

Report Title

**Updated Bioinformatics Evaluation of the DNA Sequences Flanking the
Insertion Site in MON 87705: BLASTn and BLASTx Analyses**

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1.0 Summary

Monsanto Company has developed biotechnology-derived soybean MON 87705 with an improved fatty acid profile that results in enhanced nutritional characteristics. MON 87705 was developed to selectively suppress two key enzymes, FATB and FAD2, involved in the soybean seed fatty acid biosynthetic pathway. As a result, MON 87705 soybean oil contains lower levels of saturated fatty acids (16:0 palmitic acid and 18:0 stearic acid) and higher levels of monounsaturated 18:1 oleic acid, with an associated decrease in polyunsaturated 18:2 linoleic acid levels relative to commodity soybean oil.

In addition, MON 87705 also contains the 5-enolpyruvylshikimate-3-phosphate synthase gene derived from *Agrobacterium sp.* strain CP4 (*cp4 epsps*). Expression of the gene product (CP4 EPSPS) renders the plant tolerant to glyphosate, which is the active ingredient in the Roundup® family of agricultural herbicides. Glyphosate binds to the endogenous plant EPSPS enzyme and blocks the biosynthesis of shikimate-3-phosphate, thereby depriving plants of aromatic amino acids (Haslam, 1993; Steinrücken *et al.*, 1984). The CP4 EPSPS protein is structurally similar and functionally identical to endogenous plant EPSPS enzymes but has a much reduced affinity for glyphosate relative to endogenous plant EPSPS (Padgett *et al.*, 1996). Introduction of the *cp4 epsps* gene into MON 87705 allows for the production of aromatic amino acids in the presence of glyphosate (Padgett *et al.*, 1996).

A bioinformatics evaluation was performed to determine if any endogenous open reading frames (ORFs) were disrupted by the insertion of the transfer DNA (T-DNA) present in MON 87705 or whether ORFs from the soybean genome are present in the flanking genomic DNA adjacent to the T-DNA after transformation. This evaluation was accomplished by submitting the DNA sequence flanking the insertion site of MON 87705 to a BLASTn and a BLASTx bioinformatics analyses. BLASTn is an alignment search, which compares a nucleotide query sequence flanking the insertion site against a DNA sequence database. BLASTx is a sequence alignment search, which compares conceptual translation products of a six-frame DNA query sequence against a protein database. Results of these analyses confirm that it is unlikely that endogenous ORF(s) have been disrupted by the insertion of T-DNA in MON 87705. While BLASTn alignments with both the Expressed Sequence Tag (EST) and non-redundant sequence databases yielded significant *E*-scores, all alignments displayed less than 95% identity. BLASTx alignments yielded significant *E*-scores with RNA-directed DNA polymerase, a class of proteins contained in retrotransposons. Inspection of the aligned regions of the query sequence revealed that in order to maintain the alignment, the sequence translation jumped from frame to frame and contained numerous stop codons. Indicating the sequence alignment does not reflect a putative RNA-directed DNA polymerase and, therefore, the alignment sequence is not considered an ORF.

2.0 Sequence Database Preparation

The database used for the BLASTn analysis was the GenBank EST database (EST_2010) that includes 64,526,527 sequences (released January 22, 2010; Tu and Silvanovich, 2010) and the GenBank non-redundant nucleotide database (NT_2010) that includes 10,498,010 sequences

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(released January 22, 2010; Tu and Silvanovich, 2010). The database used for the BLASTx analysis was the GenBank non-redundant amino acid database (NR_2010) that includes 10,272,453 sequences (released January 22, 2010; Tu and Silvanovich, 2010).

3.0 Sequence Database Searches

The genomic DNA sequence flanking the insertion site described in Tu and Silvanovich (2009) was used as a source of the DNA for these bioinformatics search comparisons (Figure 1).

The analysis was carried out using a computer loaded with a SUSE LINUX version 10 operating system, and using the publicly available BLAST version 2.2.21 + algorithms downloaded from the National Center for Biotechnology Information (NCBI). The genomic DNA query sequence of MON 87705 was used separately for both BLASTn and BLASTx searches.

The BLASTn search was performed using the BLASTn algorithm, which compares a nucleotide query sequence (both strands) against a nucleotide sequence database (Altschul *et al.*, 1990). All settings used for the analysis were the default for NCBI BLASTn algorithm with the following exceptions: (i) the query sequence was not filtered for repetitive regions, and (ii) an *E*-score cut off of 1e-6 was used. The BLASTx search was performed using the BLASTx algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence against a protein sequence database (Altschul *et al.*, 1997). All settings used for the analysis were the default for NCBI BLAST with the following exceptions: (i) the query sequence was not filtered for repetitive regions and (ii) an *E*-score cut off of 1e-8 was used.

