155_1 FadX-1 [Calen ( 374)	443	110.0	1.9e-21
gi 155295241 gb ABT50845.1  Sequence 138315 from p ( 185)	450	111.4	3.4e-22	gi 13447100 gb AAK26632.1 AF343064_1 fatty acid co ( 374)	443	110.0	1.9e-21
gi 33766658 gb AAQ52861.1  Sequence 15 from patent ( 383)	453	112.2	3.9e-22	gi 13275554 emb CAC34032.1  unnamed protein produc ( 374)	443	110.0	1.9e-21
gi 155689135 gb ABU29145.1  Sequence 15 from paten ( 383)	453	112.2	3.9e-22	gi 189704764 gb ACE16093.1  Sequence 19 from paten ( 383)	443	110.0	1.9e-21
gi 3417601 gb AAC31698.1  delta-12 fatty acid desa ( 383)	453	112.2	3.9e-22	gi 189846857 gb ACE26355.1  Sequence 19 from paten ( 383)	443	110.0	1.9e-21
gi 215697837 dbj BAG92030.1  unnamed protein produ ( 390)	453	112.2	4e-22	gi 110623214 emb CAL24247.1  unnamed protein produ ( 218)	440	109.1	1.9e-21
gi 113611002 dbj BAF21380.1  Os07g0416900 [Oryza s ( 390)	453	112.2	4e-22	gi 110623212 emb CAL24246.1  unnamed protein produ ( 218)	440	109.1	1.9e-21
gi 27261056 dbj BAC45170.1  putative delta 12 olei ( 390)	453	112.2	4e-22	gi 155713303 gb ABU35459.1  Sequence 20 from paten ( 387)	443	110.0	1.9e-21
gi 34600644 gb AAQ78501.1  Sequence 4 from patent ( 374)	452	112.0	4.5e-22	gi 155689131 gb ABU29141.1  Sequence 9 from patent ( 387)	443	110.0	1.9e-21
gi 10278516 emb CAC09645.1  unnamed protein produc ( 374)	452	112.0	4.5e-22	gi 33766654 gb AAQ52857.1  Sequence 9 from patent ( 387)	443	110.0	1.9e-21
gi 10863192 gb AAG23930.1 AF239834_1 ELI7.9 [Petro ( 376)	452	112.0	4.5e-22	gi 198444772 gb ACH88346.1  omega-6 fatty acid des ( 173)	438	108.6	2.2e-21
gi 115392237 gb ABT96919.1  delta-12 fatty acid de ( 381)	452	112.0	4.6e-22	gi 83702515 gb ABC41578.1  endoplasmic reticulum 1 ( 388)	442	109.7	2.3e-21
gi 55509203 gb AAV52834.1  delta-12 fatty acid des ( 383)	452	112.0	4.6e-22	gi 31322141 gb AAO38035.1  delta12-fatty acid acet ( 326)	441	109.5	2.3e-21
gi 51556906 gb AAT72296.2  microsomal omega-6-desa ( 383)	452	112.0	4.6e-22	gi 107785182 gb ABF84062.1  microsomal oleate desa ( 387)	441	109.5	2.6e-21
gi 10863184 gb AAG23926.1 AF239830_1 ELI7.5 [Petro ( 384)	452	112.0	4.6e-22	gi 31322137 gb AAO38033.1  delta12-fatty acid acet ( 324)	440	109.2	2.7e-21
gi 110623234 emb CAL24257.1  unnamed protein produ ( 387)	450	111.6	6.4e-22	gi 148917610 emb CAO00496.1  unnamed protein produ ( 407)	441	109.5	2.8e-21
gi 110623232 emb CAL24256.1  unnamed protein produ ( 387)	450	111.6	6.4e-22	gi 148917612 emb CAO00497.1  unnamed protein produ ( 407)	441	109.5	2.8e-21
gi 147819968 emb CAN73788.1  hypothetical protein ( 366)	449	111.3	7.1e-22	gi 116672830 gb ABK15557.1  bi-functional microsom ( 407)	441	109.5	2.8e-21
gi 147858117 emb CAN79670.1  hypothetical protein ( 376)	449	111.3	7.3e-22	gi 189704770 gb ACE16099.1  Sequence 34 from paten ( 383)	440	109.3	3.1e-21
gi 157337660 emb CAO22006.1  unnamed protein produ ( 376)	449	111.3	7.3e-22	gi 27261181 gb AAN87573.1  delta 12 oleic acid des ( 383)	440	109.3	3.1e-21
gi 34600650 gb AAQ78507.1  Sequence 12 from patent ( 383)	448	111.1	8.7e-22	gi 189846863 gb ACE26361.1  Sequence 34 from paten ( 383)	440	109.3	3.1e-21
gi 1054843 emb CAA63432.1  D12 oleate desaturase [ ( 383)	448	111.1	8.7e-22	gi 155295235 gb ABT50839.1  Sequence 138309 from p ( 387)	440	109.3	3.1e-21
gi 48431267 gb AAT44123.1  microsomal omega-6-desa ( 362)	447	110.9	9.7e-22	gi 148917614 emb CAO00498.1  unnamed protein produ ( 417)	440	109.3	3.3e-21
gi 10945375 gb AAG24521.1 AF239835_1 fatty acid de ( 383)	447	110.9	1e-21	gi 11991243 gb AAG42260.1 AF310156_1 FadX-2 [Calen ( 372)	439	109.0	3.5e-21
gi 110623228 emb CAL24254.1  unnamed protein produ ( 387)	447	110.9	1e-21	gi 155689126 gb ABU29136.1  Sequence 4 from patent ( 372)	439	109.0	3.5e-21
gi 59956944 dbj BAD89861.1  microsomal omega-6 fat ( 387)	447	110.9	1e-21	gi 13275556 emb CAC34033.1  unnamed protein produc ( 372)	439	109.0	3.5e-21
gi 110623230 emb CAL24255.1  unnamed protein produ ( 387)	447	110.9	1e-21	gi 33766649 gb AAQ52852.1  Sequence 4 from patent ( 372)	439	109.0	3.5e-21
gi 110623206 emb CAL24243.1  unnamed protein produ ( 387)	447	110.9	1e-21	gi 83272391 gb ABC00769.1  delta-12 fatty acid ace ( 375)	439	109.0	3.5e-21
gi 110623204 emb CAL24242.1  unnamed protein produ ( 387)	447	110.9	1e-21	gi 11991460 emb CAA76158.2  delta 12 fatty acid ac ( 375)	439	109.0	3.5e-21
gi 197111724 gb ACH43026.1  omega-6 fatty acid des ( 387)	447	110.9	1e-21	gi 83272395 gb ABC029144.1  delta-12 fatty acid des ( 377)	439	109.0	3.6e-21
gi 62358441 gb AAX78904.1  fatty acid desaturase, ( 408)	447	110.9	1.1e-21	gi 2578033 emb CAA65744.1  omega-6 desaturase [Gos ( 385)	439	109.0	3.6e-21
gi 33348439 gb AAQ15765.1  fatty acid desaturase, ( 408)	447	110.9	1.1e-21	gi 91125663 gb ABE12611.1  Sequence 4 from patent ( 385)	439	109.0	3.6e-21
gi 34551088 gb AAQ74969.1  oleate desaturase [Tryp ( 408)	447	110.9	1.1e-21	gi 31322139 gb AAO38034.1  delta12-fatty acid acet ( 324)	438	108.8	3.7e-21
gi 29536058 emb CAD87607.1  unnamed protein produc ( 374)	445	110.4	1.4e-21	gi 155102616 gb ABT03239.1  Sequence 48 from paten ( 412)	439	109.1	3.8e-21
gi 28564443 emb CAD24672.1  delta 12-acyl-lipid-co ( 374)	445	110.4	1.4e-21	gi 69061719 gb AAY99778.1  delta-12 oleate desatur ( 378)	438	108.8	4.2e-21
gi 5994481 gb AAE19894.1  Sequence 4 from patent U ( 384)	445	110.4	1.4e-21	gi 134284835 gb ABO69519.1  microsomal oleate desa ( 378)	438	108.8	4.2e-21
gi 45735853 dbj BAD12887.1  putative delta-12 olea ( 388)	445	110.4	1.4e-21	gi 134284837 gb ABO69520.1  microsomal oleate desa ( 378)	438	108.8	4.2e-21
gi 110623220 emb CAL24250.1  unnamed protein produ ( 388)	445	110.4	1.4e-21	gi 60392566 gb AAX19389.1  delta-12 oleate desatur ( 378)	438	108.8	4.2e-21
gi 42408040 dbj BAD09176.1  putative delta-12 olea ( 388)	445	110.4	1.4e-21	gi 155689134 gb ABU29144.1  Sequence 14 from paten ( 378)	438	108.8	4.2e-21
gi 113537458 dbj BAF09841.1  Os02g0716500 [Oryza s ( 388)	445	110.4	1.4e-21	gi 60418976 gb AAX19895.1  delta-12 oleate desatur ( 378)	438	108.8	4.2e-21
gi 125540897 gb EAY87292.1  hypothetical protein O ( 388)	445	110.4	1.4e-21	gi 2290404 gb AAB65146.1  delta-12 oleate desatura ( 378)	438	108.8	4.2e-21
gi 125583461 gb EAY224392.1  hypothetical protein O ( 388)	445	110.4	1.4e-21	gi 60418974 gb AAX19894.1  delta-12 oleate desatur ( 378)	438	108.8	4.2e-21
gi 110623222 emb CAL24251.1  unnamed protein produ ( 388)	445	110.4	1.4e-21	gi 33766657 gb AAQ52860.1  Sequence 14 from patent ( 378)	438	108.8	4.2e-21
gi 29536063 emb CAD87609.1  unnamed protein produc ( 395)	445	110.4	1.4e-21	gi 60392568 gb AAX19390.1  delta-12 oleate desatur ( 378)	438	108.8	4.2e-21
gi 28371825 gb AAO37753.1  fatty acid conjugase [P ( 395)	445	110.4	1.4e-21	gi 69061718 gb AAY99777.1  delta-12 oleate desatur ( 378)	438	108.8	4.2e-21
gi 197035436 gb ACH16336.1  Sequence 12 from paten ( 395)	445	110.4	1.4e-21	gi 60392564 gb AAX19388.1  delta-12 oleate desatur ( 378)	438	108.8	4.2e-21
gi 155356845 gb ABU12450.1  Sequence 199919 from p ( 174)	440	109.1	1.6e-21	gi 18418649 gb AAL68981.1 AF251842_1 delta-12 olea ( 378)	438	108.8	4.2e-21
gi 194702722 gb ACF85445.1  unknown [Zea mays] ( 382)	444	110.2	1.6e-21	gi 209967428 gb AJC02341.1  seed-specific oleoyl-p ( 378)	438	108.8	4.2e-21
gi 5994480 gb AAE19893.1  Sequence 2 from patent U ( 382)	444	110.2	1.6e-21	gi 60392570 gb AAX19391.1  delta-12 oleate desatur ( 378)	438	108.8	4.2e-21
gi 31322133 gb AAO38031.1  delta12-fatty acid acet ( 382)	444	110.2	1.6e-21	gi 197111722 gb ACH43025.1  omega-6 fatty acid des ( 387)	438	108.8	4.3e-21
gi 91125664 gb ABE12612.1  Sequence 6 from patent ( 383)	444	110.2	1.6e-21	gi 168014166 gb ACA14461.1  oleate desaturase [Car ( 283)	436	108.3	4.5e-21
gi 119655554 gb ABL86147.1  delta-12 oleic acid de ( 383)	444	110.2	1.6e-21	gi 125558079 gb EAO3615.1  hypothetical protein O ( 362)	436	108.3	5.5e-21

gi 113611003 dbj BAF21381.1  Os07g0417200 [Oryza s ( 362)	436	108.3	5.5e-21	gi 91125594 gb ABE12594.1  Sequence 2 from patent ( 387)	427	106.3	2.4e-20
gi 125599974 gb EAZ239550.1  hypothetical protein O ( 362)	436	108.3	5.5e-21	gi 189846851 gb ACE26349.1  Sequence 13 from paten ( 387)	427	106.3	2.4e-20
gi 27261059 dbj BAC45173.1  putative delta 12 olei ( 362)	436	108.3	5.5e-21	gi 155713302 gb ABU35458.1  Sequence 6 from patent ( 387)	427	106.3	2.4e-20
gi 18252115 gb AAL61826.1  putative delta12 acid d ( 255)	434	107.8	5.7e-21	gi 189846876 gb ACE26374.1  Sequence 134 from pate ( 399)	427	106.3	2.5e-20
gi 155713305 gb ABU35461.1  Sequence 28 from paten ( 255)	434	107.8	5.7e-21	gi 28371823 gb AAO37752.1  delta-12 oleate desatur ( 369)	425	105.8	3.2e-20
gi 168014138 gb ACA14460.1  oleate desaturase [Car ( 380)	436	108.4	5.8e-21	gi 13443733 emb CAC34898.1  unnamed protein produc ( 377)	425	105.8	3.3e-20
gi 4530970 emb CAA03835.1  DELTA-12 DESATURASE [Co ( 382)	436	108.4	5.8e-21	gi 6634080 emb CAB64256.1  (8,11)-linoleoyl desatu ( 377)	425	105.8	3.3e-20
gi 17225559 gb AAL37475.1 AF329635_1 delta-12 fatt ( 182)	432	107.3	5.9e-21	gi 123201159 gb ABM72767.1  fatty acid desaturase, ( 375)	423	105.4	4.5e-20
gi 45272283 gb AAS57577.1  delta12-oleic acid desa ( 382)	435	108.1	6.8e-21	gi 8980833 gb AAF82294.1  microsomal oleate desatu ( 379)	422	105.2	5.3e-20
gi 31322145 gb AAO38037.1  delta12-fatty acid acet ( 326)	434	107.9	6.9e-21	gi 67090583 gb AAY67653.1  oleate desaturase [Arac ( 379)	422	105.2	5.3e-20
gi 60594769 gb AAZ29989.1  microsomal omega-6-desa ( 379)	434	107.9	7.9e-21	gi 75205885 gb ABA17989.1  Sequence 12 from patent ( 387)	422	105.2	5.4e-20
gi 115833234 gb ABJ490712.1  Sequence 6 from patent ( 379)	434	107.9	7.9e-21	gi 62789097 gb AAY07980.1  Sequence 12 from patent ( 387)	422	105.2	5.4e-20
gi 62789094 gb AAY07977.1  Sequence 6 from patent ( 379)	434	107.9	7.9e-21	gi 21507261 gb AAM57796.1  Sequence 12 from patent ( 387)	422	105.2	5.4e-20
gi 21507257 gb AAM57793.1  Sequence 6 from patent ( 379)	434	107.9	7.9e-21	gi 115833238 gb ABJ40715.1  Sequence 12 from paten ( 387)	422	105.2	5.4e-20
gi 75205882 gb ABA17986.1  Sequence 6 from patent ( 379)	434	107.9	7.9e-21	gi 143073531 gb EDC62056.1  hypothetical protein G ( 271)	419	104.4	6.4e-20
gi 91125672 gb ABE12620.1  Sequence 33 from patent ( 387)	434	107.9	8e-21	gi 8980835 gb AAF82295.1  microsomal oleate desatu ( 379)	419	104.5	8.5e-20
gi 155689127 gb ABU29137.1  Sequence 5 from patent ( 387)	434	107.9	8e-21	gi 123960857 gb ABM75640.1  Fatty acid desaturase ( 405)	419	104.5	9e-20
gi 34600651 gb AAQ78508.1  Sequence 13 from patent ( 387)	434	107.9	8e-21	gi 31322143 gb AAO38036.1  delta12-fatty acid acet ( 326)	417	104.0	1e-19
gi 155713301 gb ABU35457.1  Sequence 5 from patent ( 387)	434	107.9	8e-21	gi 27261183 gb AAN87574.1  delta 12 fatty acid con ( 386)	417	104.0	1.2e-19
gi 33766650 gb AAQ52853.1  Sequence 5 from patent ( 387)	434	107.9	8e-21	gi 58578276 emb CAI48074.1  omega-6 fatty acid des ( 304)	415	103.5	1.3e-19
gi 59956942 dbj BAD9860.1  mocosomal omega-6 fat ( 387)	434	107.9	8e-21	gi 189704778 gb AAB84107.1  Sequence 42 from paten ( 377)	416	103.8	1.4e-19
gi 5994482 gb AAE19895.1  Sequence 5 from patent U ( 387)	434	107.9	8e-21	gi 189704772 gb ACE16101.1  Sequence 36 from paten ( 377)	416	103.8	1.4e-19
gi 904152 gb AAB00859.1  microsomal omega-6 desatu ( 387)	434	107.9	8e-21	gi 189846871 gb ACE26369.1  Sequence 42 from paten ( 377)	416	103.8	1.4e-19
gi 6063030 gb AAF03100.1 AF162199_1 oleate 12-hydr ( 189)	430	106.8	8.3e-21	gi 189846865 gb ACE26363.1  Sequence 36 from paten ( 377)	416	103.8	1.4e-19
gi 33766653 gb AAQ52856.1  Sequence 8 from patent ( 399)	430	107.0	1.5e-20	gi 189704774 gb ACE16103.1  Sequence 38 from paten ( 377)	416	103.8	1.4e-19
gi 155689130 gb ABU29140.1  Sequence 8 from patent ( 399)	430	107.0	1.5e-20	gi 189846867 gb ACE26365.1  Sequence 38 from paten ( 377)	416	103.8	1.4e-19
gi 155713300 gb ABU35456.1  Sequence 4 from patent ( 399)	430	107.0	1.5e-20	gi 2613051 gb AAB84262.1  omega-6 desaturase [Arac ( 379)	416	103.8	1.4e-19
gi 6224716 gb AAF05916.1 AF182521_1 delta-12 oleic ( 399)	430	107.0	1.5e-20	gi 4092879 gb AAC99622.1  delta-12 desaturase [Bra ( 312)	413	103.1	1.9e-19
gi 60117056 gb AAX14399.1  oleate desaturase [Arac ( 379)	428	106.5	2e-20	gi 137103080 gb EBS21930.1  hypothetical protein G ( 288)	412	102.8	2e-19
gi 121104181 gb ABM47430.1  delta-12 fatty acid de ( 379)	428	106.5	2e-20	gi 143934227 gb EDH68469.1  hypothetical protein G ( 302)	412	102.8	2.1e-19
gi 71064149 gb AAZ22543.1  oleate desaturase [Arac ( 379)	428	106.5	2e-20	gi 46392790 gb AAS91160.1  delta-12 desaturase-lik ( 121)	406	101.2	2.6e-19
gi 14572857 gb AAK67829.1  delta-12 fatty acid des ( 379)	428	106.5	2e-20	gi 66734339 gb AAY53559.1  oleate desaturase [Arac ( 379)	412	102.9	2.6e-19
gi 121104183 gb ABM47431.1  delta-12 fatty acid de ( 379)	428	106.5	2e-20	gi 83286879 gb ABC00770.1  delta-12 fatty acid des ( 382)	412	102.9	2.6e-19
gi 8980831 gb AAF82293.1  microsomal oleate desatu ( 379)	428	106.5	2e-20	gi 78713359 gb ABB50536.1  Delta(12)-fatty acid de ( 391)	410	102.4	3.6e-19
gi 189846868 gb ACE26366.1  Sequence 39 from paten ( 387)	428	106.5	2.1e-20	gi 157087398 gb ABV21586.1  fatty acid desaturase ( 385)	409	102.2	4.2e-19
gi 189704773 gb ACE16102.1  Sequence 37 from paten ( 387)	428	106.5	2.1e-20	gi 164636954 gb EDR01244.1  delta-12 fatty acid de ( 394)	408	102.0	5e-19
gi 189846866 gb ACE26364.1  Sequence 37 from paten ( 387)	428	106.5	2.1e-20	gi 89305244 gb EAS03232.1  Fatty acid desaturase f ( 387)	407	101.7	5.8e-19
gi 189704775 gb ACE16104.1  Sequence 39 from paten ( 387)	428	106.5	2.1e-20	gi 141832428 gb ECT55938.1  hypothetical protein G ( 283)	405	101.2	6.1e-19
gi 38426731 gb AAR20348.1  delta-12 desaturase [Sa ( 393)	428	106.5	2.1e-20	gi 164638120 gb EDR02400.1  delta-12 fatty acid de ( 425)	407	101.8	6.2e-19
gi 155102610 gb ABT03233.1  Sequence 42 from paten ( 393)	428	106.5	2.1e-20	gi 18252113 gb AAL61825.1  putative delta12 oleic ( 255)	404	101.0	6.5e-19
gi 155102611 gb ABT03234.1  Sequence 43 from paten ( 393)	428	106.5	2.1e-20	gi 155713306 gb ABU35462.1  Sequence 30 from paten ( 255)	404	101.0	6.5e-19
gi 72002083 gb AAZ57885.1  delta(12)-fatty acid de ( 405)	428	106.5	2.2e-20	gi 78197948 gb ABB35713.1  Delta(12)-fatty acid de ( 381)	406	101.5	6.7e-19
gi 189702340 gb ACE14957.1  Sequence 2 from patent ( 378)	427	106.3	2.4e-20	gi 14572859 gb AAK67830.1 AF248740_1 truncated del ( 164)	401	100.2	7.3e-19
gi 189846878 gb ACE26376.1  Sequence 136 from pate ( 378)	427	106.3	2.4e-20	gi 197944847 gb ACH79976.1  truncated delta-12 fat ( 164)	401	100.2	7.3e-19
gi 38564776 gb AAR23815.1  delta 12 fatty acid epo ( 378)	427	106.3	2.4e-20	gi 155689129 gb ABU35455.1  Sequence 7 from patent ( 383)	404	101.0	9.2e-19
gi 5994483 gb AAE19896.1  Sequence 6 from patent U ( 387)	427	106.3	2.4e-20	gi 6224714 gb AAF05915.1  delta-12 oleic acid desa ( 383)	404	101.0	9.2e-19
gi 5955847 gb AAE07503.1  Sequence 42 from patent ( 387)	427	106.3	2.4e-20	gi 155707470 gb ABU33119.1  Sequence 57 from paten ( 383)	404	101.0	9.2e-19
gi 2492222 gb AAB80358.1 I66169 Sequence 40 from p ( 387)	427	106.3	2.4e-20	gi 155713299 gb AAO37755.1  Sequence 2 from patent ( 383)	404	101.0	9.2e-19
gi 5955845 gb AAE07501.1  Sequence 40 from patent ( 387)	427	106.3	2.4e-20	gi 33766652 gb AAQ52855.1  Sequence 7 from patent ( 383)	404	101.0	9.2e-19
gi 17909751 gb AAE82558.1  Sequence 5 from patent ( 387)	427	106.3	2.4e-20	gi 155707469 gb ABU33118.1  Sequence 53 from paten ( 383)	404	101.0	9.2e-19
gi 189704758 gb ACE16087.1  Sequence 13 from paten ( 387)	427	106.3	2.4e-20	gi 143173998 gb EDD34949.1  hypothetical protein G ( 403)	404	101.1	9.6e-19
gi 722351 gb AAC49010.1  oleate 12-hydroxylase ( 387)	427	106.3	2.4e-20	gi 138284618 gb EBY79340.1  hypothetical protein G ( 256)	400	100.0	1.2e-18
gi 155689128 gb ABU29138.1  Sequence 6 from patent ( 387)	427	106.3	2.4e-20	gi 197035435 gb ACH16335.1  Sequence 1 from patent ( 387)	402	100.6	1.3e-18
gi 33766651 gb AAQ52854.1  Sequence 6 from patent ( 387)	427	106.3	2.4e-20	gi 28371821 gb AAO37751.1  fatty acid conjugase [T ( 387)	402	100.6	1.3e-18
gi 34600652 gb AAQ78509.1  Sequence 14 from patent ( 387)	427	106.3	2.4e-20	gi 86769314 gb ABD15171.1  truncated delta-12 fatt ( 135)	396	99.0	1.4e-18
gi 2492224 gb AAB80360.1 I66171 Sequence 42 from p ( 387)	427	106.3	2.4e-20	gi 137357188 gb EBT64399.1  hypothetical protein G ( 289)	400	100.1	1.4e-18
gi 17918534 gb AAE85968.1  Sequence 5 from patent ( 387)	427	106.3	2.4e-20	gi 139693867 gb ECG82230.1  hypothetical protein G ( 276)	399	99.8	1.5e-18
gi 76007348 gb ABA38262.1  Sequence 5 from patent ( 387)	427	106.3	2.4e-20	gi 4530972 emb CAA03836.1  DELTA-12 DESATURASE [Co ( 338)	399	99.9	1.8e-18