4.0 Significance of the Alignments

An *E*-score cut-off of less than or equal to 1e-6 (for BLASTn) or 1e-8 (for BLASTx) was used because it provides the best compromise between search sensitivity while still minimizing the number of false positives. The expectation value (*E*-score) is a statistical measure of the likelihood that the observed alignment occurred by chance. Any alignments with observed *E*-scores of less than the indicated cut-off values are documented and reviewed to determine their significance. Paired nucleotide sequences are considered to be likely homologues in BLASTn comparisons when 95% or greater shared identity is observed; a high level of shared identity may be indicative of gene sequence with the potential for encoding homologous proteins.

5.0 Results and Conclusions

The results of the BLASTn comparison analysis of the genomic DNA query sequence flanking the insertion site against the GenBank EST database (EST_2010) are shown in Appendix 1. Of those search results, 71 alignments with *E*-score less than or equal to 1e-6 with the GenBank database were obtained, however, none displayed greater than 95% identity.

The results of the BLASTn comparison analysis of the genomic DNA query sequence flanking the insertion site against the GenBank non-redundant nucleotide database (NT_2010) are shown in Appendix 2. Of those search results, numerous alignments with *E*-score less than or equal to

1e-8 with the soybean genome sequence were obtained, however, none displayed greater than 95% identity.

The results of the BLASTx comparison analysis of conceptual translation products from the genomic DNA query sequence against the GenBank non-redundant protein sequence database (NR_2010) are shown in Appendix 3. BLASTx analysis yielded numerous alignments with an *E*-score less than or equal to 1e-8. Inspection of the alignments revealed many were with proteins described as being RNA-directed DNA polymerase, a class of proteins contained in retrotransposons. Inspection of the aligned regions of the query sequence revealed that in order to maintain the alignment, the sequence translation jumped from frame to frame and contained numerous stop codons. While identifying the likely source of the DNA as being a retrotransposon, it appears that the retrotransposon sequence has sustained numerous mutations such that it is incapable of encoding a protein and therefore is not considered an ORF for the purposes of this analysis.

Although both BLASTn searches yielded alignments that displayed significant *E*-scores, the absence of alignments displaying greater than 95% identity precludes the positive identification ESTs or regulatory elements flanking the T-DNA insertion site in MON 87705. Likewise, although the BLASTx search yielded alignments that displayed significant *E*-scores, these alignments did not display characteristics that are reflective of the presence of an identified protein coding sequence in the flanking genomic DNA in MON 87705. Taken together, the results of the BLASTn and BLASTx evaluations indicate that it is unlikely that ORFs at or in the flanking genomic DNA of the MON 87705 insertion site were disrupted.