gi 135637216 gb EBI91132.1	hypothetical protein G ( 350)	399	99.9	1.9e-18	gi 155090497 gb ABS96096.1	Sequence 12 from paten ( 435)	380	95.6	4.6e-17
gi 33640306 emb CAB1984.1	fatty acid desaturase, ( 392)	399	99.9	2.1e-18	gi 13605712 gb AAK32849.1	AF361837_1 AT5g05580/MOP ( 435)	380	95.6	4.6e-17
gi 33238192 gb AAQ00259.1	Fatty acid desaturase [ ( 368)	397	99.4	2.7e-18	gi 159888364 gb ABX08578.1	Hypothetical protein P ( 180)	375	94.2	4.8e-17
gi 162690784 gb EDQ77149.1	predicted protein [Phy ( 375)	397	99.4	2.7e-18	gi 143742469 gb EDG55458.1	hypothetical protein G ( 226)	376	94.5	5e-17
gi 143761874 gb EDG66538.1	hypothetical protein G ( 406)	397	99.5	2.9e-18	gi 137938899 gb EBW86311.1	hypothetical protein G ( 243)	375	94.3	6.2e-17
gi 140346041 gb ECL14042.1	hypothetical protein G ( 286)	395	98.9	3e-18	gi 141545071 gb ECS26866.1	hypothetical protein G ( 306)	376	94.6	6.4e-17
gi 140706595 gb ECM95975.1	hypothetical protein G ( 243)	394	98.7	3.1e-18	gi 143416270 gb EDE83951.1	hypothetical protein G ( 240)	374	94.1	7.2e-17
gi 143151544 gb EDD19097.1	hypothetical protein G ( 407)	396	99.2	3.4e-18	gi 143751027 gb EDG60053.1	hypothetical protein G ( 386)	376	94.7	7.8e-17
gi 123199234 gb ABM70875.1	fatty acid desaturase, ( 344)	395	99.0	3.5e-18	gi 111054802 gb ABG88130.2	ER-type omega-3 fatty ( 395)	374	94.2	1.1e-16
gi 137847989 gb EBW34483.1	hypothetical protein G ( 237)	393	98.4	3.5e-18	gi 17135417 dbj BAB77963.1	omega-3 fatty acid des ( 359)	371	93.5	1.6e-16
gi 148524113 gb ABQ81921.1	FAD2 [Brassica napus] ( 142)	390	97.6	3.7e-18	gi 4008402 emb CAB05304.1	C. elegans protein W02A ( 376)	371	93.5	1.7e-16
gi 126543957 gb ABO181199.1	fatty acid desaturase, ( 388)	395	99.0	3.9e-18	gi 62789973 gb AAY08322.1	Sequence 32 from patent ( 376)	371	93.5	1.7e-16
gi 163772970 gb EDQ86615.1	predicted protein [Mon ( 592)	397	99.6	4e-18	gi 167279412 gb ABZ32276.1	Sequence 6214 from pat ( 376)	371	93.5	1.7e-16
gi 139197177 gb ECE07780.1	hypothetical protein G ( 295)	393	98.5	4.2e-18	gi 7546993 gb AAF63745.1	AF240777_1 delta 12 fatty ( 376)	371	93.5	1.7e-16
gi 134995018 gb EBE80676.1	hypothetical protein G ( 369)	394	98.8	4.3e-18	gi 142200493 gb ECW34394.1	hypothetical protein G ( 386)	371	93.5	1.7e-16
gi 134976357 gb EBE67982.1	hypothetical protein G ( 313)	393	98.5	4.4e-18	gi 199601694 dbj BAG70950.1	omega-3 fatty acid de ( 393)	371	93.5	1.7e-16
gi 157388526 gb ABV51231.1	fatty acid desaturase, ( 388)	394	98.8	4.5e-18	gi 139519788 gb ECF63159.1	hypothetical protein G ( 218)	367	92.5	2e-16
gi 162692736 gb EDQ79092.1	predicted protein [Phy ( 375)	393	98.5	5.2e-18	gi 75704133 gb ABA23809.1	Fatty acid desaturase [ ( 359)	369	93.0	2.2e-16
gi 135754439 gb EBJ63635.1	hypothetical protein G ( 324)	392	98.3	5.3e-18	gi 140863227 gb ECO01526.1	hypothetical protein G ( 258)	366	92.3	2.7e-16
gi 155102615 gb ABT03238.1	Sequence 47 from paten ( 333)	392	98.3	5.5e-18	gi 140667895 gb ECM68585.1	hypothetical protein G ( 313)	366	92.3	3.2e-16
gi 135621037 gb ABO181141.1	hypothetical protein G ( 362)	392	98.3	5.9e-18	gi 135781697 gb EBJ80636.1	hypothetical protein G ( 309)	365	92.1	3.7e-16
gi 158279015 gb EDP04777.1	fatty acid desaturase, ( 383)	391	98.1	7.2e-18	gi 139871797 gb ECI04781.1	hypothetical protein G ( 154)	361	91.0	3.9e-16
gi 136351801 gb EBN58294.1	hypothetical protein G ( 263)	389	97.5	7.2e-18	gi 140082397 gb ECJ42398.1	hypothetical protein G ( 283)	364	91.8	4e-16
gi 142677465 gb EBY94335.1	hypothetical protein G ( 388)	391	98.1	7.3e-18	gi 142362510 gb ECS53443.1	hypothetical protein G ( 243)	362	91.3	4.9e-16
gi 135681213 gb EBJ18314.1	hypothetical protein G ( 271)	388	97.3	8.7e-18	gi 6503049 gb AAF14564.1	AF181726_1 delta-12 fatty ( 206)	361	91.1	5e-16
gi 143848454 gb EDH06493.1	hypothetical protein G ( 401)	390	97.9	8.8e-18	gi 143131753 gb EDD04630.1	hypothetical protein G ( 186)	360	90.8	5.3e-16
gi 138318032 gb EBY94335.1	hypothetical protein G ( 275)	388	97.3	8.8e-18	gi 142755055 gb EDA34189.1	hypothetical protein G ( 406)	363	91.7	6.4e-16
gi 136250130 gb EBM89171.1	hypothetical protein G ( 406)	390	97.9	8.9e-18	gi 119214806 gb ABL61262.1	chloroplast omega-3 de ( 445)	363	91.7	6.9e-16
gi 33327237 gb AAQ08982.1	delta-12 fatty acid des ( 233)	387	97.0	8.9e-18	gi 155689133 gb ABU29143.1	Sequence 13 from paten ( 375)	362	91.4	7e-16
gi 143821886 gb EDG87315.1	hypothetical protein G ( 237)	387	97.1	9.1e-18	gi 45643651 gb AAS72901.1	delta9 fatty acid conju ( 375)	362	91.4	7e-16
gi 145386893 gb ABP65296.1	omega-6 fatty desatura ( 350)	389	97.6	9.2e-18	gi 33766656 gb AAQ52859.1	Sequence 13 from patent ( 375)	362	91.4	7e-16
gi 140859315 gb ECN98726.1	hypothetical protein G ( 255)	386	96.8	1.1e-17	gi 140670558 gb ECM70517.1	hypothetical protein G ( 320)	361	91.2	7.2e-16
gi 116787072 gb ABK24364.1	unknown [Picea sitchen ( 375)	388	97.4	1.1e-17	gi 3133289 gb AAC110354.1	omega-3 desaturase [Pela ( 407)	362	91.5	7.5e-16
gi 17064784 gb AAL32546.1	temperature-sensitive o ( 435)	388	97.4	1.3e-17	gi 140541495 gb ECM16089.1	hypothetical protein G ( 235)	359	90.7	7.6e-16
gi 20259912 gb AAM13303.1	temperature-sensitive o ( 435)	388	97.4	1.3e-17	gi 137615387 gb EBV06629.1	hypothetical protein G ( 195)	358	90.4	7.6e-16
gi 143419214 gb EDE85479.1	hypothetical protein G ( 406)	387	97.2	1.4e-17	gi 13840635 emb CAE20424.1	fatty acid desaturase, ( 379)	361	91.2	8.2e-16
gi 137278133 gb EBT20260.1	hypothetical protein G ( 250)	384	96.4	1.5e-17	gi 125661171 gb ABN49521.1	fatty acid desaturase ( 389)	361	91.2	8.4e-16
gi 143165925 gb EDD29220.1	hypothetical protein G ( 327)	385	96.7	1.6e-17	gi 50295115 gb AAT72937.1	putative fatty acid des ( 389)	361	91.2	8.4e-16
gi 59956948 dbj BAD89863.1	microsomal omega-6 fat ( 337)	384	96.4	2e-17	gi 112099617 gb ABI10354.1	Sequence 15 from paten ( 351)	360	91.0	9.1e-16
gi 144160439 gb EDJ30569.1	hypothetical protein G ( 413)	385	96.7	2e-17	gi 45385976 gb AAS59833.1	chloroplast omega-3 des ( 439)	361	91.3	9.3e-16
gi 137689128 gb EBV46724.1	hypothetical protein G ( 246)	382	95.9	2.1e-17	gi 123964087 gb ABM78843.1	fatty acid desaturase, ( 380)	360	91.0	9.7e-16
gi 143784241 gb EDG76662.1	hypothetical protein G ( 407)	384	96.5	2.3e-17	gi 10050182 gb AAE27089.1	Sequence 17 from patent ( 156)	355	89.6	1e-15
gi 134798877 gb EBD51227.1	hypothetical protein G ( 410)	383	96.3	2.7e-17	gi 112099624 gb ABI10360.1	Sequence 21 from paten ( 369)	359	90.8	1.1e-15
gi 137783082 gb EBV97124.1	hypothetical protein G ( 293)	381	95.7	2.8e-17	gi 164521894 gb ABY60736.1	microsomal omega-3 fat ( 371)	359	90.8	1.1e-15
gi 144165642 gb EBL15614.1	hypothetical protein G ( 445)	383	96.3	2.9e-17	gi 118430556 gb ABK91881.1	omega-3 fatty acid des ( 433)	359	90.8	1.3e-15
gi 136361108 gb EBN64632.1	hypothetical protein G ( 389)	382	96.0	3e-17	gi 1694625 dbj BAA11475.1	omega-3 fatty acid desa ( 441)	359	90.8	1.3e-15
gi 141897758 gb ECU01814.1	hypothetical protein G ( 208)	378	95.0	3.4e-17	gi 21668486 dbj BAC01274.1	plastid omega-3 fatty ( 441)	359	90.8	1.3e-15
gi 135985651 gb EBL15614.1	hypothetical protein G ( 401)	381	95.8	3.6e-17	gi 62789972 gb AAY08321.1	Sequence 14 from patent ( 374)	358	90.5	1.3e-15
gi 136755838 gb EBQ19318.1	hypothetical protein G ( 402)	381	95.8	3.6e-17	gi 141233760 gb ECQ54809.1	hypothetical protein G ( 176)	354	89.4	1.3e-15
gi 143629305 gb EDF94875.1	hypothetical protein G ( 406)	381	95.8	3.7e-17	gi 138583392 gb ECA60096.1	hypothetical protein G ( 162)	353	89.2	1.4e-15
gi 45643653 gb AAS72902.1	trans-delta12 oleic aci ( 380)	380	95.5	4.1e-17	gi 137479245 gb EBU32506.1	hypothetical protein G ( 237)	355	89.7	1.4e-15
gi 33766655 gb AAQ52858.1	Sequence 11 from patent ( 380)	380	95.6	4.1e-17	gi 167293297 gb ABZ46161.1	Sequence 20099 from pa ( 347)	357	90.3	1.4e-15
gi 155689132 gb ABU29142.1	Sequence 11 from paten ( 380)	380	95.6	4.1e-17	gi 186468713 gb ACC84514.1	fatty acid desaturase ( 359)	357	90.3	1.5e-15
gi 471093 dbj BAA04504.1	plastid fatty acid desat ( 435)	380	95.6	4.6e-17	gi 46849975 gb AAT02410.1	chloroplast omega-3 fat ( 439)	358	90.6	1.5e-15
gi 10178135 dbj BAB11547.1	temperature-sensitive ( 435)	380	95.6	4.6e-17	gi 136982607 gb EBR54408.1	hypothetical protein G ( 151)	352	88.9	1.6e-15
gi 516045 gb AAA65621.1	omega-3 fatty acid desatu ( 435)	380	95.6	4.6e-17	gi 195612756 gb ACG28208.1	omega-3 fatty acid des ( 408)	357	90.3	1.7e-15
gi 497219 gb AAB60302.1	chloroplast linoleate des ( 435)	380	95.6	4.6e-17	gi 141128901 gb ECP82841.1	hypothetical protein G ( 234)	354	89.5	1.7e-15
gi 18700268 gb AAL77744.1	AT5g05580/MOP10_12 [Ara ( 435)	380	95.6	4.6e-17	gi 135595996 gb EBI65603.1	hypothetical protein G ( 166)	352	89.0	1.7e-15

gi 124423282 emb CAK88077.1  unnamed protein produ ( 358) 356 90.1 1.7e-15	gi 112099618 gb ABI10355.1  Sequence 16 from paten ( 358) 348 88.2 6.2e-15
gi 112099614 gb ABI10351.1  Sequence 12 from paten ( 361) 356 90.1 1.7e-15	gi 32479366 gb AAP82169.2  omega-3 fatty acid desa ( 435) 349 88.5 6.2e-15
gi 112099622 gb ABI10358.1  Sequence 19 from paten ( 352) 355 89.8 2e-15	gi 32442202 gb AAP82170.1  omega-3 fatty acid desa ( 435) 349 88.5 6.2e-15
gi 126633024 emb CAM55477.1  unnamed protein produ ( 172) 351 88.8 2.1e-15	gi 112099635 gb ABI10369.1  Sequence 30 from paten ( 362) 348 88.2 6.2e-15
gi 110084514 gb ABG49414.1  chloroplast omega-3 fa ( 455) 356 90.1 2.1e-15	gi 33638914 emb CAE07211.1  fatty acid desaturase, ( 382) 348 88.3 6.5e-15
gi 157351193 emb CAO41380.1  unnamed protein produ ( 456) 356 90.1 2.1e-15	gi 4321399 gb AAD15744.1  omega-3 fatty acid desat ( 391) 348 88.3 6.6e-15
gi 215700937 dbj BAG92361.1  unnamed protein produ ( 385) 355 89.9 2.2e-15	gi 136003587 gb EBL26327.1  hypothetical protein G ( 242) 345 87.5 7.1e-15
gi 76803810 gb ABA55806.1  omega-3 fatty acid desa ( 385) 355 89.9 2.2e-15	gi 23345023 gb AAN17503.1  omega-3 fatty acid desa ( 444) 348 88.3 7.4e-15
gi 77552800 gb ABA95596.1  Omega-3 fatty acid desa ( 385) 355 89.9 2.2e-15	gi 11691870 emb CAC18722.1  putative plastidial w- ( 449) 348 88.3 7.4e-15
gi 113648433 dbj BAF28945.1  Os12g0104400 [Oryza s ( 385) 355 89.9 2.2e-15	gi 140855361 gb ECN95873.1  hypothetical protein G ( 211) 344 87.2 7.5e-15
gi 5305302 gb AAD41576.1 AF056565_1 fatty acid des ( 163) 350 88.5 2.3e-15	gi 162135888 gb ABX82798.1  microsomal omega-3 fat ( 377) 347 88.0 7.5e-15
gi 870784 gb AAA70334.1  omega-3 fatty acid desatu ( 447) 355 89.9 2.4e-15	gi 141450291 gb ECR77185.1  hypothetical protein G ( 219) 344 87.2 7.7e-15
gi 112099620 gb ABI10356.1  Sequence 17 from paten ( 377) 354 89.6 2.5e-15	gi 143454309 gb EDF05453.1  hypothetical protein G ( 269) 345 87.5 7.8e-15
gi 125661167 gb ABN49519.1  fatty acid desaturase ( 388) 354 89.6 2.5e-15	gi 142738209 gb EDA21987.1  hypothetical protein G ( 245) 344 87.2 8.4e-15
gi 167292274 gb ABZ45138.1  Sequence 19076 from pa ( 333) 353 89.4 2.6e-15	gi 156219508 gb EDD040389.1  predicted protein [Nem ( 361) 346 87.8 8.5e-15
gi 112099627 gb ABI10362.1  Sequence 23 from paten ( 368) 353 89.4 2.9e-15	gi 112099637 gb ABI10370.1  Sequence 31 from paten ( 369) 346 87.8 8.7e-15
gi 190613766 gb ACE80931.1  omega-3 fatty acid des ( 445) 354 89.7 2.9e-15	gi 139079064 gb ECD26660.1  hypothetical protein G ( 235) 343 87.0 9.6e-15
gi 91992438 gb ABE72960.1  chloroplast omega-3 fat ( 455) 354 89.7 2.9e-15	gi 699390 gb AAA86690.1  delta-15 lineoyl desatura ( 436) 346 87.8 1e-14
gi 414732 gb AAA73511.1  linoleoyl desaturase ( 460) 354 89.7 2.9e-15	gi 112099623 gb ABI10359.1  Sequence 20 from paten ( 363) 345 87.6 1e-14
gi 158307132 gb ABW28749.1  omega-3 fatty acid des ( 353) 352 89.2 3.2e-15	gi 156990674 gb ABU96743.1  chloroplast omega-3 fa ( 446) 346 87.8 1e-14
gi 126633508 emb CAM55719.1  unnamed protein produ ( 437) 353 89.4 3.3e-15	gi 139550120 gb ECF83668.1  hypothetical protein G ( 149) 340 86.2 1.1e-14
gi 4240385 gb AAD13527.1  omega-3 fatty acid desat ( 437) 353 89.4 3.3e-15	gi 74275357 gb ABA02172.1  fatty acid desaturase 3 ( 392) 345 87.6 1.1e-14
gi 76803815 gb ABA55807.1  chloroplast omega-3 fat ( 438) 353 89.4 3.3e-15	gi 145036529 gb ABP30234.1  Sequence 8 from patent ( 392) 345 87.6 1.1e-14
gi 116001285 emb CAL49894.1  unnamed protein produ ( 363) 352 89.2 3.3e-15	gi 135295560 gb EBG69212.1  hypothetical protein G ( 153) 340 86.2 1.1e-14
gi 162684238 gb EDQ70642.1  predicted protein [Phy ( 445) 353 89.4 3.3e-15	gi 196191998 gb EDX86962.1  Fatty acid desaturase ( 351) 344 87.3 1.1e-14
gi 137798840 gb EBW06016.1  hypothetical protein G ( 213) 349 88.3 3.4e-15	gi 541653 dbj BAA03106.1  omega-3-desaturase [Arab ( 446) 345 87.6 1.2e-14
gi 1777376 dbj BAA11397.1  w-3 fatty acid desatura ( 381) 352 89.2 3.4e-15	gi 10050176 gb AAE27083.1  Sequence 5 from patent ( 446) 345 87.6 1.2e-14
gi 136237708 gb EBM80780.1  hypothetical protein G ( 231) 349 88.4 3.6e-15	gi 12321881 gb AAG50977.1 AC073395_19 omega-3 fatt ( 446) 345 87.6 1.2e-14
gi 199601696 dbj BAG70949.1  omega-3 fatty acid de ( 390) 351 88.9 4.1e-15	gi 468434 dbj BAA05040.1  plastid fatty acid desat ( 446) 345 87.6 1.2e-14
gi 171700755 gb ACB53736.1  fatty acid desaturase ( 349) 350 88.7 4.4e-15	gi 6016681 gb AAF01508.1 AC009991_4 omega-3 fatty ( 446) 345 87.6 1.2e-14
gi 126633530 emb CAM55730.1  unnamed protein produ ( 429) 351 89.0 4.5e-15	gi 155090496 gb ABS96095.1  Sequence 10 from paten ( 446) 345 87.6 1.2e-14
gi 125535471 gb EAY81959.1  hypothetical protein O ( 355) 350 88.7 4.5e-15	gi 408481 gb AAA61773.1  omega-3 fatty acid desatu ( 446) 345 87.6 1.2e-14
gi 125578209 gb EAZ19355.1  hypothetical protein O ( 355) 350 88.7 4.5e-15	gi 154813792 gb ABS86961.1  chloroplast omega-3 fa ( 451) 345 87.6 1.2e-14
gi 112099641 gb ABI10373.1  Sequence 34 from paten ( 356) 350 88.7 4.5e-15	gi 118489331 gb ABK96470.1  unknown [Populus trich ( 452) 345 87.6 1.2e-14
gi 3550663 emb CAA07638.1  w-3 desaturase [Solanum ( 431) 351 89.0 4.5e-15	gi 160334210 gb ABX24525.1  omega-3 fatty acid des ( 377) 344 87.3 1.2e-14
gi 113735150 dbj BAF30809.1  omega-3-desaturase [E ( 434) 351 89.0 4.5e-15	gi 1826897616 gb ABD48788.1  endoplasmic reticulum 1 ( 383) 344 87.3 1.2e-14
gi 125575925 gb EAA217147.1  hypothetical protein O ( 362) 350 88.7 4.5e-15	gi 195635609 gb ACG37273.1  omega-3 fatty acid des ( 384) 344 87.3 1.2e-14
gi 126632956 emb CAM55443.1  unnamed protein produ ( 443) 351 89.0 4.6e-15	gi 189308128 gb ACD86948.1  fatty acyl desaturase ( 226) 341 86.5 1.3e-14
gi 195627062 gb ACG35361.1  omega-3 fatty acid des ( 443) 351 89.0 4.6e-15	gi 162684694 gb EDQ71094.1  predicted protein [Phy ( 441) 344 87.4 1.4e-14
gi 2446998 dbj BAA22441.1  fatty acid desaturase [ ( 443) 351 89.0 4.6e-15	gi 141069087 gb ECP40955.1  hypothetical protein G ( 257) 341 86.6 1.4e-14
gi 140727720 gb ECN10408.1  hypothetical protein G ( 294) 348 88.2 5.2e-15	gi 137359343 gb EBT65630.1  hypothetical protein G ( 213) 340 86.3 1.4e-14
gi 110168938 gb ABG53478.1  Delta(12)-fatty acid d ( 357) 349 88.5 5.2e-15	gi 10050177 gb AAE27084.1  Sequence 7 from patent ( 378) 343 87.1 1.4e-14
gi 126633418 emb CAM55674.1  unnamed protein produ ( 432) 350 88.7 5.2e-15	gi 144576748 gb ABO94816.1  predicted protein [Ost ( 387) 343 87.1 1.5e-14
gi 141315775 gb ECQ99409.1  hypothetical protein G ( 203) 346 87.6 5.3e-15	gi 155306965 gb ABT62569.1  Sequence 150039 from p ( 164) 338 85.8 1.6e-14
gi 134989727 gb EBE77060.1  hypothetical protein G ( 204) 346 87.6 5.3e-15	gi 162680781 gb EDQ67214.1  predicted protein [Phy ( 431) 343 87.1 1.6e-14
gi 110725975 gb ABG88131.1  chloroplast omega-3 fa ( 436) 350 88.7 5.3e-15	gi 158593298 gb EDP31893.1  Fatty acid desaturase ( 376) 342 86.9 1.7e-14
gi 141072386 gb ECP43211.1  hypothetical protein G ( 252) 347 87.9 5.4e-15	gi 140220184 gb ECK34119.1  hypothetical protein G ( 151) 337 85.5 1.7e-14
gi 139790774 gb ECH48637.1  hypothetical protein G ( 255) 347 87.9 5.4e-15	gi 50508696 dbj BAD31200.1  putative omega-3 fatty ( 327) 341 86.6 1.7e-14
gi 138713287 gb ECB49397.1  hypothetical protein G ( 211) 346 87.7 5.4e-15	gi 33146890 dbj BAC79888.1  putative omega-3 fatty ( 327) 341 86.6 1.7e-14
gi 112099616 gb ABI10353.1  Sequence 14 from paten ( 375) 349 88.5 5.5e-15	gi 14787742 emb CAC44309.1  C. elegans protein Y67 ( 402) 342 86.9 1.8e-14
gi 167294087 gb ABZ46951.1  Sequence 20889 from pa ( 318) 348 88.2 5.6e-15	gi 125585886 gb EAA226550.1  hypothetical protein O ( 402) 342 86.9 1.8e-14
gi 5101874 emb CAB45155.1  omega-3 desaturase [Ver ( 387) 349 88.5 5.6e-15	gi 140832739 gb ECN82765.1  hypothetical protein G ( 285) 340 86.4 1.8e-14
gi 164683927 gb AAC98967.2  omega-3 fatty acid des ( 387) 349 88.5 5.6e-15	gi 124422313 emb CAK87150.1  unnamed protein produ ( 358) 341 86.6 1.9e-14
gi 10050178 gb AAE27085.1  Sequence 9 from patent ( 404) 349 88.5 5.8e-15	gi 108707600 gb ABF95395.1  Omega-3 fatty acid des ( 458) 342 86.9 2e-14
gi 143646242 gb EDG04607.1  hypothetical protein G ( 405) 349 88.5 5.8e-15	gi 140870390 gb ECO06627.1  hypothetical protein G ( 150) 336 85.3 2e-14
gi 136026861 gb EBL41763.1  hypothetical protein G ( 131) 343 86.9 5.9e-15	gi 50508695 dbj BAD31199.1  putative omega-3 fatty ( 413) 341 86.7 2.1e-14
gi 143564685 gb EDF66080.1  hypothetical protein G ( 284) 347 88.0 5.9e-15	gi 57014072 gb AAW32557.1  FAD8 [Oryza sativa (jap ( 413) 341 86.7 2.1e-14
gi 7378667 emb CAB85467.1  chloroplast omega-3 fat ( 429) 349 88.5 6.1e-15	gi 113612269 dbj BAF22647.1  Os07g0693800 [Oryza s ( 413) 341 86.7 2.1e-14

gi 29837190 dbj BAC75572.1  putative omega-3 fatty ( 413) 341 86.7 2.1e-14	gi 190898702 gb ACE97864.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 215704382 dbj BAG93816.1  unnamed protein produ ( 413) 341 86.7 2.1e-14	gi 190898656 gb ACE97845.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 88606639 dbj BAE79786.1  plastid omega-3 fatty ( 413) 341 86.7 2.1e-14	gi 190898654 gb ACE97841.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 125601618 gb EAZ41194.1  hypothetical protein O ( 413) 341 86.7 2.1e-14	gi 190898652 gb ACE97839.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 88606635 dbj BAE79784.1  plastid omega-3 fatty ( 413) 341 86.7 2.1e-14	gi 190898662 gb ACE97844.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 215692568 dbj BAG87988.1  unnamed protein produ ( 413) 341 86.7 2.1e-14	gi 190898666 gb ACE97846.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 125992363 emb CAM35355.1  unnamed protein produ ( 413) 341 86.7 2.1e-14	gi 190898674 gb ACE97850.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 6752907 gb AAF27933.1 AF222989_1 omega-3 fatty ( 438) 341 86.7 2.2e-14	gi 190898692 gb ACE97859.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 88606633 dbj BAE79783.1  plastid omega-3 fatty ( 459) 341 86.7 2.3e-14	gi 190898710 gb ACE97868.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 88606637 dbj BAE79785.1  plastid omega-3 fatty ( 459) 341 86.7 2.3e-14	gi 190898708 gb ACE97867.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14
gi 142738149 gb EDA21944.1  hypothetical protein G ( 397) 340 86.4 2.4e-14	gi 138639648 gb ECA97978.1  hypothetical protein G ( 291) 332 84.5 6.5e-14
gi 159025986 emb CAO87893.1  unnamed protein produ ( 273) 338 85.9 2.4e-14	gi 88606667 dbj BAE79800.1  omega-3-desaturase [Cy ( 435) 334 85.1 6.6e-14
gi 118430554 gb ABK91880.1  omega-3 fatty acid des ( 449) 340 86.5 2.6e-14	gi 110565255 emb CAL23344.1  unnamed protein produ ( 361) 333 84.8 6.7e-14
gi 141991317 gb ECU67281.1  hypothetical protein G ( 280) 337 85.7 2.9e-14	gi 60220822 emb CAI58910.1  unnamed protein produc ( 361) 333 84.8 6.7e-14
gi 159029904 emb CO90958.1  unnamed protein produ ( 345) 338 85.9 2.9e-14	gi 76059322 emb CAJ30855.1  unnamed protein produc ( 361) 333 84.8 6.7e-14
gi 166088576 dbj BAG03284.1  omega 3 acyl-lipid de ( 350) 338 86.0 2.9e-14	gi 126633856 emb CAM55884.1  unnamed protein produ ( 361) 333 84.8 6.7e-14
gi 112099634 gb ABI10368.1  Sequence 29 from paten ( 354) 338 86.0 3e-14	gi 140244294 gb ECK50946.1  hypothetical protein G ( 300) 332 84.5 6.7e-14
gi 196177223 gb EDX7231.1  Fatty acid desaturase ( 358) 338 86.0 3e-14	gi 143426844 gb EDE89318.1  hypothetical protein G ( 338) 332 84.6 7.4e-14
gi 116055853 emb CAL57938.1  delta 12 fatty acid d ( 442) 339 86.2 3.1e-14	gi 190898670 gb ACE97848.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 112099633 gb ABI10367.1  Sequence 28 from paten ( 366) 338 86.0 3.1e-14	gi 190898696 gb ACE97861.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 47028567 gb AAT09135.1  omega-3 fatty acid desa ( 383) 338 86.0 3.2e-14	gi 190898678 gb ACE97852.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 14124415 gb AAE60611.1  Sequence 2 from patent ( 402) 338 86.0 3.3e-14	gi 190898704 gb ACE97865.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 67581027 gb AAY69963.1  Sequence 2 from patent ( 402) 338 86.0 3.3e-14	gi 190898684 gb ACE97855.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 27278515 gb AAN93253.1  Sequence 2 from patent ( 402) 338 86.0 3.3e-14	gi 190898720 gb ACE97873.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 91145259 gb ABE21477.1  Sequence 30 from patent ( 402) 338 86.0 3.3e-14	gi 190898700 gb ACE97863.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 784870 gb AAA67369.1  fatty acid desaturase ( 402) 338 86.0 3.3e-14	gi 190898712 gb ACE97869.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 155102614 gb ABT03237.1  Sequence 46 from paten ( 409) 338 86.0 3.4e-14	gi 190898726 gb ACE97876.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 142522375 gb ECY68815.1  hypothetical protein G ( 307) 336 85.5 3.6e-14	gi 190898724 gb ACE97875.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 112099632 gb ABI10366.1  Sequence 27 from paten ( 373) 337 85.7 3.6e-14	gi 190898716 gb ACE97871.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 100501800 gb AAE27087.1  Sequence 13 from patent ( 453) 338 86.0 3.7e-14	gi 190898658 gb ACE97842.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 408792 gb AAA61776.1  omega-3 fatty acid desatu ( 453) 338 86.0 3.7e-14	gi 190898676 gb ACE97851.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 27902573 gb AAO24263.1  microsomal omega-3-fatt ( 376) 337 85.7 3.7e-14	gi 190898706 gb ACE97866.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 144583207 gb ABP01320.1  microsomal omega three ( 376) 337 85.7 3.7e-14	gi 190898690 gb ACE97858.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 34787276 dbj BAC87757.1  microsomal omega-3 fat ( 376) 337 85.7 3.7e-14	gi 190898698 gb ACE97862.1  fatty acid desaturase ( 197) 329 83.8 7.6e-14
gi 157004277 gb ABV00680.1  microsomal omega-3 fat ( 376) 337 85.7 3.7e-14	gi 190898722 gb ABP00334.1  predicted protein [Ost ( 362) 331 84.4 9.2e-14
gi 118430552 gb ABK91879.1  omega-3 fatty acid des ( 386) 337 85.7 3.7e-14	gi 147845818 emb CAN80104.1  hypothetical protein ( 452) 332 84.6 9.4e-14
gi 74275359 gb ABA02173.1  fatty acid desaturase 3 ( 391) 337 85.7 3.8e-14	gi 157356207 emb CAO50134.1  unnamed protein produ ( 452) 332 84.6 9.4e-14
gi 2447000 dbj BAA22442.1  fatty acid desaturase [ ( 398) 337 85.8 3.8e-14	gi 167148 gb AAA32994.1  linoleic acid desaturase ( 383) 331 84.4 9.6e-14
gi 2446996 dbj BAA22440.1  fatty acid desaturase [ ( 398) 337 85.8 3.8e-14	gi 112099604 gb ABI10344.1  Sequence 3 from patent ( 383) 331 84.4 9.6e-14
gi 147848500 emb CAK24051.1  Fatty acid desaturase ( 331) 336 85.5 3.9e-14	gi 155090495 gb ABS96094.1  Sequence 2 from patent ( 383) 331 84.4 9.6e-14
gi 169884460 gb ACA98173.1  omega-3 acyl-lipid des ( 350) 336 85.5 4e-14	gi 112099611 gb ABI10349.1  Sequence 10 from paten ( 383) 331 84.4 9.6e-14
gi 2197199 gb AAB61352.1  omega-3 desaturase [Syn ( 350) 336 85.5 4e-14	gi 27278516 gb AAN93254.1  Sequence 8 from patent ( 383) 331 84.4 9.6e-14
gi 41581197 emb CAF18425.1  omega 3 acyl-lipid des ( 359) 336 85.5 4.1e-14	gi 408483 gb AAA61778.1  omega-3 fatty acid desatu ( 386) 331 84.4 9.7e-14
gi 112099630 gb ABI10365.1  Sequence 26 from paten ( 360) 336 85.5 4.1e-14	gi 3420053 gb AAC31854.1  omega-3 fatty acid desat ( 386) 331 84.4 9.7e-14
gi 143598148 gb EDF79303.1  hypothetical protein G ( 321) 335 85.2 4.4e-14	gi 112099605 gb ABI10345.1  Sequence 4 from patent ( 386) 331 84.4 9.7e-14
gi 112099621 gb ABI10357.1  Sequence 18 from paten ( 362) 335 85.3 4.9e-14	gi 10050175 gb AAE27082.1  Sequence 2 from patent ( 386) 331 84.4 9.7e-14
gi 1786066 gb AAB72241.1  omega-3 fatty acid desat ( 438) 336 85.5 4.9e-14	gi 20465899 gb AAM20102.1  putative omega-3 fatty ( 386) 331 84.4 9.7e-14
gi 214028096 gb ABS587969.2  omega-3 fatty acid des ( 372) 335 85.3 5e-14	gi 471091 dbj BAA04505.1  fatty acid desaturase [A ( 386) 331 84.4 9.7e-14
gi 122937801 gb ABM68629.1  omega-3 fatty acid des ( 372) 335 85.3 5e-14	
gi 213053824 gb ACJ39217.1  fatty acid desaturase ( 452) 336 85.6 5e-14	
gi 140220232 gb ECK34154.1  hypothetical protein G ( 257) 333 84.7 5e-14	
gi 190898694 gb ACE97860.1  fatty acid desaturase ( 197) 331 84.2 5.5e-14	
gi 46981930 gb AAN62759.2  omega-3 fatty acid desa ( 435) 335 85.3 5.7e-14	
gi 1754795 gb AAB39387.1  omega-3 fatty acid desat ( 438) 335 85.3 5.7e-14	
gi 164521896 gb ABY60737.1  chloroplast omega-3 fa ( 451) 335 85.3 5.8e-14	
gi 154354069 gb ABS76144.1  chloroplast omega-3 fa ( 453) 335 85.3 5.9e-14	
gi 112099643 gb ABI10374.1  Sequence 35 from paten ( 329) 333 84.8 6.2e-14	
gi 190898688 gb ACE97857.1  fatty acid desaturase ( 197) 330 84.0 6.5e-14	