6.0 References

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GTGTATGTGG	ATGATATCAT	TTTTGGTGCT	ACTAATGAAA	TGCTCTATGA	AGATTTTTCT	60
AAGTTAATGC	AAACTGAGTT	TGAAATGAGC	ATGATGGGAG	AGCTAAAATT	CTTCCTTGGA	120
CTGCAAATAA	AGCAAACACC	CCAAGGCATT	TACATTCATC	AGACCAAGTA	TGTGAAAAAT	180
TAGTTGAAGA	AGTTCAACAT	AAGTGATGAA	AAAGAGATGA	AGACTTTTAT	GCATCCCACT	240
ACACATCTTG	GA CTGGATGA	GGAATCAATG	AAGGTGGACG	TGACTCAATA	CAAAGCAATG	300
ATTGGATCAC	TGCTCTATCT	TAATGCTTCT	AGGCCTTATA	TAATTTTTAG	TGTTTTATTA	360
TGTGCAAGAT	TCCAAAAGGA	ACCAAGGGAA	GTTCATTTAA	CTGCAGTTAA	ACCTATATTC	420
TAATATTTAA	TTAGA ACTCA	TAACCTTGGT	CTTATGCTTA	AGAGAAGAGA	TAGTTTCAGA	480
CTCATGAGCT	ATTGAGATGT	GGACTATGTT	GGTGATAAAG	TCGAAAGAAA	AAGTACAAGT	540
GGAAGTTGTC	ACTTTATAGG	TGGCAACTTA	GTCAC TTGGA	TATGGAAGAA	G TAGGGATCA	600
ACTACATTGT	TC ACTGCTGA	AGTAGAATGC	GTGTCAGTAG	CCATGGAGGT	TACCCTCGAC	660
ATTGAAGACC	CCAAGAAATA	GGTTCAAAGT	TTTGGAATC	CACAGGGTCA	GAGCACAAGT	720
GCAAGTTTCA	AGTATCAAGG	CAGCAACGAA	GCTATATCGT	AGGTAGGGGA	GTTTAGTGGT	780
ACCAATAATG	CCCAAACACC	CACTGGTGGG	ACTCAAAATC	TACAAGGGGA	GAGCAGAATG	840
TCTTCTACAT	CATCAATATC	CAAACCAAGA	TTCTCAAGAC	CGTGAAACAA	AGGATCTCAA	900
ACCATTCTTT	ATGTTGAGTA	TGTCAAATGA	AGAGACTCAG	GGTGTTGTTA	TC ACTGCGGT	960
TTGGCCTTTG	GGCCAAGGCA	CCGTTGTCCT	GAAAAAATA	TGAGAGTTGT	AATACTCGCT	1020
AAGGATGAGT	AGATTAATGA	AGACGGGGAG	ATCATAGGAT	TAAAAAATGA	GAATGAGGAA	1080
GAATGTGAGG	AAGTTTTGGA	GATGGTTTGC	TAGCGGATGG	ATTTGT CAGT	TTGTTCCGCA	1140
GGTGGGCTAA	CCCAGCCTCA	AGCATGAAGC	TTAGGTGAGA	ATTATAGGGG	CAAGAGGTGA	1200
TAATCTTGAT	TGACAATAGG	GCAAGCCACA	ACTTTATATC	CAACAAATTG	GTACATAAAT	1260
TGGGACTCAG	CATAGATCCC	ACAAAGCCCT	ATTATATGAG	ATTGGGGGAT	AGTAACCGCA	1320
AATCCACTCA	AGGATGTTGT	AAGAACTTAA	AAAATAGTTG	GGAGCTTATA	CCATGGTAGG	1380
ATATTTCTAT	CTATTTAAGT	TGGGAGGAGT	GGACCTAATT	ATTGGAGTTG	CTTAGTTGGA	1440
AACATTGGGA	GAAATTAAGG	TGAATTGGAG	GACCCTAAGT	ATGTCTTTTG	TCCACCAAGA	1500
TCAGAATATG	GTGATCAAGG	AGATCTTGGT	TTATTGAAGA	CAATGATCAT	TTTGAGAACA	1560
TTGCAAAAAA	TAGTTAGCAA	GGAAGTTGAG	ATGATGTTCA	TGTTGTGGGT	AATTGAAAGC	1620
AACTATGTGG	AACAAATTGA	TTTAACAAAG	AACCAAGAAA	ATTAGTTGTA	GCAAGTACTG	1680
ATAGAGTTTG	CTACAGTTTT	TCAGGACCTA	AGGGTTTACC	ACCATCTAGA	GAGGTTGATC	1740
ACAAGATTGC	AATTAAGTCC	GGGGCATATC	CAGATAATGT	TAGGCCTTAT	CGTTACCCCC	1800
ACTTACAGAA	GAATGAGATA	AAA ACTCTAG	TGGTTGAGAT	GTTATGATTG	GGGATTATTA	1860
GACTAAGCAA	TAGCTCCTAT	TCTAGCCCAG	TAATTTTGGT	AAAAAGGAAA	GATGGAAGTT	1920
GACGATTATG	TATGGATTAT	CAGGCTTTAA	GTAAGGCTAC	AGTCCCAGAC	AAGTTCCTGA	1980
TTCCTGTCAT	GAAAGAGTTG	TTGGATGAGT	TAAATGGACC	CATCCACTTC	TCTAAAATAG	2040
ATCTAAAGGC	AAGGTATCAC	CAAATCAGAA	TGCACAAACC	TACCTTCAGA	ACTCACCAAG	2100
GACATTATGA	ATCTCCAGTG	ATGCCATTTG	GATTAACAAA	CACCCCGACC	ACGTTCCAAT	2160
GAGCTATGAA	TGCCACACTG	AAACCGTTCC	TTCGTAGGTA	TGTGGTAGTG	TTCTTTGATG	2220
ACATTTTGGT	CTATAGTAAG	TCTTGGAAG	CCCATTTGGA	TCATTTGAGT	TAGGTGTTGG	2280

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CCAGGTTATT AGAACATTAT TTCTTCACAA ATGTTTTTAA AAAAAAATGT AGTTTTGGTC 2340
AAATTAAGGC GGGTTGCTTA GGGCACGTTA TCTCTAAAGA AGGAGTTTTG ATGAGGCCAT 2400
TTTGTAGTGG CCAATGCCTA AAACCTCCTAA GACTTTGAGA GGGTTTTTTGG AACTTACAGG 2460
TTATTATAAA AGGTCCATTT GCAATTATGG GAAGATAGCT CGCCCATTGA TTGATCTATT 2520
AAAGTAAGGA AATTTTAAGT GGAATGAGGA TAGTATTAAG GCTTCCATAC AATTACAACA 2580
AGCTATTACC ACAATACCAA CACTATCCAT GCTTGATTTT TCAAAACAAT TCTCCATAGA 2640
ATGTGATGCC TCGGGGAAGG GAATTGGAGT TGTTCTAACA CAAGATAGAA AGCAAATTGC 2700
TTATTTCAAC AAGGCATTAA AAGATTTGAC TCTTTCTAAA TCTATGTATG AAAAGGAATC 2760
AATGGCTCTT GTCTTAGCCA TACAACATTG GAGGCCTTAT CTTCCGGATT AGAAATTTAC 2820
TATATACATT GACCAAAAAA GTTTGAGATA TCTACTAGAT CAGCGAATTA CAACTCAACC 2880
AACAATATTG GGTAGCCAAG TTGCTGGGGT ATGAGTTTGA CATTGTGTAT AAGGTGGGGG 2940
CTTCAAACAA GGTTGTTGAT GCTCTATCTA GAAGAGATGA AGACAAAGAA TTGCAGGGCA 3000
TTTCTAGACC TTTCTGGAAA GACATAACAA AAATTAATGA AGAAGTTCAG AAGGATCCCG 3060
CGTTGGCTAA AATCCGAGAA GAATTGAAGG ATAATCTAGA TTCACACCCT CAGTACACCC 3120
TGGAGTGTGA CATATTATAC TTCAGAGGGA GGTTGGTCCT ATTAGCTTCT TCATTGTGGA 3180
TTCCAAAGTT ACTACAAGAA TTCCAGACTT CTCTTATGGG AGGGCACTCG GGTATTTACA 3240
TAACTTATAG AAGAATCACT CAATCGCTTT ATTGGATACC AATAAAGGGA GAAATCACTA 3300
AGTTTGTGGT TGC GTGTCAT GTGGGCCAAA GAAGTAAATA TCAAGCATCC TCTCCAGCAG 3360
GTTTACTACA ACCTTTGCCA ATTCCAAATG CTATTTGGGA AGAAATTAGT ATGAATTTTA 3420
TTGTAGGTAT GCTAAAATCA AAAGGGTTTG ATGTTATACT AGTAGAGGTC GACAAGTTAA 3480
GCAAATATAG ATATTTTATT GTGATTAAGC ACCCATACTT TGCTAGGTCT ATTGTTGATG 3540
TTAAAGAAAT AATTTGGTTG CTTGAGGTGC CTATATCTAT TGTTAGCGAC AGTGACCTTA 3600
TTTTTATGAG TCATTTTTTTG CAAGAATTAT TCAAA 3635