gi 17381020 gb AAL36322.1  putative omega-3 fatty ( 386) 331 84.4 9.7e-14	gi 5305300 gb AAD41575.1 AF056563_1 unknown [Brass ( 165) 315 80.5 6e-13
gi 112099613 gb ABI10350.1  Sequence 11 from paten ( 386) 331 84.4 9.7e-14	gi 5305760 gb AAD41802.1 AF140057_1 unknown [Brass ( 165) 315 80.5 6e-13
gi 1197795 dbj BAA05514.1  microsomal omega-3 fatt ( 386) 331 84.4 9.7e-14	gi 112099615 gb ABI10352.1  Sequence 13 from paten ( 359) 319 81.6 6.1e-13
gi 62789969 gb AAY08318.1  Sequence 11 from patent ( 389) 331 84.4 9.7e-14	gi 155362912 gb ABU18517.1  Sequence 205986 from p ( 162) 314 80.3 6.9e-13
gi 164521898 gb ABY60738.1  omega-3 fatty acid des ( 454) 331 84.4 1.1e-13	gi 5305756 gb AAD41801.1 AF140055_1 unknown [Brass ( 166) 314 80.3 7.1e-13
gi 113735152 dbj BAF30810.1  omega-3-desaturase [E ( 340) 329 83.9 1.2e-13	gi 408492 gb AAA61775.1  omega-3 fatty acid desatu ( 377) 318 81.4 7.4e-13
gi 137646878 gb EBV23208.1  hypothetical protein G ( 240) 327 83.3 1.2e-13	gi 91125673 gb ABE12621.1  Sequence 34 from patent ( 377) 318 81.4 7.4e-13
gi 154813794 gb ABS86962.1  omega-3 fatty acid des ( 386) 329 83.9 1.3e-13	gi 112099602 gb ABI10343.1  Sequence 2 from patent ( 377) 318 81.4 7.4e-13
gi 62789968 gb AAY08317.1  Sequence 10 from patent ( 387) 329 83.9 1.3e-13	gi 112099610 gb ABI10348.1  Sequence 9 from patent ( 377) 318 81.4 7.4e-13
gi 125559707 gb EAZ05243.1  hypothetical protein O ( 250) 326 83.1 1.5e-13	gi 49355342 gb AAT65204.1  omega-3 fatty acid desa ( 378) 318 81.4 7.4e-13
gi 32306982 gb AAP78965.1  omega-3 fatty acid desa ( 443) 329 84.0 1.5e-13	gi 112099601 gb ABI10342.1  Sequence 1 from patent ( 380) 318 81.4 7.5e-13
gi 45385321 gb AAM77643.2 AF517831_1 chloroplast o ( 449) 329 84.0 1.5e-13	gi 62319074 dbj BAD94215.1  omega-3 fatty acid des ( 206) 314 80.3 8.4e-13
gi 10050179 gb AAE27086.1  Sequence 11 from patent ( 380) 328 83.7 1.5e-13	gi 197111726 gb ACH43027.1  microsomal omega-3 fat ( 380) 317 81.2 8.8e-13
gi 34787274 dbj BAC87756.1  microsomal omega-3 fat ( 380) 328 83.7 1.5e-13	gi 189014682 gb ACD69577.1  omega-3 fatty acid des ( 380) 317 81.2 8.8e-13
gi 157004275 gb ABV00679.1  microsomal omega-3 fat ( 380) 328 83.7 1.5e-13	gi 137943424 gb EBW88866.1  hypothetical protein G ( 332) 316 80.9 9.2e-13
gi 408794 gb AAA61777.1  omega-3 fatty acid desatu ( 380) 328 83.7 1.5e-13	gi 600598 dbj BAA02924.1  delta 15 desaturase [Syn ( 359) 316 80.9 9.8e-13
gi 27902575 gb AAO24264.1  microsomal omega-3-fatt ( 380) 328 83.7 1.5e-13	gi 167275943 gb ABZ28807.1  Sequence 2745 from pat ( 359) 316 80.9 9.8e-13
gi 1357460 dbj BAA28358.1  omega-3 fatty acid desa ( 383) 328 83.7 1.5e-13	gi 1653388 dbj BAA18302.1  delta 15 desaturase [Sy ( 359) 316 80.9 9.8e-13
gi 139522922 gb ECF65248.1  hypothetical protein G ( 318) 327 83.4 1.6e-13	gi 139034378 gb ECC95336.1  hypothetical protein G ( 151) 311 79.6 1e-12
gi 190898668 gb ACE97847.1  fatty acid desaturase ( 197) 324 82.6 1.7e-13	gi 193299732 gb ABU54076.2  omega 3 desaturase O3D ( 434) 315 80.7 1.3e-12
gi 112099640 gb ABI10372.1  Sequence 33 from paten ( 349) 327 83.4 1.7e-13	gi 112099644 gb ABI10375.1  Sequence 36 from paten ( 329) 313 80.2 1.5e-12
gi 116061930 emb CAL52648.1  delta 12 fatty acid d ( 442) 328 83.7 1.7e-13	gi 136211167 gb EBM62811.1  hypothetical protein G ( 189) 310 79.4 1.5e-12
gi 162696041 gb EDQ82382.1  predicted protein [Phy ( 380) 327 83.5 1.8e-13	gi 155707466 gb ABU33115.1  Sequence 6 from patent ( 358) 313 80.2 1.6e-12
gi 94959240 gb ABF47510.1  truncated delta-12 fatt ( 107) 320 81.6 1.9e-13	gi 182916824 gb ACC10859.1  Sequence 4 from patent ( 358) 313 80.2 1.6e-12
gi 190898672 gb ACE97849.1  fatty acid desaturase ( 197) 323 82.4 2e-13	gi 145025096 gb ABP24253.1  Sequence 44 from paten ( 358) 313 80.2 1.6e-12
gi 190898660 gb ACE97843.1  fatty acid desaturase ( 197) 323 82.4 2e-13	gi 155070722 gb ABS91067.1  Sequence 54 from paten ( 358) 313 80.2 1.6e-12
gi 162677068 gb EDQ63543.1  predicted protein [Phy ( 364) 326 83.2 2e-13	gi 118822322 gb ABL20744.1  Sequence 4 from patent ( 358) 313 80.2 1.6e-12
gi 14488094 gb AAK63867.1 AF389295_1 AT3g11170/F9F ( 446) 327 83.5 2.1e-13	gi 144998359 gb ABP16932.1  Sequence 28 from paten ( 358) 313 80.2 1.6e-12
gi 20908084 gb AAM26725.1  AT3g11170/F9F8_4 [Arabi ( 446) 327 83.5 2.1e-13	gi 160830402 emb CAP40271.1  unnamed protein produ ( 358) 313 80.2 1.6e-12
gi 23345025 gb AAN17504.1  microsomal omega-3 fatt ( 386) 326 83.2 2.1e-13	gi 38426733 gb AAR20444.1  omega-3 fatty acid desa ( 358) 313 80.2 1.6e-12
gi 60220802 emb CAI58900.1  unnamed protein produc ( 361) 325 83.0 2.4e-13	gi 155102608 gb ABT03231.1  Sequence 26 from paten ( 358) 313 80.2 1.6e-12
gi 160830400 emb CAP40270.1  unnamed protein produ ( 361) 325 83.0 2.4e-13	gi 155102613 gb ABT03236.1  Sequence 45 from paten ( 358) 313 80.2 1.6e-12
gi 76059302 emb CAJ30845.1  unnamed protein produc ( 361) 325 83.0 2.4e-13	gi 112099647 gb ABI10377.1  Sequence 38 from paten ( 251) 311 79.7 1.6e-12
gi 76059411 emb CAJ30870.1  unnamed protein produc ( 361) 325 83.0 2.4e-13	gi 157347450 emb CAO18087.1  unnamed protein produ ( 368) 313 80.3 1.6e-12
gi 126633852 emb CAM55882.1  unnamed protein produ ( 361) 325 83.0 2.4e-13	gi 6466197 gb AAF12821.1 AF200717_1 omega-3 fatty ( 451) 314 80.5 1.6e-12
gi 141620606 gb ECS58022.1  hypothetical protein G ( 212) 322 82.2 2.4e-13	gi 24466994 dbj BAA22439.1  fatty acid desaturase [ ( 262) 311 79.7 1.7e-12
gi 155281603 gb ABT37207.1  Sequence 124677 from p ( 381) 325 83.0 2.5e-13	gi 162686680 gb EDQ73067.1  predicted protein [Phy ( 383) 313 80.3 1.7e-12
gi 21668465 dbj BAA07785.3  plastid omega-3 fatty ( 381) 325 83.0 2.5e-13	gi 138707809 gb ECB45598.1  hypothetical protein G ( 261) 310 79.5 1.9e-12
gi 112099638 gb ABI10371.1  Sequence 32 from paten ( 348) 324 82.8 2.7e-13	gi 15811218 gb AAL08867.1  omega-3 fatty acid desa ( 302) 310 79.5 2.2e-12
gi 112099629 gb ABI10364.1  Sequence 25 from paten ( 356) 323 82.5 3.2e-13	gi 139690344 gb ECG79948.1  hypothetical protein G ( 252) 309 79.2 2.2e-12
gi 138600399 gb ECA72044.1  hypothetical protein G ( 306) 322 82.3 3.3e-13	gi 159888363 gb ABX08577.1  Hypothetical protein P ( 141) 305 78.2 2.6e-12
gi 62789966 gb AAY08315.1  Sequence 8 from patent ( 397) 323 82.6 3.5e-13	gi 112099664 gb ABI10390.1  Sequence 69 from paten ( 382) 310 79.6 2.7e-12
gi 138259907 gb EBY63590.1  hypothetical protein G ( 235) 320 81.7 3.6e-13	gi 141437295 gb ECR82204.1  hypothetical protein G ( 177) 305 78.3 3.1e-12
gi 136011793 gb EBL31511.1  hypothetical protein G ( 197) 319 81.5 3.7e-13	gi 140939661 gb ECO53532.1  hypothetical protein G ( 194) 305 78.3 3.3e-12
gi 53952283 gb AAV02280.1  Sequence 14237 from pat ( 110) 315 80.4 4.3e-13	gi 5305296 gb AAD41573.1 AF056561_1 unknown [Brass ( 163) 304 78.0 3.4e-12
gi 27902577 gb AAO24265.1  microsomal omega-3-fatt ( 380) 321 82.1 4.7e-13	gi 141373649 gb ECR37601.1  hypothetical protein G ( 177) 304 78.0 3.6e-12
gi 188509991 gb ACD56667.1  omega-3 fatty acid des ( 380) 321 82.1 4.7e-13	gi 134996864 gb EBE81927.1  hypothetical protein G ( 171) 303 77.8 4.1e-12
gi 15430570 dbj BAB18135.2  microsomal omega-3 fat ( 380) 321 82.1 4.7e-13	gi 61162223 dbj BAD36812.2  microsomal omega-3 fat ( 381) 307 78.9 4.3e-12
gi 189014684 gb ACD69578.1  omega-3 fatty acid des ( 380) 321 82.1 4.7e-13	gi 143457875 gb EDF08039.1  hypothetical protein G ( 165) 302 77.5 4.7e-12
gi 287562 dbj BAA03306.1  hypothetical protein [Vi ( 380) 321 82.1 4.7e-13	gi 138993987 gb ECC71640.1  hypothetical protein G ( 172) 302 77.6 4.9e-12
gi 157004279 gb ABY00681.1  microsomal omega-3 fat ( 380) 321 82.1 4.7e-13	gi 141025864 gb ECP12238.1  hypothetical protein G ( 174) 302 77.6 4.9e-12
gi 113548266 dbj BAF11709.1  Os03g0290300 [Oryza s ( 276) 319 81.6 4.9e-13	gi 135975138 gb EBL08479.1  hypothetical protein G ( 176) 302 77.6 5e-12
gi 62789967 gb AAY08316.1  Sequence 9 from patent ( 413) 321 82.1 5e-13	gi 38564809 gb AAR23833.1  delta-12 oleate desatur ( 419) 306 78.7 5.4e-12
gi 158283651 gb EDP09401.1  chloroplast glycerolip ( 418) 321 82.1 5e-13	gi 76007352 gb BAD38266.1  Sequence 9 from patent ( 302) 304 78.1 5.7e-12
gi 118638729 gb ABL09485.1  omega-3 fatty acid des ( 418) 321 82.1 5e-13	gi 17918538 gb AAE85972.1  Sequence 9 from patent ( 302) 304 78.1 5.7e-12
gi 5305298 gb AAD41574.1 AF056562_1 unknown [Brass ( 169) 316 80.8 5.2e-13	gi 17909755 gb AAE82562.1  Sequence 9 from patent ( 302) 304 78.1 5.7e-12
gi 187424523 gb ACD03846.1  omega-3 fatty acid des ( 436) 321 82.1 5.2e-13	gi 141619566 gb ECS57491.1  hypothetical protein G ( 186) 301 77.3 6.1e-12
gi 3452132 gb AAC32756.1  putative oleate 12-desat ( 181) 316 80.8 5.5e-13	gi 110739886 dbj BAF01848.1  omega-3 fatty acid de ( 225) 302 77.6 6.1e-12

gi 141103895 gb ECP65231.1	hypothetical protein G ( 123)	296	76.1	9.5e-12	gi 167018792 gb ABZ05366.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 137018838 gb EBR74904.1	hypothetical protein G ( 153)	296	76.2	1.1e-11	gi 167018790 gb ABZ05365.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 139880277 gb ECI09568.1	hypothetical protein G ( 178)	296	76.2	1.3e-11	gi 167018864 gb ABZ05402.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 136984566 gb EBR55532.1	hypothetical protein G ( 195)	295	76.0	1.6e-11	gi 167018728 gb ABZ05334.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 112099625 gb ABI10361.1	Sequence 22 from paten ( 351)	298	76.8	1.7e-11	gi 167018722 gb ABZ05331.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 599592 dbj BAA05515.1	microsomal omega-3 acid ( 379)	298	76.8	1.8e-11	gi 167018778 gb ABZ05359.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 21668484 dbj BAC01273.1	microsomal omega-3 fat ( 379)	298	76.8	1.8e-11	gi 167018696 gb ABZ05318.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 137790912 gb EBW01485.1	hypothetical protein G ( 170)	292	75.3	2.3e-11	gi 167018826 gb ABZ05383.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 136351800 gb EBN58293.1	hypothetical protein G ( 255)	294	75.8	2.4e-11	gi 167018724 gb ABZ05332.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 155311457 gb ABT67061.1	Sequence 154531 from p ( 145)	290	74.8	2.8e-11	gi 167018846 gb ABZ05393.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 155327923 gb ABT83527.1	Sequence 170997 from p ( 138)	289	74.5	3.2e-11	gi 167018762 gb ABZ05351.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 154354067 gb ABS76143.1	chloroplast omega-3 fa ( 248)	292	75.4	3.2e-11	gi 167018760 gb ABZ05350.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 17918537 gb AAE85971.1	Sequence 8 from patent ( 309)	292	75.4	3.9e-11	gi 167018690 gb ABZ05315.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 17909754 gb AAE82561.1	Sequence 8 from patent ( 309)	292	75.4	3.9e-11	gi 167018756 gb ABZ05348.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 154354067 gb ABS76143.1	Sequence 8 from patent ( 309)	292	75.4	3.9e-11	gi 167018768 gb ABZ05354.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 157337097 emb CAO21443.1	unnamed protein produ ( 329)	292	75.4	4.1e-11	gi 167018738 gb ABZ05339.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 155367161 gb ABU22766.1	Sequence 210235 from p ( 138)	287	74.1	4.3e-11	gi 167018698 gb ABZ05319.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 144600655 gb ABP01593.1	microsomal omega-3 fat ( 105)	285	73.6	4.7e-11	gi 167018794 gb ABZ05367.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 134987868 gb EBE75801.1	hypothetical protein G ( 171)	286	73.9	6.1e-11	gi 167018832 gb ABZ05386.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 139880513 gb ECI09723.1	hypothetical protein G ( 157)	285	73.7	6.6e-11	gi 167018812 gb ABZ05326.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 5057564 gb AAD41803.1	AF140059_1 fatty acid des ( 177)	284	73.5	8.6e-11	gi 167018730 gb ABZ05385.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 141600306 gb ECS52576.1	hypothetical protein G ( 173)	283	73.2	9.9e-11	gi 167018862 gb ABZ05401.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 157337096 emb CAO21442.1	unnamed protein produ ( 329)	286	74.1	1.1e-10	gi 167018776 gb ABZ05358.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 17402595 dbj BAB78717.1	omega-3 fatty acid des ( 418)	287	74.3	1.1e-10	gi 167018700 gb ABZ05320.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 210028781 emb CAR94991.1	unnamed protein produ ( 115)	280	72.4	1.1e-10	gi 167018770 gb ABZ05355.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 138224268 gb EBY53079.1	hypothetical protein G ( 139)	281	72.7	1.1e-10	gi 167018802 gb ABZ05371.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 17224294 gb AAL36934.1	AF213482_1 delta-15 desa ( 390)	285	73.9	1.4e-10	gi 167018740 gb ABZ05340.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 6900316 emb CAB71341.1	omega-3 fatty acid desa ( 164)	280	72.5	1.5e-10	gi 167018718 gb ABZ05329.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 137799086 gb EBW06156.1	hypothetical protein G ( 136)	278	72.0	1.8e-10	gi 167018858 gb ABZ05399.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 155363868 gb ABU19473.1	Sequence 206942 from p ( 169)	279	72.3	1.8e-10	gi 167018796 gb ABZ05368.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 141600305 gb ECS52575.1	hypothetical protein G ( 123)	277	71.8	1.9e-10	gi 167018800 gb ABZ05370.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 155334563 gb ABT90167.1	Sequence 177637 from p ( 137)	277	71.8	2.1e-10	gi 167018814 gb ABZ05377.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 139974114 gb ECI74768.1	hypothetical protein G ( 122)	276	71.5	2.2e-10	gi 167018744 gb ABZ05342.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 139351796 gb ECE59526.1	hypothetical protein G ( 135)	276	71.6	2.4e-10	gi 167018758 gb ABZ05349.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 144600653 gb ABP01592.1	microsomal omega-3 fat ( 105)	274	71.0	2.7e-10	gi 167018716 gb ABZ05328.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 125543438 gb EAY89577.1	hypothetical protein O ( 387)	279	72.5	3.6e-10	gi 167018732 gb ABZ05336.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 140139588 gb ECJ80227.1	hypothetical protein G ( 140)	273	70.9	4e-10	gi 167018766 gb ABZ05353.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 5305752 gb AAD41800.1	AF140053_1 unknown [Brass ( 157)	273	70.9	4.4e-10	gi 167018774 gb ABZ05357.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 112099645 gb ABI10376.1	Sequence 37 from paten ( 321)	272	70.9	9.5e-10	gi 167018808 gb ABZ05374.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 179185401 gb AAE85974.1	Sequence 11 from patent ( 224)	270	70.3	9.6e-10	gi 167018828 gb ABZ05384.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 62789096 gb AAY07979.1	Sequence 10 from patent ( 224)	270	70.3	9.6e-10	gi 167018810 gb ABZ05375.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 115833236 gb ABJ40714.1	Sequence 10 from paten ( 224)	270	70.3	9.6e-10	gi 167018806 gb ABZ05373.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 215072601 gb AAM57795.1	Sequence 10 from patent ( 224)	270	70.3	9.6e-10	gi 167018848 gb ABZ05394.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 17909757 gb AAE82564.1	Sequence 11 from patent ( 224)	270	70.3	9.6e-10	gi 167018838 gb ABZ05389.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 5305304 gb AAD41577.1	Sequence 10 from patent ( 224)	270	70.3	9.6e-10	gi 167018682 gb ABZ05311.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 76007354 gb ABA38268.1	Sequence 11 from patent ( 224)	270	70.3	9.6e-10	gi 167018704 gb ABZ05322.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 408490 gb AAA61774.1	omega-3 fatty acid desatu ( 329)	272	70.9	9.7e-10	gi 167018804 gb ABZ05372.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 140855362 gb ECN95874.1	hypothetical protein G ( 136)	265	69.1	1.4e-09	gi 167018788 gb ABZ05364.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 5305308 gb AAD41579.1	AF056568_1 unknown [Brass ( 106)	262	68.3	1.8e-09	gi 167018784 gb ABZ05362.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 5305306 gb AAD41578.1	AF056567_1 unknown [Brass ( 104)	261	68.1	2.1e-09	gi 167018764 gb ABZ05352.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 5305304 gb AAD41577.1	AF056566_1 unknown [Brass ( 108)	261	68.1	2.2e-09	gi 167018856 gb ABZ05398.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 112099663 gb ABI10389.1	Sequence 68 from paten ( 379)	264	69.1	3.9e-09	gi 167018798 gb ABZ05369.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 112099666 gb ABI10391.1	Sequence 70 from paten ( 384)	262	68.6	5.4e-09	gi 167018824 gb ABZ05382.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 140873904 gb EC009092.1	hypothetical protein G ( 227)	259	67.8	5.5e-09	gi 167018730 gb ABZ05335.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 144600657 gb ABP01594.1	microsomal omega-3 fat ( 105)	254	66.5	6.4e-09	gi 167018840 gb ABZ05390.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 134135879 gb ABO56993.1	fatty acid desaturase ( 365)	260	68.1	7e-09	gi 167018816 gb ABZ05378.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 142490019 gb ECY45889.1	hypothetical protein G ( 103)	253	66.2	7.4e-09	gi 167018860 gb ABZ05400.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09
gi 137372058 gb EBT72798.1	hypothetical protein G ( 137)	254	66.5	8e-09	gi 167018726 gb ABZ05333.1	fatty acid desaturase ( 118)	253	66.3	8.3e-09