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Figure 1. The MON 87705 insertion site and flanks.

Base pairs 1-895 of the query sequence represent the 5' flanking sequence, bases 896-931 represent 36 bp that were likely deleted in MON 87705 upon insertion of the T-DNA, and base pairs 932-3635 of the query sequence represent the 3' flanking sequence.

Appendix 1. BLASTn against EST_2010 database results for the insertion site of MON 87705

BLASTN 2.2.21+

Reference:
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Database: All GenBank+EMBL+DDBJ+PDB sequences from EST Divisions
64,526,527 sequences; 35,552,074,586 total letters

Query= OmniSoy_seq
Length=3635

Sequences producing significant alignments:			Score (Bits)	E Value
gi 192310286 gb FK002614.1	GLPAT26TF JCVI-SOY1 Glycine max cDNA...	253	5e-63	
gi 157978736 gb EX527008.1	MTGland-A073_2007-08-21/MTGland-73_F...	183	7e-42	
gi 46455310 gb CN449584.1	GUO_cDNA_22_35 Flower bud cDNA librar...	141	2e-29	
gi 46455309 gb CN449583.1	GUO_cDNA_47_53 Flower bud cDNA librar...	136	9e-28	
gi 120531684 gb EH259817.1	JGI_ACBU874.fwd ACBU Phakopsora pach...	129	1e-25	
gi 224932199 gb GO262098.1	VBL1_27_C18_E001.g1 Normalized cDNA ...	125	2e-24	
gi 46454183 gb CN448457.1	GUO_cDNA_35_05 Flower bud cDNA librar...	122	2e-23	
gi 46454182 gb CN448456.1	Guo_cDNA_04_34 Flower bud cDNA librar...	122	2e-23	
gi 46453255 gb CN447529.1	GUO_cDNA_52_96 Flower bud cDNA librar...	122	2e-23	
gi 31394403 gb CD473135.1	nad03-14ms3-d02 Nad03 Nuphar advena c...	118	3e-22	
gi 46454077 gb CN448351.1	GUO_cDNA_13_09 Flower bud cDNA librar...	114	3e-21	
gi 46453381 gb CN447655.1	GUO_cDNA_19_65 Flower bud cDNA librar...	114	3e-21	
gi 182387416 gb FF383845.1	MOOA815TF MOO Vigna unguiculata cDNA...	113	1e-20	
gi 55782938 dbj AU286657.2	AU286657 zinnia cultured mesophyll c...	113	1e-20	
gi 164499654 gb FD382994.1	Nad03b_88_C09_C005.g1 Nuphar advena ...	111	4e-20	
gi 195282201 gb FG449368.1	010531KAFB002933HT (KAFB) Actinidia ...	109	1e-19	
gi 188328064 gb EY649972.1	CS00-C1-100-005-F09-CT.F Sweet orang...	109	1e-19	
gi 188237040 gb EY653154.1	CS00-C1-100-041-B11-CT.F Sweet orang...	109	1e-19	
gi 46455765 gb CN450039.1	GUO_cDNA_05_64 Flower bud cDNA librar...	107	5e-19	
gi 46455764 gb CN450038.1	GUO_cDNA_52_77 Flower bud cDNA librar...	107	5e-19	
gi 46455763 gb CN450037.1	GUO_cDNA_50_03 Flower bud cDNA librar...	107	5e-19	
gi 46455762 gb CN450036.1	GUO_cDNA_27_01 Flower bud cDNA librar...	107	5e-19	
gi 46454834 gb CN449108.1	Guo_cDNA_02_72 Flower bud cDNA librar...	104	6e-18	
gi 15545428 gb BI643218.1	RS4_G06 Sugar beet root cDNA library ...	102	2e-17	
gi 48113381 gb CN857670.1	000722AAAA006665HT (AAAA) Royal Gala ...	100	7e-17	
gi 156641404 emb AM791024.1	AM791024 COL, cold overnight librar...	98.7	2e-16	
gi 109856434 gb DW485413.1	GH_RMIRS_052_G05_F Cotton Normalized...	96.9	8e-16	
gi 109856433 gb DW485412.1	GH_RMIRS_052_G05_035_R Cotton Normal...	96.9	8e-16	
gi 211988850 emb CU515454.1	CU515454 ROOTS_KZ0ABF Theobroma cac...	95.1	3e-15	
gi 29632689 gb CB637698.1	OSJNEa04L24.r OSJNEa Oryza sativa Jap...	89.7	1e-13	
gi 152004321 gb EV414029.1	AE193 Subtractive cDNA libraries of ...	87.8	4e-13	
gi 63058835 gb CX289981.1	C02019B11SK IF1 Citrus clementina cDN...	87.8	4e-13	
gi 51368899 gb CV009675.1	zfi01-3ms3-d09 Zfi01 Zamia fischeri c...	87.8	4e-13	
gi 24248782 dbj AU288662.1	AU288662 zinnia cultured mesophyll c...	87.8	4e-13	
gi 13480893 gb BG510236.1	sac64c03.y1 Gm-cl072 Glycine max cDNA...	87.8	4e-13	
gi 218842191 gb FC898759.1	IC0AAA66CG03RM1 IVIA1 Citrus clemen...	86.0	1e-12	
gi 156659462 emb AM827013.1	AM827013 seedling library, SL Nicot...	86.0	1e-12	
gi 110868371 gb DY287020.1	IC0AAA66CG03RM1 CitNFL Citrus clemen...	86.0	1e-12	
gi 45622839 dbj BP066094.1	BP066094 Lotus japonicus mature nodu...	86.0	1e-12	

gi 156700574 emb AM797360.1	AM797360 COL, cold overnight librar...	84.2	5e-12
gi 156677621 emb AM825109.1	AM825109 DL, diurnal library Nicoti...	84.2	5e-12
gi 156640135 emb AM788043.1	AM788043 seedling library, SL Nicot...	84.2	5e-12
gi 46453545 gb CN447819.1	GUO_cDNA_40_33 Flower bud cDNA librar...	84.2	5e-12
gi 34949210 gb CA095903.1	SCACCL6007A10.g CL6 Saccharum officin...	82.4	2e-11
gi 195283410 gb FG452295.1	010603KAFB006601HT (KAFB) Actinidia ...	80.6	6e-11
gi 88903506 dbj CI089044.1	CI089044 Oryza sativa (japonica cult...	77.0	8e-10
gi 35262416 gb CA214784.1	SCQGF1095H02.g FL1 Saccharum officin...	77.0	8e-10
gi 29637310 gb CB642319.1	OSJNEb02H03.r OSJNEb Oryza sativa Jap...	77.0	8e-10
gi 191204749 gb EY403248.1	pOP-CNH03809_EST_C_1_pSK_SK CNH (Oil...	75.2	3e-09
gi 195292065 gb FG421266.1	000717KUFA005629HT (KUFA) Actinidia ...	75.2	3e-09
gi 82451690 gb DV678310.1	CGN-16034 Pericarp Coffea canephora c...	75.2	3e-09
gi 74062044 gb DT577266.1	nad03-44ms4-e04 Nad03 Nuphar advena c...	75.2	3e-09
gi 33796553 gb CF324144.1	HDN--05-L23.g1 OshDAC1-overexpressing...	75.2	3e-09
gi 33793606 gb CF322687.1	HDN--01-M14.g1 OshDAC1-overexpressing...	75.2	3e-09
gi 33793150 gb CF322456.1	HDN--01-B18.g1 OshDAC1-overexpressing...	75.2	3e-09
gi 159611412 gb EY065030.1	CATF8607.fwd CATF Artemisia annua, T...	73.4	9e-09
gi 35241521 gb CA204346.1	SCSGFL1077E10.b FL1 Saccharum officin...	73.4	9e-09
gi 35241364 gb CA204270.1	SCSGFL1077E10.g FL1 Saccharum officin...	73.4	9e-09
gi 223436193 gb GO026487.1	LJMBV62TFC JCVI-LJ2 Lotus japonicus ...	71.6	3e-08
gi 86171752 gb DY032284.1	zfi02-7ms1-f12 Zfi02 Zamia fischeri c...	71.6	3e-08
gi 81292868 gb DV666982.1	CGN-5051 Pericarp Coffea canephora cD...	71.6	3e-08
gi 27248563 dbj BJ566743.1	BJ566743 Ipomoea nil mixture of flow...	71.6	3e-08
gi 212117680 emb CU513805.1	CU513805 ROOTS_KZ0ABF Theobroma cac...	69.8	1e-07
gi 29674721 gb CB670996.1	OSJNEe04F17.f OSJNEe Oryza sativa Jap...	69.8	1e-07
gi 29668050 gb CB664325.1	OSJNEd09P16.f OSJNEd Oryza sativa Jap...	69.8	1e-07
gi 268791897 gb DV639029.1	SUR01-172-E09-A-070.b Sugarcane root...	68.0	4e-07
gi 198161641 gb FL876194.1	CCGI9746.b1 CCGI Panicum virgatum et...	68.0	4e-07
gi 193570388 gb FK526257.1	454GmaGlobSeed260889 Soybean Seeds C...	68.0	4e-07
gi 86170565 gb DY031561.1	zfi02-12ms1-a17 Zfi02 Zamia fischeri ...	68.0	4e-07
gi 82771030 gb DV864592.1	CRP4324 Creeping bentgrass EST Agrost...	68.0	4e-07
gi 46454835 gb CN449109.1	Guo_cDNA_02_01 Flower bud cDNA librar...	68.0	4e-07