gi 167018772 gb ABZ05356.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 167018818 gb ABZ05379.1	fatty acid desaturase	( 111)	217	58.0	2.4e-06
gi 167018710 gb ABZ05325.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 50261903 gb AAT72504.1	AT4G30950 [Arabidopsis	( 203)	220	58.9	2.4e-06
gi 167018742 gb ABZ05341.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 167018822 gb ABZ05381.1	fatty acid desaturase	( 110)	216	57.8	2.7e-06
gi 167018786 gb ABZ05363.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 33634986 emb CAE20972.1	Fatty acid desaturase,	( 361)	221	59.2	3.4e-06
gi 167018708 gb ABZ05324.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 488509 dbj BAA02921.1	delta 12 desaturase [Syn	( 349)	220	59.0	3.8e-06
gi 167018836 gb ABZ05388.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 2696717 dbj BAA23881.1	chloroplast w6 desatura	( 424)	221	59.3	3.8e-06
gi 167018782 gb ABZ05361.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 158277870 gb EDP03637.1	omega-6-FAD, chloropla	( 424)	221	59.3	3.8e-06
gi 167018680 gb ABZ05310.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 194342553 gb EDX23519.1	fatty acid desaturase	( 367)	219	58.8	4.7e-06
gi 167018702 gb ABZ05321.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 111055893 gb EAT77013.1	hypothetical protein S	( 374)	219	58.8	4.7e-06
gi 167018754 gb ABZ05347.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 141139091 gb ECP89709.1	hypothetical protein G	( 108)	212	56.9	5.1e-06
gi 167018688 gb ABZ05314.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 76059320 emb CAJ30854.1	unnamed protein produc	( 418)	219	58.8	5.2e-06
gi 167018686 gb ABZ05313.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 126633854 emb CAM55883.1	unnamed protein produ	( 418)	219	58.8	5.2e-06
gi 167018748 gb ABZ05344.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 60220820 emb CAI58909.1	unnamed protein produc	( 418)	219	58.8	5.2e-06
gi 167018780 gb ABZ05360.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 17135418 dbj BAB77964.1	phosphatidylcholine de	( 350)	218	58.5	5.3e-06
gi 167018736 gb ABZ05338.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 493225 dbj BAA03435.1	fatty-acid desaturase [A	( 350)	218	58.5	5.3e-06
gi 167018868 gb ABZ05404.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 167292275 gb ABZ45139.1	Sequence 19077 from pa	( 350)	218	58.5	5.3e-06
gi 167018720 gb ABZ05330.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 75704134 gb ABA23810.1	Fatty acid desaturase [	( 350)	218	58.5	5.3e-06
gi 167018684 gb ABZ05312.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 1653254 dbj BAA18169.1	fatty acid desaturase [	( 351)	217	58.3	6.2e-06
gi 167018866 gb ABZ05403.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 40652 emb CAA37584.1	unnamed protein product [	( 351)	217	58.3	6.2e-06
gi 167018694 gb ABZ05317.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 167275936 gb ABZ28800.1	Sequence 2738 from pat	( 351)	217	58.3	6.2e-06
gi 167018750 gb ABZ05345.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 108863908 gb ABA91057.2	Omega-3 fatty acid des	( 415)	217	58.4	7.1e-06
gi 167018854 gb ABZ05397.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 138773117 gb ECB81856.1	hypothetical protein G	( 111)	210	56.4	7.1e-06
gi 167018752 gb ABZ05346.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 137634104 gb EBV16995.1	hypothetical protein G	( 153)	211	56.7	8e-06
gi 167018706 gb ABZ05323.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 137012142 gb EBR71172.1	hypothetical protein G	( 125)	209	56.2	9.2e-06
gi 167018852 gb ABZ05396.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 159028367 emb CAO87265.1	unnamed protein produ	( 346)	214	57.6	9.8e-06
gi 167018870 gb ABZ05405.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 141103894 gb ECP65230.1	hypothetical protein G	( 133)	208	56.0	1.1e-05
gi 167018844 gb ABZ05392.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 166090471 dbj BAG05179.1	delta 12 acyl-lipid d	( 346)	213	57.4	1.1e-05
gi 167018812 gb ABZ05376.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 41581195 emb CAF18424.1	delta 12 acyl-lipid de	( 350)	213	57.4	1.2e-05
gi 167018746 gb ABZ05343.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 143683191 gb EDG25391.1	hypothetical protein G	( 274)	211	56.9	1.3e-05
gi 167018734 gb ABZ05337.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 118487416 gb ABK95536.1	unknown [Populus trich	( 444)	213	57.5	1.4e-05
gi 167018820 gb ABZ05380.1	fatty acid desaturase	( 118)	253	66.3	8.3e-09	gi 149390715 gb ABR25375.1	omega 6 fatty acid des	( 79)	203	54.8	1.6e-05
gi 155289548 gb ABT45152.1	Sequence 132622 from p	( 224)	250	65.7	2.3e-08	gi 54873456 gb AAV41001.1	chloroplast fatty acid	( 443)	211	57.0	1.9e-05
gi 62789970 gb AAY08319.1	Sequence 12 from patent	( 289)	251	66.0	2.4e-08	gi 55772330 dbj BAD70771.1	fatty acid desaturase	( 345)	209	56.5	2.2e-05
gi 138003596 gb EBX22343.1	hypothetical protein G	( 103)	244	64.2	3.1e-08	gi 46196514 gb AAS80930.1	omega-(3) fatty acid de	( 345)	209	56.5	2.2e-05
gi 162669532 gb EDQ56117.1	predicted protein [Phy	( 173)	244	64.3	4.8e-08	gi 35214308 dbj BAC91676.1	delta 12 acyl-lipid de	( 355)	209	56.5	2.2e-05
gi 167018692 gb ABZ05316.1	fatty acid desaturase	( 118)	241	63.5	5.5e-08	gi 42408692 dbj BAD09911.1	putative Omega-6 fatty	( 414)	209	56.5	2.5e-05
gi 155102612 gb ABT03235.1	Sequence 44 from paten	( 359)	246	64.9	6.4e-08	gi 42408677 dbj BAD09897.1	putative Omega-6 fatty	( 414)	209	56.5	2.5e-05
gi 167018714 gb ABZ05327.1	fatty acid desaturase	( 117)	240	63.3	6.5e-08	gi 167293298 gb ABZ46162.1	Sequence 20100 from pa	( 347)	208	56.3	2.5e-05
gi 169887016 gb ACB00730.1	phosphatidylcholine de	( 347)	245	64.7	7.3e-08	gi 186468714 gb ACC84515.1	fatty acid desaturase	( 353)	208	56.3	2.6e-05
gi 6649528 gb AAF21445.1	U36388_2 delta-12 desatur	( 347)	245	64.7	7.3e-08	gi 196176135 gb EDX71152.1	Fatty acid desaturase	( 354)	208	56.3	2.6e-05
gi 488511 dbj BAA02922.1	delta_12 desaturase [Syn	( 347)	245	64.7	7.3e-08	gi 58013371 gb AAW63039.1	plastidial delta-12 ole	( 443)	209	56.5	2.7e-05
gi 147847464 emb CAK23015.1	Fatty acid desaturase	( 354)	245	64.7	7.4e-08	gi 155090528 gb ABS96125.1	Sequence 72 from paten	( 418)	206	55.8	4.1e-05
gi 140312354 gb ECK90461.1	hypothetical protein G	( 118)	238	62.8	8.9e-08	gi 493068 gb AAA92800.1	chloroplast omega-6 fatty	( 418)	206	55.8	4.1e-05
gi 134412622 gb EBB20102.1	hypothetical protein G	( 120)	237	62.6	1.1e-07	gi 623344 emb CAA55121.1	n-6 fatty acid desaturas	( 447)	206	55.9	4.3e-05
gi 34600646 gb AAQ78503.1	Sequence 8 from patent	( 59)	233	61.5	1.1e-07	gi 154813796 gb ABS86963.1	chloroplast delta-12 f	( 447)	206	55.9	4.3e-05
gi 10278520 emb CAC09647.1	unnamed protein produc	( 59)	233	61.5	1.1e-07	gi 114384177 gb ABI73993.1	omega-6 fatty acid des	( 447)	206	55.9	4.3e-05
gi 137892068 gb EBW59749.1	hypothetical protein G	( 117)	233	61.7	2e-07	gi 7269997 emb CAB79813.1	chloroplast omega-6 fat	( 448)	206	55.9	4.3e-05
gi 186469984 gb ACB85610.1	delta 12 desaturase [A	( 350)	238	63.1	2.2e-07	gi 15010640 gb AAK73979.1	AT4g30950/F6I18_140 [Ar	( 448)	206	55.9	4.3e-05
gi 805064 emb CAA60415.1	delta 12 desaturase [Art	( 351)	238	63.1	2.2e-07	gi 2980771 emb CAA18198.1	chloroplast omega-6 fat	( 448)	206	55.9	4.3e-05
gi 147851166 emb CAK28660.1	Fatty acid desaturase	( 351)	237	62.9	2.6e-07	gi 16604360 gb AAL24186.1	AT4g30950/F6I18_140 [Ar	( 448)	206	55.9	4.3e-05
gi 141492535 gb ECS50464.1	hypothetical protein G	( 161)	229	60.9	4.8e-07	gi 18958032 gb AAL79589.1	AT4g30950/F6I18_140 [Ar	( 448)	206	55.9	4.3e-05
gi 155289549 gb ABT45153.1	Sequence 132623 from p	( 328)	232	61.7	5.4e-07	gi 16604468 gb AAL24240.1	AT4g30950/F6I18_140 [Ar	( 448)	206	55.9	4.3e-05
gi 35213192 dbj BAC90564.1	delta 12 acyl-lipid de	( 352)	231	61.5	6.7e-07	gi 21593581 gb AAM65548.1	chloroplast omega-6 fat	( 448)	206	55.9	4.3e-05
gi 7381157 gb AAF61413.1	AF134896_1 delta 12 desat	( 352)	231	61.5	6.7e-07	gi 142830407 gb EDA90356.1	hypothetical protein G	( 380)	205	55.6	4.4e-05
gi 3452135 gb AAC32757.1	putative oleate 12-desat	( 161)	225	60.0	9.1e-07	gi 140563764 gb ECM22629.1	hypothetical protein G	( 95)	197	53.4	4.9e-05
gi 143452461 gb EDF04111.1	hypothetical protein G	( 127)	223	59.4	1e-06	gi 196191947 gb EDX86911.1	Fatty acid desaturase	( 346)	203	55.1	5.6e-05
gi 123963403 gb ABM78159.1	Fatty acid desaturase,	( 361)	228	60.8	1.1e-06	gi 136641202 gb EBP45594.1	hypothetical protein G	( 287)	201	54.6	6.6e-05
gi 138327289 gb EBY99311.1	hypothetical protein G	( 118)	219	58.5	1.8e-06	gi 5821436 dbj BAA83822.1	chloroplast w6 desatura	( 421)	203	55.2	6.6e-05

gi 156900672 gb ABU96742.1 chloroplast omega-6 fa ( 440) 203 55.2 6.8e-05	gi 154358245 gb ABS79146.1 At4g30950-like protein ( 111) 184 50.5 0.00044
gi 142370756 gb ECX58803.1 hypothetical protein G ( 116) 195 53.0 8e-05	gi 171699545 gb ACB52526.1 fatty acid desaturase ( 349) 190 52.1 0.00044
gi 167018834 gb ABZ05387.1 fatty acid desaturase ( 102) 193 52.5 9.8e-05	gi 154358193 gb ABS79120.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 167018842 gb ABZ05391.1 fatty acid desaturase ( 102) 193 52.5 9.8e-05	gi 154358187 gb ABS79117.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 112099608 gb ABI10347.1 Sequence 6 from patent ( 217) 196 53.4 0.00011	gi 154358195 gb ABS79121.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 112099662 gb ABI10388.1 Sequence 64 from paten ( 218) 196 53.4 0.00012	gi 154358203 gb ABS79125.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 139465389 gb ECF29015.1 hypothetical protein G ( 152) 193 52.6 0.00014	gi 154358183 gb ABS79115.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 162682735 gb EDQ69151.1 predicted protein [Phy ( 342) 197 53.7 0.00014	gi 154358191 gb ABS79119.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 112099607 gb ABI10346.1 Sequence 5 from patent ( 283) 196 53.5 0.00014	gi 154358247 gb ABS79147.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 139342629 gb ECE56642.1 hypothetical protein G ( 119) 191 52.1 0.00015	gi 154358189 gb ABS79118.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 167018850 gb ABZ05395.1 fatty acid desaturase ( 100) 190 51.8 0.00016	gi 154358205 gb ABS79126.1 At4g30950-like protein ( 112) 184 50.5 0.00044
gi 112099669 gb ABI10393.1 Sequence 72 from paten ( 218) 194 52.9 0.00016	gi 154358239 gb ABS79143.1 At4g30950-like protein ( 113) 184 50.5 0.00044
gi 49355354 gb AAT65208.1 omega-6 desaturase [Bra ( 443) 197 53.8 0.00018	gi 12655937 gb AAK00664.1 AF229392_1 omega 6 reduc ( 201) 187 51.3 0.00045
gi 155316475 gb ABT72079.1 Sequence 159549 from p ( 81) 188 51.3 0.00018	gi 125603557 gb EAZ42882.1 hypothetical protein O ( 370) 190 52.2 0.00046
gi 112099667 gb ABI10392.1 Sequence 71 from paten ( 283) 194 53.0 0.0002	gi 125561683 gb EAX07131.1 hypothetical protein O ( 372) 190 52.2 0.00047
gi 110165097 gb ABG49637.1 fatty acid desaturase ( 351) 195 53.3 0.0002	gi 68348070 gb AAY95676.1 delta 12 desaturase [Ps ( 659) 193 53.0 0.00047
gi 33639203 emb CAB08211.1 possible fatty acid de ( 378) 195 53.3 0.00021	gi 146218708 emb CAM96526.1 putative chloroplast ( 167) 185 50.8 0.00053
gi 116787557 gb ABT04556.1 unknown [Picea sitchen ( 460) 196 53.6 0.00021	gi 88911216 gb ABD58898.1 chloroplast omega-6 fat ( 439) 190 52.2 0.00053
gi 134996528 gb EBE81702.1 hypothetical protein G ( 394) 195 53.3 0.00022	gi 5305312 gb AAD41581.1 AF056571_1 unknown [Brass ( 141) 184 50.6 0.00053
gi 84787828 gb ABC64010.1 putative fatty acid des ( 344) 194 53.1 0.00023	gi 112099651 gb ABI10380.1 Sequence 41 from paten ( 141) 184 50.6 0.00053
gi 112659969 gb AAK00662.1 AF229390_1 omega 6 reduc ( 202) 191 52.2 0.00024	gi 61620777 gb AAX47480.1 microsomal omega-6-des ( 151) 184 50.6 0.00057
gi 457631 gb AAA50157.1 omega-6 desaturase ( 443) 195 53.3 0.00024	gi 12655931 gb AAK00661.1 AF229389_1 omega 6 reduc ( 222) 186 51.1 0.00057
gi 154358219 gb ABS79133.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 140516970 gb ECM08249.1 hypothetical protein G ( 246) 185 50.9 0.00073
gi 154358243 gb ABS79145.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 5305310 gb AAD41580.1 AF056570_1 unknown [Brass ( 141) 182 50.1 0.00073
gi 154358221 gb ABS79134.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 112099652 gb ABI10381.1 Sequence 42 from paten ( 141) 182 50.1 0.00073
gi 154358235 gb ABS79141.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 140873905 gb ECO09093.1 hypothetical protein G ( 68) 178 49.0 0.00075
gi 154358201 gb ABS79124.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 134906514 gb EBE21366.1 hypothetical protein G ( 261) 185 50.9 0.00076
gi 154358217 gb ABS79132.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 142875988 gb EDB20702.1 hypothetical protein G ( 191) 183 50.4 0.00081
gi 154358207 gb ABS79127.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 112099648 gb ABI10378.1 Sequence 39 from paten ( 257) 183 50.5 0.001
gi 154358213 gb ABS79130.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 1785856 dbj BAA11396.1 w-3 fatty acid desatura ( 269) 183 50.5 0.0011
gi 154358181 gb ABS79114.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 138969562 gb ECC63594.1 hypothetical protein G ( 278) 183 50.5 0.0011
gi 154358231 gb ABS79139.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 113623875 dbj BAF23820.1 Os08g0440900 [Oryza s ( 184) 179 49.5 0.0015
gi 154358185 gb ABS79116.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 34600645 gb AAQ78502.1 Sequence 6 from patent ( 183) 177 49.0 0.002
gi 154358251 gb ABS79149.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 10278518 emb CAC09646.1 unnamed protein produc ( 183) 177 49.0 0.002
gi 154358211 gb ABS79129.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 138090575 gb EBX69101.1 hypothetical protein G ( 283) 179 49.6 0.0021
gi 154358233 gb ABS79140.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 143207578 gb EDD59354.1 hypothetical protein G ( 368) 180 49.9 0.0022
gi 154358249 gb ABS79148.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 136415656 gb EBO01902.1 hypothetical protein G ( 315) 179 49.6 0.0023
gi 154358199 gb ABS79123.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 144066402 gb EDI62561.1 hypothetical protein G ( 196) 176 48.8 0.0025
gi 154358237 gb ABS79142.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 157388522 gb ABV51227.1 Fatty acid desaturase, ( 368) 179 49.6 0.0026
gi 154358225 gb ABS79136.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 134825520 gb EBD68131.1 hypothetical protein G ( 220) 176 48.8 0.0028
gi 154358197 gb ABS79122.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 52346891 gb AAU39525.1 hypothetical protein BL ( 342) 178 49.4 0.0029
gi 154358227 gb ABS79137.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 46408141 emb CAG26642.1 unnamed protein produc ( 342) 178 49.4 0.0029
gi 154358209 gb ABS79128.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 52002229 gb AAU22171.1 fatty acid desaturase [ ( 342) 178 49.4 0.0029
gi 154358241 gb ABS79144.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 136733729 gb EBQ04834.1 hypothetical protein G ( 303) 177 49.1 0.0031
gi 154358229 gb ABS79138.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 108863907 gb ECS90863.1 Omega-3 fatty acid des ( 271) 176 48.9 0.0033
gi 154358215 gb ABS79131.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 459962 gb AAA50158.1 plastid omega-6 desaturas ( 424) 178 49.4 0.0035
gi 154358223 gb ABS79135.1 At4g30950-like protein ( 128) 188 51.4 0.00026	gi 91125674 gb ABE12622.1 Sequence 35 from patent ( 424) 178 49.4 0.0035
gi 162684563 gb EDQ70964.1 predicted protein [Phy ( 340) 193 52.8 0.00027	gi 33238186 gb AAQ00253.1 Fatty acid desaturase [ ( 370) 177 49.2 0.0036
gi 157330281 emb CAO45069.1 unnamed protein produ ( 301) 192 52.6 0.00028	gi 113644232 dbj BAF27373.1 Os11g0104400 [Oryza s ( 269) 175 48.7 0.0038
gi 195628958 gb ACG36241.1 hypothetical protein [ ( 443) 194 53.1 0.00029	gi 171991123 gb ACB62045.1 fatty acid desaturase ( 339) 175 48.7 0.0046
gi 162669755 gb EDQ56336.1 predicted protein [Phy ( 454) 194 53.1 0.00029	gi 141716287 gb ECS90863.1 hypothetical protein G ( 306) 174 48.5 0.005
gi 113881936 gb ABT46894.1 possible fatty acid de ( 399) 193 52.9 0.00031	gi 189184986 gb ACD82171.1 Fatty acid desaturase ( 295) 173 48.2 0.0057
gi 126559291 gb AAK00660.1 AF229388_1 omega 6 reduc ( 213) 189 51.8 0.00034	gi 108467859 gb ABF93044.1 fatty acid desaturase ( 361) 174 48.5 0.0057
gi 126559351 gb AAK00663.1 AF229391_1 omega 6 reduc ( 216) 189 51.8 0.00035	gi 24193921 gb AAN47701.1 AE011236_10 Fatty acid d ( 365) 174 48.5 0.0058
gi 493553391 gb AAT65203.1 omega-6 desaturase [Bra ( 443) 192 52.7 0.00039	gi 198248261 gb ACH3854.1 fatty acid desaturase ( 374) 174 48.5 0.0059
gi 155273457 gb ABT29061.1 Sequence 116531 from p ( 443) 192 52.7 0.00039	gi 142453372 gb ECY18908.1 hypothetical protein G ( 259) 172 48.0 0.0059
gi 136784329 gb EBQ98333.1 hypothetical protein G ( 259) 189 51.8 0.0004	gi 120324979 gb ABM19294.1 fatty acid desaturase ( 362) 173 48.3 0.0067
gi 906553891 gb ABD96230.1 possible fatty acid des ( 379) 191 52.4 0.0004	gi 45602124 gb AAS71602.1 fatty acid desaturase [ ( 365) 173 48.3 0.0068