>gi|192310286|gb|FK002614.1| GLPAT26TF JCVI-SOY1 Glycine max cDNA 5', mRNA
sequence.
Length=644

Score = 253 bits (280), Expect = 5e-63
Identities = 198/230 (86%), Gaps = 10/230 (4%)
Strand=Plus/Plus

Query	1341	AAGAACTTAAAAA-ATAGTTGGGAGCTTATACCATGGTAGGATATTTCTATCTATTTAAG	1399
Sbjct	2	AAGAACTTAAAAATACAGTTGGGAGCTTATACATGGTAGGAGACTTCTTTCTATTTGAG	61
Query	1400	TTGGGAGGAGTGGACCTAATTATTGGAGTTGCTTAGTTGGAACATTGGGAGAAATTAAG	1459
Sbjct	62	TTGGGAGGAGTGGACCTAATCTGGGAGTTGCTTGACTGGAACATTGGGAGAAATTAAG	121
Query	1460	GTGAATTGGAGGACCCTAAGTATGTCTTTTGTCCACCAAGATCAGAATATGGTGA-TCAA	1518
Sbjct	122	GTGAATTGGAGGACCCTAAGTATGTCTTTTGTCCATCAAGATCAGAATGTGTTGATTGAG	181
Query	1519	GGAGATCTTTGGTTTATTGA-AGACAATGATCATTTTGAGAACATTGCAA	1567
Sbjct	182	GGAG-TCTTTG--TGTGTTGAGAGATTAAGACCTTTTGTG---CATTGCAAA	224

>gi|157978736|gb|EX527008.1| MTGland-A073_2007-08-21/MTGland-73_F06_014_1 Medicago
truncatula
A17 glandular trichome Medicago truncatula cDNA, mRNA sequence.

Score = 183 bits (202), Expect = 7e-42
Identities = 384/561 (68%), Gaps = 20/561 (3%)
Strand=Plus/Plus

```

Query 62      AGTTAATGCAAAGTCTGAGTTTGAAGTGGAGAGCTAAAGTCTTCTTGGAC 121
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 397      AGTTAATGCAGGATGAAGTTGAAGTGGAGAGCTAAAGTCTTCTTGGAA 456

```

```

Query 122  TGCAATAAAGCAAACACCCCAAGGCATTACATTTCATCAGACCAAGTATGTGAAAAAATT 181
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 457  TTCAAATCAACCAAAGTAAAGAAGGAGTATATGTTTCATCAAACAAAATAT---ACAAAGG 513

```

```

Query 182  AG---TTGAAGAAGTTCAACATAAGTGA-TGAAAAAGAGATGAAGACTTTTATGCATCCC 237
           ||||||||||||| || ||||| ||||| ||||| ||||| |||||
Sbjct 514  AGCTTCTGAAGAAGTTCAAGCTAGAAGACTGTAAAA-TGATGAACACTCCAATGCATCCA 572

```

```

Query 238  A-CTACACATCTTGGA CTG--GATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAA 294
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 573  ACCTGCACCTTAAGCAAAGAAGATACTGGAACAGT---AGTAGACCAGAAGCTTTACAGA 629

```

```

Query 295  GCAATGATTGGATCACTGCTCTATCTTAATGCTTCTAGGCCCTATATAATTTTATGTT 354
            |  ||||| ||||| ||| | | | | ||||| ||| ||||| |||||
Sbjct 630  GGTATGATTGGTTCTCTGTTATACCTCACTGCATCTAGACCTGATATTTTATTCAGTGTA 689

```

```

Query 355 TTATTATGTGCAAGATTCCAAAAGGAACCAAGGGAAGTTCATTTAACTGCAGTTAAACCT 414
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct 690 TGCTTGTGTGCAAGATTTCATCAATCAGATCCTAGAGAATCTCATTTAACTGCAGTTAAGAGA 749