gi 126543953 gb ABO18195.1	Fatty acid desaturase, ( 368)	173	48.3	0.0068	gi 142848386 gb EDB03752.1	hypothetical protein G ( 326)	163	46.0	0.03
gi 135949122 gb EBK90918.1	hypothetical protein G ( 368)	173	48.3	0.0068	gi 139409156 gb ECE91420.1	hypothetical protein G ( 153)	159	44.9	0.03
gi 144056605 gb ED155295.1	hypothetical protein G ( 369)	173	48.3	0.0068	gi 109454449 gb ABG30654.1	fatty acid desaturase, ( 350)	163	46.0	0.032
gi 136114208 gb EBM00849.1	hypothetical protein G ( 374)	173	48.3	0.0069	gi 189335465 dbj BAG44535.1	putative fatty acid d ( 361)	163	46.0	0.033
gi 210028779 emb CAR94990.1	unnamed protein produ ( 89)	165	46.1	0.0074	gi 142399062 gb ECX78387.1	hypothetical protein G ( 368)	163	46.0	0.033
gi 143730985 gb EDG49314.1	hypothetical protein G ( 368)	172	48.0	0.008	gi 142248916 gb ECW70653.1	hypothetical protein G ( 309)	162	45.7	0.034
gi 136362146 gb EBN65337.1	hypothetical protein G ( 390)	172	48.1	0.0084	gi 160341224 gb ABX14310.1	fatty acid desaturase ( 378)	163	46.0	0.034
gi 215765755 dbj BAG87452.1	unnamed protein produ ( 162)	167	46.7	0.0089	gi 138257509 gb EBY61921.1	hypothetical protein G ( 181)	159	44.9	0.035
gi 142760554 gb EDA38161.1	hypothetical protein G ( 196)	168	47.0	0.0089	gi 135823807 gb EBK07194.1	hypothetical protein G ( 322)	162	45.7	0.035
gi 136276686 gb EBN07445.1	hypothetical protein G ( 377)	171	47.8	0.0095	gi 60172920 gb AAX14502.1	delta-8 fatty acid desa ( 476)	164	46.3	0.035
gi 155315801 gb ABT71405.1	Sequence 158875 from p ( 177)	167	46.7	0.0095	gi 60220814 emb CAI58906.1	unnamed protein produc ( 476)	164	46.3	0.035
gi 134324014 gb EBA64569.1	hypothetical protein G ( 160)	166	46.5	0.01	gi 76059314 emb CAJ30851.1	unnamed protein produc ( 476)	164	46.3	0.035
gi 137661488 gb EBV31099.1	hypothetical protein G ( 175)	166	46.5	0.011	gi 126633752 emb CAM55832.1	unnamed protein produ ( 476)	164	46.3	0.035
gi 49330597 gb AAT61243.1	delta5 acyl-lipid desat ( 319)	169	47.3	0.011	gi 40193163 gb AAR78135.1	Sequence 33 from patent ( 29)	149	42.2	0.036
gi 49179721 gb AAU55097.1	fatty acid desaturase [ ( 319)	169	47.3	0.011	gi 158473916 gb ABW47816.1	Sequence 22 from paten ( 29)	149	42.2	0.036
gi 30257588 gb AAP26818.1	fatty acid desaturase [ ( 319)	169	47.3	0.011	gi 118901317 gb ABL51032.1	Sequence 22 from paten ( 29)	149	42.2	0.036
gi 47503442 gb AAT32118.1	fatty acid desaturase [ ( 319)	169	47.3	0.011	gi 83349275 gb ABC14928.1	Sequence 33 from patent ( 29)	149	42.2	0.036
gi 143665885 gb EDG175625.1	hypothetical protein G ( 334)	169	47.3	0.012	gi 20230167 gb AAE91310.1	Sequence 33 from patent ( 29)	149	42.2	0.036
gi 118417547 gb ABK85966.1	delta5 acyl-lipid desa ( 343)	169	47.3	0.012	gi 110293129 gb ABG66302.1	omega-3 fatty acid des ( 91)	155	43.8	0.037
gi 217068320 gb ACT82570.1	fatty acid desaturase ( 343)	169	47.3	0.012	gi 142821377 gb EDA83492.1	hypothetical protein G ( 197)	159	44.9	0.037
gi 15975993 gb AAU17543.1	delta5 acyl-lipid desat ( 343)	169	47.3	0.012	gi 91800948 gb ABE63323.1	fatty acid desaturase [ ( 349)	162	45.7	0.037
gi 29896651 gb AAP09930.1	delta5 acyl-lipid desat ( 343)	169	47.3	0.012	gi 20230171 gb AAE91314.1	Sequence 37 from patent ( 36)	150	42.5	0.037
gi 143633755 gb EDF97335.1	hypothetical protein G ( 306)	168	47.1	0.013	gi 83349279 gb ABC14932.1	Sequence 37 from patent ( 36)	150	42.5	0.037
gi 123201151 gb ABM72759.1	Fatty acid desaturase, ( 368)	168	47.1	0.015	gi 40193167 gb AAR78139.1	Sequence 37 from patent ( 36)	150	42.5	0.037
gi 33640302 emb CAE19837.1	Fatty acid desaturase, ( 368)	168	47.1	0.015	gi 118901322 gb ABL51037.1	Sequence 27 from paten ( 36)	150	42.5	0.037
gi 154350851 gb ABS72930.1	putitative fatty acid ( 342)	167	46.9	0.017	gi 158473921 gb ABW47821.1	Sequence 27 from paten ( 36)	150	42.5	0.037
gi 206685961 gb ED246443.1	fatty acid desaturase ( 344)	167	46.9	0.017	gi 136840519 gb EBQ75828.1	hypothetical protein G ( 200)	159	44.9	0.038
gi 136409502 gb EBN97900.1	hypothetical protein G ( 236)	165	46.3	0.017	gi 139594873 gb ECG14809.1	hypothetical protein G ( 244)	160	45.2	0.038
gi 138556163 gb ECA41253.1	hypothetical protein G ( 287)	166	46.6	0.017	gi 78713356 gb ABB50533.1	fatty acid desaturase, ( 368)	162	45.8	0.039
gi 111608891 gb ABH11003.1	omega-6 fatty acid des ( 216)	164	46.1	0.018	gi 136740857 gb EBQ09515.1	hypothetical protein G ( 149)	157	44.4	0.04
gi 167324306 gb AB260899.1	Sequence 11698 from pa ( 344)	166	46.7	0.019	gi 88865995 gb ABD56872.1	fatty acid desaturase [ ( 330)	161	45.5	0.042
gi 136121332 gb EBM05702.1	hypothetical protein G ( 322)	165	46.4	0.022	gi 20230169 gb AAE91312.1	Sequence 35 from patent ( 36)	149	42.2	0.044
gi 136961755 gb EBR42583.1	hypothetical protein G ( 326)	165	46.4	0.022	gi 40193165 gb AAR78137.1	Sequence 35 from patent ( 36)	149	42.2	0.044
gi 143157154 gb EDD23046.1	hypothetical protein G ( 395)	166	46.7	0.022	gi 118901320 gb ABL51035.1	Sequence 25 from paten ( 36)	149	42.2	0.044
gi 136491773 gb EBO51081.1	hypothetical protein G ( 343)	165	46.4	0.023	gi 158473919 gb ABW47819.1	Sequence 25 from paten ( 36)	149	42.2	0.044
gi 42738016 gb AAS41947.1	fatty acid desaturase [ ( 343)	165	46.4	0.023	gi 83349277 gb ABC14930.1	Sequence 35 from patent ( 36)	149	42.2	0.044
gi 202301991 gb AAE91342.1	Sequence 66 from patent ( 36)	153	43.2	0.023	gi 140824677 gb ECN77005.1	hypothetical protein G ( 292)	160	45.2	0.044
gi 118901340 gb ABL51055.1	Sequence 49 from paten ( 36)	153	43.2	0.023	gi 142215690 gb ECW45999.1	hypothetical protein G ( 204)	158	44.7	0.045
gi 40193196 gb AAR78168.1	Sequence 66 from patent ( 36)	153	43.2	0.023	gi 142341924 gb ECX39321.1	hypothetical protein G ( 300)	160	45.3	0.045
gi 83349307 gb ABC14960.1	Sequence 66 from patent ( 36)	153	43.2	0.023	gi 123199229 gb ABM70870.1	Fatty acid desaturase, ( 368)	161	45.5	0.046
gi 158473939 gb ABW47839.1	Sequence 49 from paten ( 36)	153	43.2	0.023	gi 163862930 gb ABA43989.1	fatty acid desaturase ( 343)	160	45.3	0.05
gi 5955839 gb AAE07495.1	Sequence 21 from patent ( 37)	153	43.2	0.024	gi 138546994 gb ECA34812.1	hypothetical protein G ( 239)	158	44.7	0.051
gi 5955833 gb AAE07489.1	Sequence 15 from patent ( 37)	153	43.2	0.024	gi 190696256 gb ACE90341.1	probable fatty acid de ( 350)	160	45.3	0.051
gi 2492210 gb AAB80346.1	I66157 Sequence 15 from p ( 37)	153	43.2	0.024	gi 139660029 gb ECG58793.1	hypothetical protein G ( 294)	159	45.0	0.052
gi 2492216 gb AAB80352.1	I66163 Sequence 21 from p ( 37)	153	43.2	0.024	gi 141725778 gb ECS96738.1	hypothetical protein G ( 145)	155	43.9	0.054
gi 143544394 gb EDF55390.1	hypothetical protein G ( 368)	165	46.4	0.024	gi 136684917 gb EBP72872.1	hypothetical protein G ( 177)	156	44.2	0.054
gi 136003365 gb EBL26198.1	hypothetical protein G ( 368)	165	46.4	0.024	gi 143447253 gb EDF01011.1	hypothetical protein G ( 384)	160	45.3	0.055
gi 143444755 gb EDE99441.1	hypothetical protein G ( 370)	165	46.4	0.024	gi 83349276 gb ABC14929.1	Sequence 34 from patent ( 29)	146	41.5	0.059
gi 202301651 gb AAE91308.1	Sequence 31 from patent ( 29)	151	42.6	0.027	gi 40193164 gb AAR78136.1	Sequence 34 from patent ( 29)	146	41.5	0.059
gi 158473938 gb ABW47838.1	Sequence 48 from paten ( 29)	151	42.6	0.027	gi 158473917 gb ABW47817.1	Sequence 23 from paten ( 29)	146	41.5	0.059
gi 158473914 gb ABW47814.1	Sequence 20 from paten ( 29)	151	42.6	0.027	gi 118901318 gb ABL51033.1	Sequence 23 from paten ( 29)	146	41.5	0.059
gi 83349273 gb ABC14926.1	Sequence 31 from patent ( 29)	151	42.6	0.027	gi 20230168 gb AAE91311.1	Sequence 34 from patent ( 29)	146	41.5	0.059
gi 40193161 gb AAR78133.1	Sequence 31 from patent ( 29)	151	42.6	0.027	gi 40193166 gb AAR78138.1	Sequence 36 from patent ( 36)	147	41.8	0.06
gi 118901339 gb ABL51054.1	Sequence 48 from paten ( 29)	151	42.6	0.027	gi 83349278 gb ABC14931.1	Sequence 36 from patent ( 36)	147	41.8	0.06
gi 118901315 gb ABL51030.1	Sequence 20 from paten ( 29)	151	42.6	0.027	gi 118901321 gb ABL51036.1	Sequence 26 from paten ( 36)	147	41.8	0.06
gi 186464974 gb ACC80775.1	fatty acid desaturase ( 351)	164	46.2	0.027	gi 20230170 gb AAE91313.1	Sequence 36 from patent ( 36)	147	41.8	0.06
gi 88863496 gb ABD54373.1	fatty acid desaturase [ ( 362)	164	46.2	0.028	gi 158473920 gb ABW47820.1	Sequence 26 from paten ( 36)	147	41.8	0.06
gi 143600341 gb EDF80364.1	hypothetical protein G ( 312)	163	45.9	0.029	gi 143629263 gb EDF94858.1	hypothetical protein G ( 370)	159	45.1	0.063

gi 143884086 gb EDH32508.1	hypothetical protein G ( 307)	158	44.8	0.063	gi 167285169 gb ABZ38033.1	Sequence 11971 from pa ( 340)	153	43.7	0.15
gi 139693866 gb ECG82229.1	hypothetical protein G ( 87)	151	42.9	0.066	gi 136963384 gb EBR43477.1	hypothetical protein G ( 136)	148	42.3	0.16
gi 27350502 dbj BAC47512.1	blr2247 [Bradyrhizobiu ( 893)	160	45.4	0.068	gi 140930891 gb ECO47251.1	hypothetical protein G ( 199)	150	42.9	0.16
gi 115282774 gb ABI88291.1	fatty acid desaturase ( 340)	158	44.8	0.068	gi 144002551 gb EDI16748.1	hypothetical protein G ( 356)	153	43.7	0.16
gi 115517589 gb ABJ05573.1	fatty acid desaturase ( 349)	158	44.8	0.07	gi 77968224 gb ABB09604.1	Fatty acid desaturase [ ( 360)	153	43.7	0.16
gi 140248747 gb ECK54112.1	hypothetical protein G ( 304)	157	44.6	0.073	gi 198035352 emb CAR51227.1	fatty acid desaturase ( 360)	153	43.7	0.16
gi 47028617 gb AAT09160.1	delta-5 fatty acid desa ( 475)	159	45.1	0.077	gi 143529043 gb EDF47704.1	hypothetical protein G ( 252)	151	43.2	0.16
gi 61661518 gb AAx51386.1	delta-5 fatty acid desa ( 476)	159	45.1	0.077	gi 134613509 gb EBC39000.1	hypothetical protein G ( 254)	151	43.2	0.16
gi 142654294 gb ECZ61904.1	hypothetical protein G ( 225)	155	44.0	0.078	gi 5955841 gb AAE07497.1	Sequence 23 from patent ( 40)	141	40.4	0.17
gi 171192396 gb ACB43357.1	fatty acid desaturase ( 344)	157	44.6	0.081	gi 2492212 gb AAB80348.1	I66159 Sequence 17 from p ( 40)	141	40.4	0.17
gi 40193157 gb AAR78129.1	Sequence 27 from patent ( 30)	144	41.1	0.083	gi 2492218 gb AAB80354.1	I66165 Sequence 23 from p ( 40)	141	40.4	0.17
gi 118901310 gb ABL51025.1	Sequence 15 from paten ( 30)	144	41.1	0.083	gi 5955835 gb AAE07491.1	Sequence 17 from patent ( 40)	141	40.4	0.17
gi 83349269 gb ABC14922.1	Sequence 27 from patent ( 30)	144	41.1	0.083	gi 135702350 gb EBJ31380.1	hypothetical protein G ( 222)	150	42.9	0.17
gi 158473909 gb ABW47809.1	Sequence 15 from paten ( 30)	144	41.1	0.083	gi 196193075 gb EDX88034.1	Fatty acid desaturase ( 328)	152	43.4	0.17
gi 20230161 gb AAE91304.1	Sequence 27 from patent ( 30)	144	41.1	0.083	gi 142640255 gb ECZ52013.1	hypothetical protein G ( 329)	152	43.4	0.17
gi 134810286 gb EBD58450.1	hypothetical protein G ( 295)	156	44.3	0.083	gi 137677701 gb EBV40288.1	hypothetical protein G ( 236)	150	42.9	0.18
gi 182635565 gb ACB96339.1	fatty acid desaturase ( 363)	157	44.6	0.085	gi 121588613 gb ABM61193.1	fatty acid desaturase ( 349)	152	43.5	0.18
gi 140259977 gb ECK61602.1	hypothetical protein G ( 250)	155	44.1	0.085	gi 134772240 gb EBD32686.1	hypothetical protein G ( 351)	152	43.5	0.18
gi 136533675 gb EBO78016.1	hypothetical protein G ( 254)	155	44.1	0.086	gi 136921855 gb EBR20091.1	hypothetical protein G ( 242)	150	42.9	0.18
gi 136997190 gb EBR62659.1	hypothetical protein G ( 313)	156	44.3	0.088	gi 91802797 gb ABE65169.1	fatty acid desaturase [ ( 354)	152	43.5	0.18
gi 158473918 gb ABW47818.1	Sequence 24 from paten ( 29)	143	40.8	0.094	gi 142019328 gb ECU89117.1	hypothetical protein G ( 246)	150	42.9	0.19
gi 118901316 gb ABL51031.1	Sequence 21 from paten ( 29)	143	40.8	0.094	gi 5823006 gb AAD53003.1	AF076471_1 MocD [Sinorhiz ( 361)	152	43.5	0.19
gi 40193162 gb AAR78134.1	Sequence 32 from patent ( 29)	143	40.8	0.094	gi 144135916 gb EDJ12565.1	hypothetical protein G ( 363)	152	43.5	0.19
gi 118901319 gb ABL51034.1	Sequence 24 from paten ( 29)	143	40.8	0.094	gi 139074519 gb ECD23377.1	hypothetical protein G ( 254)	150	42.9	0.19
gi 83349274 gb ABC14927.1	Sequence 32 from patent ( 29)	143	40.8	0.094	gi 136348703 gb EBN56170.1	hypothetical protein G ( 318)	151	43.2	0.2
gi 20230166 gb AAE91309.1	Sequence 32 from patent ( 29)	143	40.8	0.094	gi 138159875 gb EBY09754.1	hypothetical protein G ( 224)	149	42.7	0.2
gi 158473915 gb ABW47815.1	Sequence 21 from paten ( 29)	143	40.8	0.094	gi 22778539 dbj BAC14808.1	fatty-acid desaturase ( 349)	151	43.2	0.21
gi 145046627 gb ABP33254.1	fatty acid desaturase ( 346)	156	44.4	0.095	gi 115260472 emb CAK03576.1	putative transmembran ( 362)	151	43.2	0.22
gi 155082204 gb ABS94944.1	Sequence 37 from paten ( 509)	158	44.9	0.096	gi 154156969 gb ABS64186.1	fatty acid desaturase ( 371)	151	43.2	0.22
gi 155095505 gb ABS99960.1	Sequence 37 from paten ( 509)	158	44.9	0.096	gi 143086273 gb EDC71371.1	hypothetical protein G ( 174)	147	42.2	0.22
gi 111979073 gb ABH83316.1	Sequence 37 from paten ( 509)	158	44.9	0.096	gi 141273638 gb ECQ82648.1	hypothetical protein G ( 217)	148	42.4	0.23
gi 155116369 gb ABT11295.1	Sequence 37 from paten ( 509)	158	44.9	0.096	gi 126633754 emb CAM55833.1	unnamed protein produ ( 482)	152	43.5	0.24
gi 158473923 gb ABW47823.1	Sequence 29 from paten ( 36)	144	41.1	0.096	gi 60220816 emb CAI58907.1	unnamed protein produc ( 482)	152	43.5	0.24
gi 118901324 gb ABL51039.1	Sequence 29 from paten ( 36)	144	41.1	0.096	gi 76059316 emb CAJ30852.1	unnamed protein produc ( 482)	152	43.5	0.24
gi 146218710 emb CAM96527.1	putative microsomal o ( 116)	150	42.7	0.099	gi 136665182 gb EBP60030.1	hypothetical protein G ( 275)	149	42.7	0.24
gi 206680127 gb EDZ44614.1	fatty acid desaturase ( 309)	155	44.1	0.1	gi 142643368 gb ABQ35122.1	hypothetical protein G ( 337)	150	43.0	0.24
gi 143304298 gb EDE21795.1	hypothetical protein G ( 341)	155	44.1	0.11	gi 138742267 gb ECB69817.1	hypothetical protein G ( 231)	148	42.5	0.24
gi 168990272 gb ACA37812.1	Fatty acid desaturase ( 343)	155	44.1	0.11	gi 144056168 gb EDI54978.1	hypothetical protein G ( 165)	146	41.9	0.25
gi 140942966 gb ECO55750.1	hypothetical protein G ( 238)	153	43.6	0.11	gi 83349270 gb ABC14923.1	Sequence 28 from patent ( 30)	137	39.5	0.25
gi 136001020 gb EBL24809.1	hypothetical protein G ( 242)	153	43.6	0.11	gi 118901311 gb ABL51026.1	Sequence 16 from paten ( 30)	137	39.5	0.25
gi 137209426 gb EBS81473.1	hypothetical protein G ( 166)	151	43.1	0.11	gi 20230162 gb AAE91305.1	Sequence 28 from patent ( 30)	137	39.5	0.25
gi 143423631 gb EDE87807.1	hypothetical protein G ( 382)	155	44.2	0.12	gi 158473910 gb ABW47810.1	Sequence 16 from paten ( 30)	137	39.5	0.25
gi 137327946 gb EBT47954.1	hypothetical protein G ( 291)	153	43.6	0.13	gi 40193158 gb AAR78130.1	Sequence 28 from patent ( 30)	137	39.5	0.25
gi 137844667 gb EBW32573.1	hypothetical protein G ( 78)	146	41.7	0.13	gi 124872059 gb EAY63775.1	Fatty acid desaturase ( 360)	150	43.0	0.25
gi 169817288 gb ACA91871.1	fatty acid desaturase ( 360)	154	43.9	0.14	gi 146406616 gb ABQ35122.1	putative fatty acid de ( 374)	150	43.0	0.26
gi 134461097 gb EBB48299.1	hypothetical protein G ( 140)	149	42.6	0.14	gi 143029156 gb EDC29503.1	hypothetical protein G ( 385)	150	43.0	0.27
gi 3411183 gb AAC31186.1	putative hydrocarbon oxy ( 361)	154	43.9	0.14	gi 143139481 gb EDD10306.1	hypothetical protein G ( 385)	150	43.0	0.27
gi 167285093 gb ABZ37957.1	Sequence 11895 from pa ( 363)	154	43.9	0.14	gi 139308454 gb ECE49396.1	hypothetical protein G ( 267)	148	42.5	0.27
gi 150031672 gb ABR63788.1	fatty acid desaturase ( 363)	154	43.9	0.14	gi 138908835 gb ECC37941.1	hypothetical protein G ( 193)	146	42.0	0.29
gi 14022428 dbj BAB49037.1	probable hydrocarbon o ( 363)	154	43.9	0.14	gi 142744786 gb EDA26768.1	hypothetical protein G ( 351)	149	42.8	0.29
gi 58532810 gb AAW78909.1	fatty acid desaturase [ ( 66)	145	41.5	0.14	gi 52349044 gb AAU41678.1	Des [Bacillus lichenifo ( 352)	149	42.8	0.29
gi 142884493 gb EBD26892.1	hypothetical protein G ( 301)	153	43.7	0.14	gi 52004370 gb AAU24312.1	fatty acid desaturase [ ( 352)	149	42.8	0.29
gi 137811454 gb EBW13315.1	hypothetical protein G ( 250)	152	43.4	0.14	gi 135839244 gb EBK16908.1	hypothetical protein G ( 94)	142	40.9	0.29
gi 143312578 gb EBD26503.1	hypothetical protein G ( 383)	154	43.9	0.14	gi 143268760 gb EDE02855.1	hypothetical protein G ( 295)	148	42.5	0.3
gi 135404309 gb EBH41061.1	hypothetical protein G ( 318)	153	43.7	0.14	gi 105893807 gb ABF76972.1	fatty acid desaturase ( 360)	149	42.8	0.3
gi 139033775 gb ECC94899.1	hypothetical protein G ( 277)	152	43.4	0.15	gi 116648791 gb ABK09432.1	fatty acid desaturase ( 360)	149	42.8	0.3
gi 138189358 gb EBY30327.1	hypothetical protein G ( 278)	152	43.4	0.15	gi 142388028 gb ECX70339.1	hypothetical protein G ( 301)	148	42.5	0.3
gi 14023557 dbj BAB50163.1	fatty acid desaturase ( 340)	153	43.7	0.15	gi 140964139 gb ECO70818.1	hypothetical protein G ( 250)	147	42.2	0.3

gi 140218683 gb ECK33115.1	hypothetical protein G ( 172)	145	41.7	0.3
gi 114340763 gb ABI66043.1	fatty acid desaturase ( 311)	148	42.5	0.31
gi 137385866 gb EBT80458.1	hypothetical protein G ( 85)	141	40.6	0.32
gi 135644423 gb EBI95603.1	hypothetical protein G ( 268)	147	42.3	0.32
gi 136177948 gb EBM40697.1	hypothetical protein G ( 222)	146	42.0	0.32
gi 142269902 gb ECW86122.1	hypothetical protein G ( 155)	144	41.4	0.33
gi 143763977 gb EDG66623.1	hypothetical protein G ( 334)	148	42.5	0.33
gi 40193195 gb AAR78167.1	Sequence 65 from patent ( 29)	135	39.0	0.33
gi 158473913 gb ABW47813.1	Sequence 19 from paten ( 29)	135	39.0	0.33
gi 20230198 gb AAE91341.1	Sequence 65 from patent ( 29)	135	39.0	0.33
gi 118901314 gb ABL51029.1	Sequence 19 from paten ( 29)	135	39.0	0.33
gi 83349306 gb ABC14959.1	Sequence 65 from patent ( 29)	135	39.0	0.33
gi 138383837 gb EBZ29515.1	hypothetical protein G ( 295)	147	42.3	0.35
gi 163664008 gb ABY31375.1	fatty acid desaturase ( 358)	148	42.6	0.35
gi 124894086 gb EAY67966.1	Fatty acid desaturase ( 361)	148	42.6	0.35
gi 138456706 gb EBZ80160.1	hypothetical protein G ( 254)	146	42.0	0.36
gi 142447364 gb ECY14572.1	hypothetical protein G ( 317)	147	42.3	0.37
gi 139773585 gb ECH36273.1	hypothetical protein G ( 226)	145	41.8	0.38
gi 140553831 gb ECM19576.1	hypothetical protein G ( 236)	145	41.8	0.4
gi 157682103 gb ABV63247.1	fatty acid desaturase ( 351)	147	42.3	0.4
gi 36958688 gb AAQ87156.1	putative hydrocarbon ox ( 361)	147	42.3	0.41
gi 86284822 gb ABC93881.1	hydrocarbon oxigenase p ( 362)	147	42.3	0.41
gi 190699629 gb ACE93713.1	hydrocarbon oxigenase ( 362)	147	42.3	0.41
gi 142373528 gb ECX60602.1	hypothetical protein G ( 301)	146	42.1	0.41
gi 140968244 gb EC073358.1	hypothetical protein G ( 80)	139	40.1	0.41
gi 140827068 gb ECN78717.1	hypothetical protein G ( 319)	146	42.1	0.43
gi 138361544 gb EBZ15949.1	hypothetical protein G ( 277)	145	41.8	0.45
gi 114227321 gb ABI57120.1	fatty acid desaturase ( 349)	146	42.1	0.47
gi 141112148 gb ECP71052.1	hypothetical protein G ( 242)	144	41.5	0.47
gi 196170643 gb ACG71616.1	Linoleoyl-CoA desatura ( 364)	146	42.1	0.48
gi 142120546 gb ECV74038.1	hypothetical protein G ( 302)	145	41.8	0.49
gi 3378264 gb AAD03847.1	unknown (Novosphingobium ( 309)	145	41.8	0.5
gi 145322189 gb ABP64133.1	fatty acid desaturase ( 309)	145	41.8	0.5
gi 135247052 gb EBG40726.1	hypothetical protein G ( 258)	144	41.6	0.5
gi 142407392 gb ECX84610.1	hypothetical protein G ( 181)	142	41.0	0.51
gi 134772826 gb EBD33094.1	hypothetical protein G ( 276)	144	41.6	0.53
gi 135954332 gb EBK94439.1	hypothetical protein G ( 283)	144	41.6	0.54
gi 143117833 gb EDC94407.1	hypothetical protein G ( 134)	140	40.5	0.54
gi 141828284 gb ECT53004.1	hypothetical protein G ( 295)	144	41.6	0.56
gi 192283939 gb ACF00320.1	fatty acid desaturase ( 357)	145	41.9	0.56
gi 2492201 gb AAB80337.1	I66148 Sequence 6 from pa ( 37)	133	38.6	0.56
gi 5955840 gb AAE07496.1	Sequence 22 from patent ( 37)	133	38.6	0.56
gi 2492217 gb AAB80353.1	I66164 Sequence 22 from p ( 37)	133	38.6	0.56
gi 5955824 gb AAE07480.1	Sequence 6 from patent U ( 37)	133	38.6	0.56
gi 217063951 gb ACJ78201.1	fatty acid desaturase ( 361)	145	41.9	0.56
gi 49177306 gb AAT52682.1	fatty acid desaturase [ ( 361)	145	41.9	0.56
gi 29894149 gb AAP07440.1	Fatty acid desaturase [ ( 361)	145	41.9	0.56
gi 42735462 gb AAS39401.1	fatty acid desaturase [ ( 361)	145	41.9	0.56
gi 49331599 gb AAT62245.1	possible fatty acid des ( 361)	145	41.9	0.56
gi 47500784 gb AAT29460.1	fatty acid desaturase [ ( 361)	145	41.9	0.56
gi 51978352 gb AAU19902.1	possible fatty acid des ( 361)	145	41.9	0.56
gi 118415337 gb ABK83756.1	fatty acid desaturase ( 361)	145	41.9	0.56
gi 30253902 gb AAP24397.1	fatty acid desaturase [ ( 361)	145	41.9	0.56
gi 14024924 dbj BAB51526.1	putative hydrocarbon o ( 363)	145	41.9	0.57
gi 135993001 gb EBL20112.1	hypothetical protein G ( 250)	143	41.3	0.57
gi 137615900 gb EBV06925.1	hypothetical protein G ( 257)	143	41.3	0.58
gi 143213186 gb EDD63444.1	hypothetical protein G ( 332)	144	41.6	0.62
gi 137862788 gb EBW42988.1	hypothetical protein G ( 231)	142	41.1	0.62

gi 135475063 gb EBH88481.1	hypothetical protein G ( 135)	139	40.3	0.64
gi 138053809 gb EBX48750.1	hypothetical protein G ( 241)	142	41.1	0.65
gi 139857852 gb ECH95363.1	hypothetical protein G ( 245)	142	41.1	0.66
gi 138433799 gb EBZ64427.1	hypothetical protein G ( 297)	143	41.4	0.66
gi 136763277 gb EBQ24339.1	hypothetical protein G ( 246)	142	41.1	0.66
gi 142439034 gb ECY08406.1	hypothetical protein G ( 299)	143	41.4	0.66
gi 209539265 gb ACI59198.1	fatty acid desaturase ( 362)	144	41.6	0.66
gi 141714707 gb ECS89892.1	hypothetical protein G ( 252)	142	41.1	0.67
gi 143369933 gb EDE60968.1	hypothetical protein G ( 209)	141	40.8	0.67
gi 196193799 gb EDX88758.1	Fatty acid desaturase ( 373)	144	41.7	0.68
gi 140460181 gb ECL89651.1	hypothetical protein G ( 83)	136	39.5	0.69
gi 56680208 gb AAV96874.1	fatty acid desaturase f ( 314)	143	41.4	0.69
gi 2492204 gb AAB80340.1	I66151 Sequence 9 from pa ( 40)	132	38.4	0.7
gi 5955827 gb AAE07483.1	Sequence 9 from patent U ( 40)	132	38.4	0.7
gi 2492198 gb AAB80334.1	I66145 Sequence 3 from pa ( 40)	132	38.4	0.7
gi 5955821 gb AAE07477.1	Sequence 3 from patent U ( 40)	132	38.4	0.7
gi 135351893 gb EBH05844.1	hypothetical protein G ( 269)	142	41.1	0.71
gi 144124815 gb EDJ04372.1	hypothetical protein G ( 326)	143	41.4	0.71
gi 136058406 gb EBL62852.1	hypothetical protein G ( 339)	143	41.4	0.73
gi 84366874 dbj BAE68032.1	putative RtxC homolog ( 346)	143	41.4	0.75
gi 3064243 gb AAC38355.1	membrane bound delta 5 a ( 352)	143	41.4	0.76
gi 2619012 gb AAB84436.1	fatty acid desaturase [B ( 352)	143	41.4	0.76
gi 2634311 emb CAB13810.1	fatty acid desaturase [ ( 352)	143	41.4	0.76
gi 167296359 gb ABZ49223.1	Sequence 23161 from pa ( 352)	143	41.4	0.76
gi 46408065 emb CAG26605.1	unnamed protein produc ( 352)	143	41.4	0.76
gi 58425606 gb AAW74643.1	RtxC [Xanthomonas oryza ( 355)	143	41.4	0.76
gi 144115985 gb EDI97942.1	hypothetical protein G ( 360)	143	41.4	0.77
gi 163860553 gb ABY41612.1	fatty acid desaturase ( 361)	143	41.4	0.77
gi 144212727 gb EDJ68662.1	hypothetical protein G ( 299)	142	41.1	0.77
gi 186929487 emb CAC48958.2	MocD [Sinorhizobium m ( 363)	143	41.4	0.78
gi 141672141 gb ECS73663.1	hypothetical protein G ( 253)	141	40.9	0.79
gi 135299436 gb EBG71506.1	hypothetical protein G ( 371)	143	41.4	0.79
gi 136241577 gb EBM83404.1	hypothetical protein G ( 177)	139	40.3	0.8
gi 142467276 gb ECY29127.1	hypothetical protein G ( 326)	142	41.2	0.83
gi 140347395 gb ECL15019.1	hypothetical protein G ( 284)	141	40.9	0.87
gi 143772505 gb EDG70880.1	hypothetical protein G ( 285)	141	40.9	0.87
gi 138585842 gb ECA61869.1	hypothetical protein G ( 236)	140	40.6	0.87
gi 39648523 emb CAE27044.1	putative fatty acid de ( 355)	142	41.2	0.89
gi 134519477 gb EBB82703.1	hypothetical protein G ( 202)	139	40.4	0.9
gi 84787975 gb ABC64157.1	hypothetical protein EL ( 304)	141	40.9	0.92
gi 193786708 dbj BAG52031.1	unnamed protein produ ( 210)	139	40.4	0.93
gi 45503662 emb CAF86845.1	unnamed protein produc ( 210)	139	40.4	0.93
gi 136020166 gb EBL37299.1	hypothetical protein G ( 270)	140	40.7	0.98
gi 139522233 gb ECF64931.1	hypothetical protein G ( 272)	140	40.7	0.98

>>gi|88181398|gb|EAQ88866.1| hypothetical protein CHGG\_0 (400 aa)  
 initn: 1699 init1: 964 opt: 1886 Z-score: 2327.3 bits: 439.6 E(): 1.2e-120  
 Smith-Waterman score: 1886; 67.519% identity (84.399% similar) in 391 aa  
 overlap (32-422:15-397)

	10	20	30	40	50	60
del_15	AVTTRSHKAAAATEPEVVSTGVDAVSAAPSSSSSSSSSQSAEPIEYPIDKITIRDAIPDH					
		:	:	:	:	:
gi 881	MATTTTTTTRRRRAAEVKSAPIKLVGEPQYPIQITIRDAIPAH					
		10	20	30	40	
		70	80	90	100	110
						120

del\_15 CFRPRVWISMAYFIRDFAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIWI  
gi|881 CFPVPTWRSGLYVFRDVSMAAALGWAFTYISQIEDFTWRVAVWLVYGYLQGLVCTGIWI

del\_15 LAHECGHGAFSRHTWFNNVWGIGHSFLLVVPYFSWKFSHRHRHRTGHMEKDMAFVPATE  
gi|881 LAHEAGHGAFSVHQKLNDDVVGWTLHLSALLVVPYFSWKFSHRHRHRTGHMEKDMAFVPHTK

del\_15 ADRNQRKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKGSQWETG  
gi|881 ADREKRRLADLYLDRE---LFEDIPVQLFKLLAHQLAGWQMYLLFNVSAGSDSQSKAS

del\_15 KGGMGWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYIYQAAQVVGWQMVGLLYFQQ  
gi|881 ----WVRVSHFEPPTSAVFRPSEALYVAITDIGLLIVAGLLYLASTVVGWKMVFLMYGVP

del\_15 YFWVHHHLVAITYLHHTHEEVHFDADSWTFVKGALATVDRDFGFIGKHLFHNIIDHHV  
gi|881 YFWVHHHLVAITYLHHTHDPVHHFEADSWTFVKGALATVDRDFGVGRHLFHGIIDTHVI

del\_15 HHLFPRIPFYAAEATNSIRPMLGPLYHRDDRSFMGQLWYNFTHCKWVVPDPQVPGALI  
gi|881 HHLFPRIPFYKAEATEAIKPLLGDLYHREERSFMGQLWSTFTQCKYVEADPAAPGALKW

del\_15 AHTVQS  
gi|881 AEKK  
400

>>gi|170940419|emb|CAP65646.1| unnamed protein product [ (399 aa)  
initn: 1727 initl: 937 opt: 1884 Z-score: 2324.8 bits: 439.1 E(): 1.6e-120  
Smith-Waterman score: 1884; 65.517% identity (84.975% similar) in 406 aa  
overlap (19-424:1-398)

del\_15 MAVTTRSHKAAAATEPEVVSTGVDVAVSAAAPSSSSSSSSQKSAEPIEYDPIKTIRDAIPD  
gi|170 MATAITTTETRSRKANGGAVLKTQVVEYDPIQTIRDAIPA

del\_15 HCFRPRVWISMAYFIRDFAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIW  
gi|170 HCFEPTIILHSMAYVFRDLIMAGALGWAFTYIPQINDSIVRGLAWALYGYLQGLVLTGVW

del\_15 ILAHECGHGAFSRHTWFNNVWGIGHSFLLVVPYFSWKFSHRHRHRTGHMEKDMAFVPAT  
gi|170 ILAHEAGHGAFSKHQFNDDVVGWVLSALMVYFSWKFSHRHRHRTGHMEKDMAFVPAT

del\_15 EADRNRKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKGSQWET  
gi|170 KEDRQKRRLADLYLDRE---LFEDVPLVQLVKLIFHQLAGWQMYLLFNATAGPASKQRE--

del\_15 GKGGMWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYIYQAAQVVGWQMVGLLYFQ  
gi|170 --GG--WLRVSHFEPPTSAVFRPSEAVYIFITDVGLAIVGYCLYLASTMVGWKMVFLMYGQ

del\_15 QYFWVHHHLVAITYLHHTHEEVHFDADSWTFVKGALATVDRDFGFIGKHLFHNIIDHHV  
gi|170 AYFWVHHHLVAITYLHHTHDPVPHFDAENWTFVKGALATVDRDFGVGRHLFHGIIDTHV

del\_15 VHHLFPRIPFYAAEATNSIRPMLGPLYHRDDRSFMGQLWYNFTHCKWVVPDPQVPGALI  
gi|170 VHHLFPRIPFYKAEATEAIKPVVGDLYHQKGSFLGSLWKTFTTCKYVEADPTVPGTLK

del\_15 WAHTVQS  
gi|170 WAESK

>>gi|167276960|gb|ABZ29824.1| Sequence 3762 from patent (429 aa)  
initn: 2630 initl: 1862 opt: 1871 Z-score: 2308.3 bits: 436.2 E(): 1.3e-119  
Smith-Waterman score: 2515; 86.014% identity (86.014% similar) in 429 aa  
overlap (49-417:1-429)

del\_15 VSTGVDVAVSAAAPSSSSSSSSQKSAEPIEYDPIKTIRDAIPDHCFRPRVWISMAYFIRDF  
gi|167 PDIKTIRDAIPDHCFRPRVWISMAYFIRDF

del\_15 AMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIWILAHECGHGAFSRHTWFN  
gi|167 AMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIWILAHECGHGAFSRHTWFN

del\_15 NVMGWIGHSFLLVVPYFSWKFSHRHRHRTGHMEKDMAFVPATEADRNRKLANLYMDKET  
gi|167 NVMGWIGHSFLLVVPYFSWKFSHRHRHRTGHMEKDMAFVPATEADRNRKLANLYMDKET





Smith-Waterman score: 1369; 52.868% identity (75.062% similar) in 401 aa overlap (30-427:2-393)

del\_15 MAVTTRSHKAAAATEPEVVSTGVDVAVSAAAPSSSSSSSSQKSAEPIEYDPDIKTIRDAIPD
gi|114 MATSTMTLRKSPVEQDESVPSLTKLTKDAIPK

del\_15 HCFRPRVWISMAYFIRDFAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIW
gi|114 DCFESSVVTSLLYLARDILYCAALTYAAFQ-IHLLPWLSLRVAAWTAYGFLGQCGVGTGLW

del\_15 ILAHECGHGAFSRHTWFNNVMGWIGHSFLLVPYFSWKFSHHRHRRFTGHMEKDMAFVPAT
gi|114 ILAHECGHGAFSRYQGPNDFVGVWATHSFLMVPYFSWKFTHARHHRRTGHMEKDTVFVFPWT

del\_15 EADRNQRKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKSKQWET
gi|114 DDQLAQKKNVRLEQLKHLAE---ETPIVSFVQLVAHQFLGWQLYLLVNVTAG--AKSCPD

del\_15 GKGGMGWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYIYLYQAAQVVG-WQMVGLLYF
gi|114 GSAEV-W-PASHFNPFSLFTSSQWIYIALSDLGLAIMGAVLYYAATQIGAWNVV-LLYV

del\_15 QQYFVWHHLVAITYLHHTHEEVHFDADSWTFVKALATVDRDFGFIGKHLFHNIIIDHH
gi|114 VPFVWHHLVAITYLQHTHPAVPHYTAETWTYTKGALATIDRTTGFGRHFHEIIDYH

del\_15 VVHHLFPRIPFYAAEATNSIRPMLGPLYHRD-DRSFMGQLWYNFTHCKWVVPDPQ-VPG
gi|114 VVHHLFSRIPFYKAERATKAIQPLLGENYHEQKDESFLYSLMMTFRKCIYVSDKGRGMPG

del\_15 ALIWAHTVQS
gi|114 VLHFVRAEESQ

>>gi|134082006|emb|CAK46691.1| unnamed protein product [ (398 aa)
initn: 1189 initl: 626 opt: 1349 Z-score: 1664.4 bits: 316.9 E(): 9.9e-84
Smith-Waterman score: 1349; 51.918% identity (76.471% similar) in 391 aa
overlap (35-419:9-389)

del\_15 TRSHKAAAATEPEVVSTGVDVAVSAAAPSSSSSSSSQKSAEPIE----YDPDIKTIRDAIPD

gi|134 MAELRKVPASQAAQQQQPIHNDNDVPSLTKLTKDAIPE
10 20 30

del\_15 HCFRPRVWISMAYFIRDFAMAFGLGYLAWQYIPLIASTPLRYGAWALYGYLQGLVCTGIW
gi|134 ECFDSSVVTSLLYLARDILYCAALTYAAFQ-HIHLPSLPLRALAWAVYGFQCGVGTGIW

del\_15 ILAHECGHGAFSRHTWFNNVMGWIGHSFLLVPYFSWKFSHHRHRRFTGHMEKDMAFVPAT
gi|134 ILAHECGHGAFSKHQTFNDIVGWAHNSFLMVPYFSWKITHARHHRRTGHMEKDTVFVFPWT

del\_15 EADRNQRKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKSKQWET
gi|134 DNELAKKK--NVRIEQ-LKHLTEETPIVSFLQLIGHQLFGWQLYFLNVTAGPKSLPENR

del\_15 GKGGMGWLRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYIYLYQAAQVVG-WQMVGLLYF
gi|134 PIRGAA---SHFNPFGLFTKSYFISIALTDLGLLIMGSILYASTQIGAWNVV-LLYF

del\_15 QQYFVWHHLVAITYLHHTHEEVHFDADSWTFVKALATVDRDFGFIGKHLFHNIIIDHH
gi|134 VPYLWVHHLVAITYLQHTHPAVPHYTAESWTYTKGALATIDRSIGFIGRHFHEIIDYH

del\_15 VVHHLFPRIPFYAAEATNSIRPMLGPLYHRD-DRSFMGQLWYNFTHCKWVVPDPQVPGA
gi|134 VVHHLFSRIPFYKAEEATRAIQPLLGVNYHEEKESFLYSLMTTFRKCIYV-SDGKKNV

del\_15 LIWAHTVQS
gi|134 LHFVLPPEAK

>>gi|83776412|dbj|BAE66531.1| unnamed protein product [A (392 aa)
initn: 1158 initl: 625 opt: 1337 Z-score: 1649.7 bits: 314.2 E(): 6.5e-83
Smith-Waterman score: 1337; 52.604% identity (75.781% similar) in 384 aa
overlap (39-419:9-383)

del\_15 KAAAATEPEVVSTGVDVAVSAAAPSSSSSSSSQKSAEPIEYDPDIKTIRDAIPDHCFRPRVW
gi|837 MAELHNRKAEKAIKDTPTTLKELKDAIPKCFESSAV

del\_15 KAAAATEPEVVSTGVDVAVSAAAPSSSSSSSSQKSAEPIE----YDPDIKTIRDAIPD





>>gi|160707460|gb|EAT91011.2| hypothetical protein SNOG\_ (979 aa)  
initn: 1074 initl: 1074 opt: 1238 Z-score: 1521.5 bits: 291.8 E(): 9e-76  
Smith-Waterman score: 1238; 47.044% identity (72.494% similar) in 389 aa  
overlap (38-420:18-399)