```

```

Query 415 ATATTCTAATATTTAATTAGAAGCTCATAACCTTGGTCTTATGCTTAAGAGAAGAGATAG- 473
          || ||| ||| | | ||| ||| |||| | | || ||| ||| |||
Sbjct 750 ATCTTCAGGTATCTGAAAGGAACAACCTAATCTTGGACTCCTGTATAGGA-AATCCCTAGA 808

```

Query 474 TTTCAGACTCATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAAGAAAAAG 533
|| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 809 TTATAAGTTGATTGGATTCTGTGATGCTGATTATGCTGGTGATAGGATTGAAAGAAAATC 868

```

Query    534  TACAAGTGAAGTTGTCACTT  554
          || ||||| ||||| ||
Sbjct    869  AACCAGTGGAAATTGTCAATT  889

```

```
>gi|46455310|gb|CN449584.1| GUO_cDNA_22_35 Flower bud cDNA library from Lycoris  
longituba  
Lycoris longituba cDNA clone GUO_cDNA_22_35.T3_034.ab1, mRNA  
sequence.  
Length=673
```

Score = 141 bits (156), Expect = 2e-29
Identities = 111/133 (83%), Gaps = 0/133 (0%)
Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTTCTAAG 63
|||||
Sbjct 58 TATGTTGATGATATTATATTTGGTGCTACTAATAAAATCTTTGTCAAGATTTTCCAAG 117

Query 64 **TTAATGCAAAGTGAAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCCTTGGACTG** 123

```

Sbjct  118  || ||||| | | ||||||||||||||||||| ||||| || ||||| ||
          TTTATGCATAGGAAATTTGAAATGAGCATGATGGGTGAGCTAAACTTTATCCTTGGCCCT 177

Query   124  CAAATAAAGCAA 136
          ||||| |||||
Sbjct  178  CAAATCAAGCAA 190

```

>gi|46455309|gb|CN449583.1| GUO_cDNA_47_53 Flower bud cDNA library from Lycoris
longituba
Lycoris longituba cDNA clone GUO_cDNA_47_53.T3_052.ab1, mRNA
sequence.
Length=488

Score = 136 bits (150), Expect = 9e-28
Identities = 110/133 (82%), Gaps = 0/133 (0%)
Strand=Plus/Plus

```

Query 4      TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
             |||||
Sbjct 61     TATGTTGATGATATTATATGTGGTGCTACTAATAAAATTCTTGTCAAGATTTTCCAAG 120

```

```

Query    64      TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAAATCTTCCTTGGA CTG      123
          || |||| | | ||||||||||||||| ||||| | ||||| ||
Sbjct   121      TTTATGCATAGGAAATTTGAAATGAGCATGATGGGTGAGCTAAACTTTATCCTTGCCCTT      180

```

```

Query 124  CAAATAAGCAAA 136
           ||||| |||||
Sbjct 181  CAAATCAAGCAAA 193

```

>gi|120531684|gb|EH259817.1| JGI_ACBU874.fwd ACBU Phakopsora pachyrhizi infected
soybean leaf
tissue 6-8 days post inoculation with TW72-1 urediniospores
Glycine max cDNA clone ACBU874 5', mRNA sequence.
Length=632

Score = 129 bits (142), Expect = 1e-25
Identities = 193/267 (72%), Gaps = 8/267 (2%)
Strand=Plus/Plus

Query	2630	TTCTCCATAGAATGTGATGCCTCGGGGAAGGGAATTGGAGTGTGTTCTAACACAAGATAGA	2689
Sbjct	361	TTTTCCATTGAATGTGATGCTTCGCGAAACAGGGATAGGAGCTGTGTTAACACAAGGGAAA	420

Query 2690 AAGCAAATTGCTTATTTC AACAGGCATTAAAGATTTGACTCTTTC-TAAATCTATGTA 2748
 |||||
 Sbjct 421 CGTCCAATTGCATATTTCAGCAAAGGGTTTAGCT- ACTTCAGTTTAAAGTAAATCTATGTA 479

Query 2749 TGAAAAGGAATCAATGGCTCTTGTCTTAGCCATACAACATTGGAGGCCTTATCT-TCCGG 2807
|||||
Sbjct 480 CGAGAAGGAGTTAATGGCTTTGGTCTTAGCAGTCAGACATTGGAGGCCTTACCTATTGGG 539

Query 2808 ATTAGA-AATTACTATATACATTGACCAAAAAAGTTTGAGATATCTACTAGATCAGCGA 2866
|||||
Sbjct 540 A--AGACGATTCCTGTAATTCACTGACCAAAAAAGCTTGAAGTACTTGCTAGAACAACGG 597

```

Query    2867  ATTACAATCT--AACCAACAATATTGG    2891
          || || || || || || || || || ||
Sbjct    598   ATAACCACTCCAAATCAACAGAATTGG    624

```

>gi|224932199|gb|GO262098.1| VBL1_27_C18_E001.g1 Normalized cDNA library from cotyledon and young leaves of peanut Arachis hypogaea cDNA, mRNA sequence.
Length=708