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10 20 30 40 50 60
del_15 HKAAAATEPEVVSTGVDVSAAPSSSSSSSSQKSAEPIEYDPDIKTIRDAIPDHCFRPRV
gi|160 MATTTTTVTERKAPVMMATKGAATTPV--PDVKTLRDAIPAHCFERSL
10 20 30 40
del_15 WISMAYFIRDFAMAFGLGY----LAWQYIPLIASTPLRYGAWALYGLQLGVCTGIWILA
gi|160 VRSMGYVVRDLVAVSTLFYSATLLARADLPLYL SAPL----WTLYSFVTGCFEFTGLWILA
50 60 70 80 90 100
del_15 HECGHAFAFRHTWFNVMGWIGHSFLLVPYFVSWKFSHRRHRRFTGHMEKDMAFVPAE-A
gi|160 HECGHDSFSPYLVNATMGWILHSMMLLVFFSWKFSHARRHRYHNHMEKDTVFVFNKKA
110 120 130 140 150 160
del_15 DRNQKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKSKQWETGK
gi|160 EKAANPAAPTIVEKIMDHTAADAPIFISIASLAVHQLFGWPAYILINAGAGVNS--MVRSNR
170 180 190 200 210 220
del_15 GGMGWLVRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYILYQAAQVVGWQMVGLLYFQQY
gi|160 KETPKYKQSHLDPTSDVFTAGEQPFFVALSNVGLITFTVLYQVSKSLGGLNFTFLYGLPL
230 240 250 260 270 280
del_15 FVWHHLVAITYLHHTHEEVHFDADSWTFVKALATVDRDFGFIGKHLFHNIDHHVHVH
gi|160 LWMNHVIVAITYLHHTHEDAAYEADWTFVKALSTIDREFGFIGRHIHFGIIEYHVHVH
290 300 310 320 330 340
del_15 HLFPRIPFYAAEATNSIRPMLGPLYHRDDRSFMGLWYNFTHCKWVVPDPQVP-GALLW
gi|160 HMFPRIPFYHCEATWAVAPLLGERYIEQRTNFFADLWEAFTTCKYVVPVPGTGAKAGALVS
350 360 370 380 390 400
del_15 AHTVQS
gi|160 LGSWGMKMRMRLAAKVIDVFIQFASMWLRRAVLLVVKRNGPHTKLPKPPQPPNPNDALC
410 420 430 440 450 460
```

>>gi|150408460|gb|EDN04001.1| hypothetical protein HCAG\_ (472 aa)  
initn: 1167 initl: 525 opt: 1174 Z-score: 1447.2 bits: 277.0 E(): 1.2e-71  
Smith-Waterman score: 1179; 43.488% identity (68.837% similar) in 430 aa  
overlap (6-411:14-439)

```
10 20 30 40
del_15 MAVTTRSHKAAAATEPEVVSTGVDVSAAPSSSSSSSS--SQKSAEPI----
gi|150 MTSTALPKRRALNRNSPTDYSTEACVSPDLSLRPS-PSSTSLSSIASDVQQEPLKLVLD
10 20 30 40 50
del_15 -----EYPD--IKTIRDAIPDHCFRPRVWISMAYFIRDFAMAFGLGYLAWQYI-P-LIA
gi|150 TYGTPFEIPDFTIKQIRDAIPAHCFERSALRSLSYVARDISCLAGTFYLFHNYVTPYIPI
60 70 80 90 100 110
del_15 STPLRYGAWALYGLQLGVCTGIWILAHECGHGAFAFRHTWFNVMGWIGHSFLLVPYFSW
gi|150 STPVVRLWGLYAFQLGFGTGLWIMAHECGHQAFAFRHTWFNVMGWIGHSFLLVPYFSW
120 130 140 150 160 170
del_15 KFSHRRHRRFTGHMEKDMAFVPAEADNRQRKLANLYMDKETAEMFEDVPIVQLVKLIAH
gi|150 KISHSKHKKATGNLERDMVFPKTRVVFASRF---GYIAHELHELMETPIQTAVHVVVLQ
180 190 200 210 220 230
del_15 QLAWQMYLLFNVSAGKSKQWETGKG-GM--GWLR-VSHFEPSSAVFRNSEAIYIALSD
gi|150 QLFGWPMYILISNVTGNHCHQRQPEGRGKENGFRGWNHFNPSPLYEAKHAPLILLSD
240 250 260 270 280 290
del_15 LGLMIMGYILYQAAQVVGWQMVGLLYFQQYFVWHHLVAITYLHHTHEEVHFDADSWTF
gi|150 LGLILAGSALFWVWKNFGWANLAVWYFLPYLWVNHHLVAITYLQHTDPTLPHYSPQAWTF
300 310 320 330 340 350
del_15 VKGALATVDRDFGFIGKHLFHNIDHHVHHLFPRIPFYAAEATNSIRPMLGPLYHRDD
gi|150 TRGAAATIDREFGFIGRNIHFGIETHVLHVVSTIPFYHADEASEAIKPIMGKHYRSDT
360 370 380 390 400 410
del_15 R----SFMGLWYNFTHCKWVVPDPQVPGALIWAHTVQS
gi|150 ELGSLGFLRSLWRSARTCQWVPECEGAKGEHGVYFFRNRRNIGVVKPAVMTSPSSS
420 430 440 450 460 470
```

>>gi|90301761|gb|EAS31392.1| hypothetical protein CIMG\_0 (445 aa)  
initn: 1186 initl: 534 opt: 1165 Z-score: 1436.5 bits: 274.9 E(): 4.9e-71  
Smith-Waterman score: 1165; 44.417% identity (70.146% similar) in 412 aa  
overlap (20-417:10-416)

```
10 20 30 40 50
del_15 MAVTTRSHKAAAATEPEVVSTGVDVSAAPSSSSSSSSQKSAEPIEYPD--IKTIRDAI
gi|903 MESPRHSPSTSLSSSLASEALAEAGSSKLLDITYGNEFEIPNFTTKEIRDAI
10 20 30 40 50
```

```

60      70      80      90      100     110
del_15 PDHCFRPRVWISMAFYFIRDFAMAFGLGYLAWQ-YI-PL-IASTPLRYGAWALYGYLQGLV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|903 PAHCFKRDGIRGLLYVFRDLA-CLGVTFYAFHNYVTPENIPSTPIRAGLWALYTFVQGLF
      60      70      80      90      100

120     130     140     150     160     170
del_15 CTGIWILAHECGHGAFSRHTWFNNVMGIGHSEFLLVPYFSWKFSHRHRHRTGHMEKDMA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|903 GTGIWVLAHECGHQSFSKLVNDTVGWILHSSLLVPYFSWKISHGKHHKATGNLERDMV
      110     120     130     140     150     160

180     190     200     210     220     230
del_15 FVPATEADRNQRKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQMYLLFNVSAGKGS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|903 FVPKTR---REQYASRMGYFVHQLNEVMEETPIQAATNLILQQLFGWPMYLLSNVTGHNHH
      170     180     190     200     210     220

240     250     260     270     280     290
del_15 KQWETGKG----GMGWLVRVSHFEPSSAVFRNSEAIYIALSDLGLMIMGYIILYQAAQVVG
. . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|903 ECQREGRGKGGKNGM-FTGVNHFNPSSPLYEAKDAKLIVLSDIGLLIMGSILYALGQRF
      230     240     250     260     270     280

300     310     320     330     340     350
del_15 WQMVGLLYFQQYFVWHHLVAITYLHHTHEEVHFDADSWTFVKGALATVDRDFGFIGKH
: . . : : : : : : : : : : : . . . : : : : : : : : : : : : : : : : : : : : : : : : :
gi|903 WTNLLVWYFIPYLWVNHHLVAITYLQHTDPSLPHYHSSVWNFARGAAATIDREFGFIGRQ
      290     300     310     320     330     340

360     370     380     390     400
del_15 LFHNIIDHHVVHHLFPRIPFYAAEATNSIRPMLGPLYHRDDRS----FMGQLWYNFTHC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|903 LFHGIETHVLHHYVSTIPFYNADEATEAIKVKVMGKHYRSDTKGSGSLGFIRALWRSTRMC
      350     360     370     380     390     400

410     420
del_15 KWVVPDPQVPGALIWAHTVQS
: : : . . :
gi|903 QWVEPSEGAQEGKDVLFRRNRNGLGPRPLVVEPEEGKAK
      410     420     430     440

>>gi|159131376|gb|EDP56489.1| oleate delta-12 desaturase (469 aa)
  initn: 1128 initl: 515 opt: 1143 Z-score: 1409.0 bits: 269.9 E(): 1.7e-69
Smith-Waterman score: 1143; 40.610% identity (68.779% similar) in 426 aa
overlap (4-417:24-445)

10      20      30      40
del_15 MAVTTRSHKAAAATEPEVVSTGVDVAASAAPSSSSSSSSQ
. . : . . : : : : : : : : : : : : : : : : :
gi|159 MSSTALPKRVALHRNPTTESSVPSVSHSPFDSRQSPSSTSLSSMASDAEKTSSKMIDT
      10      20      30      40      50      60

50      60      70      80      90
del_15 KSAEPIEYD--IKTIRDAIPDHCFRPRVWISMAFYFIRDFAMAFGLGYLAWQYI-P-LIA
. . : . . : : : : : : . . : : : : : : . . : . . : . . : . . : . . : . . : . . :
gi|159 YGNE-FKIPDYTIKQIRDAIPAHCYQSAATSLYVFRDMAILASVFYVFNHYVTPETVP

```

```

70      80      90      100     110
del_15 STPLRYGAWALYGYLQGLVCTGIWILAHECGHGAFSRHTWFNNVMGIGHSEFLLVPYFSW
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 SMPVRRVLTIIYTVVQGLVGTGVWVLAHECGHQAFTSKVLNNDTVGWICHSLLLVPYFSW
      120     130     140     150     160     170

160     170     180     190     200     210
del_15 KFSHRRHRHRTGHMEKDMAFVPATEADRNQRKLANLYMDKETAEMFEDVPIVQLVKLIAH
: : : : : : : : : : : : : : : : . . : . . : : : : : : : : : : : : : : : : :
gi|159 KISHGKHHKATGNIARDMVFVPKTREEYATRIGRAAH---ELSELMEETPILTATNLVLQ
      180     190     200     210     220     230

220     230     240     250     260     270
del_15 QLAGWQMYLLFNVSAGKSKQWETGKGG---MGWLR-VSHFEPSSAVFRNSEAIYIALSD
: : : : : : : : : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 QLFGWPMYLLTNVTGHNHHERQPEGRGKGRNGYFGGVNHFNPSSPLYEAKDAKLIVLSD
      240     250     260     270     280     290

280     290     300     310     320     330
del_15 LGLMIMGYIILYQAAQVVGWQMVGLLYFQQYFVWHHLVAITYLHHTHEEVHFDADSWTF
: : : : : : : : : . . : . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 LGLFLVGSLLYIGSTYGLNLLVWYGIPLYLWVNHHLVAITYLQHTDPTLPHYQPEAWDF
      300     310     320     330     340     350

340     350     360     370     380
del_15 VKGALATVDRDFGFIGKHLFHNIIDHHVVHHLFPRIPFYAAEATNSIRPMLGPLY----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 TRGAAATIDRDFGVGRHIFHGIETHVLHHYVSTIPFYHADEASEAIQKVMGPHYRSEA
      360     370     380     390     400     410

390     400     410     420
del_15 HRDDRSFMGQLWYNFTHCKWVVPDPQVPGALIWAHTVQS
: . . : . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 HTGWTGFLKALWTSARTCQWVEPTEGAKGESQYVLFYRNINGIGVPPAKIPAK
      420     430     440     450     460

>>gi|145025092|gb|ABP24249.1| Sequence 34 from patent US (477 aa)
  initn: 1110 initl: 513 opt: 1141 Z-score: 1406.4 bits: 269.5 E(): 2.3e-69
Smith-Waterman score: 1141; 42.271% identity (69.082% similar) in 414 aa
overlap (21-418:47-453)

10      20      30      40      50
del_15 MAVTTRSHKAAAATEPEVVSTGVDVAASAAPSSSSSSSSQKSAEPIEYD
. . . : . . : : : . . . : : : . . . : : :
gi|145 TVTSTTVTDESAAVSPSDSPRHSASSTSLSSMSEVDIAKPKSEYGMVLDTYGNQFVDP
      20      30      40      50      60      70

60      70      80      90      100
del_15 --IKTIRDAIPDHCFRPRVWISMAFYFIRDFAM---AFGLGY--LAWQYIPLIASTPLRYG
: : : : : : : : : . . . : : : : : : . . . : . . : : : : : : : : : : : : : : : : :
gi|145 FTIKDIYNAIPKHCFKRSALKGYILRDIVLLTTFSIWNFVTPPEYIP---STPARAG
      80      90      100      110      120      130

110     120     130     140     150     160
del_15 AWALYGYLQGLVCTGIWILAHECGHGAFSRHTWFNNVMGIGHSEFLLVPYFSWKFSHRHR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```





340 350 360 370 380 390  
del\_15 TVDRDFGFIGKHLFHNIIDHHVVHHLFPRIPFYAAEEATNSIRPMLGPLYHRD----DRS  
gi|155 TIDREMGFIGRHLHGIIETHVLHHYVSSIPFYNADEATEAIKPIMGKHYRADVQDGRG

400 410 420  
del\_15 FMGQLWYNFTHCKWVVPDPQVPGALIWAHTVQS  
gi|155 FIRAMYRSARMCQWVEPSAGAEGAGKGVLFRRNRNNVGTTPPAVIKQVA

>>gi|155070719|gb|ABS91064.1| Sequence 46 from patent US (477 aa)  
initn: 1110 initl: 513 opt: 1141 Z-score: 1406.4 bits: 269.5 E(): 2.3e-69  
Smith-Waterman score: 1141; 42.271% identity (69.082% similar) in 414 aa  
overlap (21-418:47-453)

10 20 30 40 50  
del\_15 MAVTTRSHKAAAATEPEVVSTGVDVAVSAAPSSSSSSSQKSAEPIEYPD  
gi|155 TVTSTTVTDESAAVSPSDSPRHSASSTLSMSSEVDIAKPKSEYGVMLDTYGNQFEVFPD

60 70 80 90 100  
del\_15 --IKTIRDAIPDHCFRPRVWISMAFYRDFAM--AFGLGY--LAWQYIPLIASTPLRYG  
gi|155 FTIKDIYNAIPKHCFKRSALKGYGILRDIVLLTTFSIWYNFVTPYIYIP---STPARAG

110 120 130 140 150 160  
del\_15 AWALYGYLQGLVCTGIWILAHECGHGAFSRHTWFNNVMGWIGHSFLLVPYFSWKFSHHRH  
gi|155 LWAVYTVLQGLFGTGLWVIAHECGHGAFSDSRIINDITGWLHSSLLVPYFSWQISHRKH

170 180 190 200 210 220  
del\_15 HRFTGHMEKDMAFVPAEADRNRKLANLYMDKETAEMFEDVPIVQLVKLIAHQLAGWQM  
gi|155 HKATGNMERDMVFPVPT---REQQATRLGKMTHELALHTTEETPAFTLLMLVLQQLVGVWPN

230 240 250 260 270  
del\_15 YLLFNVSAGKSKQWETGK-----GMGWLVRVSHFEPSSAVFRNSEAIYIALSDLGLMIM  
gi|155 YLITNVVTGHNYHERQREGRGKGNGLGG-GVNHFDPRSPLYENSADAKLIVLSDIGIGLM

280 290 300 310 320 330  
del\_15 GYILYQAAQVVGQVGLLYFQQYFVWHHLVAITYLHHTHEEVHFDADSWTFVKGALA  
gi|155 ATALYFLVQKFGFYNAIWFVYPYLWVNHHLVAITFLQHTDPTLPHYNDENWVFRGAAA

340 350 360 370 380 390  
del\_15 TVDRDFGFIGKHLFHNIIDHHVVHHLFPRIPFYAAEEATNSIRPMLGPLYHRD----DRS  
gi|155 TIDREMGFIGRHLHGIIETHVLHHYVSSIPFYNADEATEAIKPIMGKHYRADVQDGRG

370 380 390 400 410 420  
400 410 420  
del\_15 FMGQLWYNFTHCKWVVPDPQVPGALIWAHTVQS  
gi|155 FIRAMYRSARMCQWVEPSAGAEGAGKGVLFRRNRNNVGTTPPAVIKQVA

>>gi|119412672|gb|EAW22613.1| oleate delta-12 desaturase (469 aa)  
initn: 1128 initl: 513 opt: 1140 Z-score: 1405.3 bits: 269.2 E(): 2.7e-69  
Smith-Waterman score: 1140; 40.610% identity (68.779% similar) in 426 aa  
overlap (4-417:24-445)

10 20 30 40  
del\_15 MAVTTRSHKAAAATEPEVVSTGVDVAVSAAPSSSSSSSQ  
gi|119 MSSTALPKRVALHRNPTDSSVPSVSHSPFDSRQSPSTLSMSMASDAENTSGRMIDT

50 60 70 80 90  
del\_15 KSAEPIEYPD--IKTIRDAIPDHCFRPRVWISMAFYRDFAMAFGLGYLAWQYI-P-LIA  
gi|119 YGNE-FKIPDYTIKQIRDAIPAHCYQRSVAVTSLYYVFRDMAILLATVYVFNHYVTPETVP

100 110 120 130 140 150  
del\_15 STPLRYGAWALYGYLQGLVCTGIWILAHECGHGAFSRHTWFNNVMGWIGHSFLLVPYFSW  
gi|119 SMPVVRVWLVAIYTIQGLVGTGVWVLAHECGHGAFSFSKVLNDTVGWICHSLLLVPYFSW

160 170 180 190 200 210  
del\_15 KFSHHRHHRFTGHMEKDMAFVPAEADRNRKLANLYMDKETAEMFEDVPIVQLVKLIAH  
gi|119 KISHGKHKHATGNRIARDMVFPKTRIEYASRIGRAVH---ELSELMEETPILATNLVLQ

220 230 240 250 260 270  
del\_15 QLAGWQMYLLFNVSAGKSKQWETGKGG---MGWLR-VSHFEPSSAVFRNSEAIYIALSD  
gi|119 QLFGWPMYLLTNVTGHNHHERQPEGRGKGRNGYFGGVNHFNPSPLYEAKDAKLIVLSD

280 290 300 310 320 330  
del\_15 LGLMIMGYILYQAAQVVGQVGLLYFQQYFVWHHLVAITYLHHTHEEVHFDADSWTF  
gi|119 LGLFLVGSLLYYIGSTYGLWLNLLVWYGIPYLWVNHHLVAITFLQHTDPTLPHYRPEAWDF

340 350 360 370 380  
del\_15 VKGALATVDRDFGFIGKHLFHNIIDHHVVHHLFPRIPFYAAEEATNSIRPMLGPLY----  
gi|119 TRGAAATIDRDFGVGRHIFHGIETHVLHHYVSTIPFYHADEASEAIQKVMGPHYRSEA

390 400 410 420  
del\_15 HRDDRSFMGQLWYNFTHCKWVVPDPQVPGALIWAHTVQS

gi|119 HTGWTGFFKALWTSARTCQWVEPTEGAKGESQHVLFYRNINGIGVPPAKIPAK  
420 430 440 450 460

427 residues in 1 query sequences  
3787527556 residues in 14717352 library sequences  
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start: Tue Oct 20 14:41:34 2009 done: Tue Oct 20 15:07:36 2009  
Total Scan time: 1517.490 Total Display time: 15.080

Function used was FASTA [version 3.4t26 July 7, 2006]

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Database checksum values:

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Tue Oct 20 15:07:38 CDT 2009 /home/andre/db/TOX_2009	fa2987b358e662a0d03802f0cfba9676
Tue Oct 20 15:09:46 CDT 2009 /home/andre/db/PRT_2009	a155ebc7632842e917ba5dd4ccea1dc09