Score = 125 bits (138), Expect = 2e-24
Identities = 123/159 (77%), Gaps = 0/159 (0%)
Strand=Plus/Minus

```
Query 1 GTGTATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCT 60
      || ||||| ||||| || ||||| || ||||| || || ||||| ||
Sbjct 420 GTTTATGTTGATGATATTATCTTTGGTTCGGCTAATGAGGATTTGTGTGCAGATTTTGCT 361

Query 61 AAGTTAATGCAAACGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCCTCCTGGA 120
      ||| || || || ||||| ||||| ||||| ||||| || || ||
Sbjct 360 AAGCTTATGACAAATGAATTGTATGAGCATGATGGGAGAGCTCAATTTCTTCTAGGC 301

Query 121 CTGCAAATAAAGCAAACACCCCAAGGCATTACATTCAT 159
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 300 TTGCAAATAAAGCAAACGTTAGAAAGGCATATTCATTCAT 262
```

>gi|46454183|gb|CN448457.1| GUO_cDNA_35_05 Flower bud cDNA library from Lycoris longituba
Lycoris longituba cDNA clone GUO_cDNA_35_05.T3_004.ab1, mRNA sequence.
Length=440

Score = 122 bits (134), Expect = 2e-23
Identities = 106/132 (80%), Gaps = 0/132 (0%)
Strand=Plus/Minus

```
Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
      ||||| ||||| ||||| ||||| ||||| ||||| || || ||||| |||
Sbjct 338 TATGTTGATGCCATCATATTTGGTTCTACTAATGAAACTCTTTGTCAAGAATTTTCAAG 279

Query 64 TTAATGCAAACGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCCTCCTGGACTG 123
      || ||||| || ||||| ||||| ||||| ||||| || || ||||| ||
Sbjct 278 TTTATGCATATGGAATTTGAAATGAGCATGATGGGTGAGCTTAACTTCATCCTTGGCCTT 219

Query 124 CAAATAAAGCAA 135
      ||||| || |||
Sbjct 218 CAAATCAAACAA 207
```

>gi|46454182|gb|CN448456.1| Guo_cDNA_04_34 Flower bud cDNA library from Lycoris longituba
Lycoris longituba cDNA clone Guo_cDNA_04_34.T3_041.ab1, mRNA sequence.
Length=691

Score = 122 bits (134), Expect = 2e-23
Identities = 106/132 (80%), Gaps = 0/132 (0%)
Strand=Plus/Minus

```
Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
      ||||| ||||| ||||| ||||| ||||| ||||| || || ||||| |||
Sbjct 346 TATGTTGATGCCATCATATTTGGTTCTACTAATGAAACTCTTTGTCAAGAATTTTCAAG 287

Query 64 TTAATGCAAACGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCCTCCTGGACTG 123
      || ||||| || || ||||| ||||| ||||| ||||| || || ||||| ||
Sbjct 286 TTTATGCATATGGAATTTGAAATGAGCATGATGGGTGAGCTTAACTTCATCCTTGGCCTT 227
```

```
Query 124 CAAATAAAGCAA 135
      ||||| || |||
Sbjct 226 CAAATCAAACAA 215
```

>gi|46453255|gb|CN447529.1| GUO_cDNA_52_96 Flower bud cDNA library from Lycoris longituba
Lycoris longituba cDNA clone GUO_cDNA_52_96.T3_096.ab1, mRNA sequence.
Length=465

Score = 122 bits (134), Expect = 2e-23
Identities = 106/132 (80%), Gaps = 0/132 (0%)
Strand=Plus/Plus

```
Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
      ||||| ||||| ||||| ||||| ||||| ||||| || || ||||| |||
Sbjct 298 TATGTGGATGACATCATATTTGGTTCTACTAATGAGCTTCTTTGTCAAGAATTTTCTAAG 357

Query 64 TTAATGCAAACGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCCTCCTGGACTG 123
      || ||||| || || ||||| ||||| ||||| ||||| || || ||||| ||
Sbjct 358 TTTATGCATAGGAAATTCGAAATGAGCATGATGGGTGAGCTTAAATTCATTCTTGGCCTT 417

Query 124 CAAATAAAGCAA 135
      ||||| || |||
Sbjct 418 CAAATGAAACAA 429
```

>gi|31394403|gb|CD473135.1| nad03-14ms3-d02 Nad03 Nuphar advena cDNA clone nad03-14ms3-d02
5', mRNA sequence.
Length=244

Score = 118 bits (130), Expect = 3e-22
Identities = 109/136 (80%), Gaps = 4/136 (2%)
Strand=Plus/Plus

```
Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATG--AAGATTTTCTA 61
      ||||| ||||| || || ||||| ||||| ||||| || ||||| || |||
Sbjct 109 TATGTTGATGACATAATATTTGGTTCTACTAATGA--TTCTCTTTGTAAGAATTTGCTA 166

Query 62 AGTTAATGCAAACGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCCTCCTGGAC 121
      || ||||| || ||||| ||||| ||||| || ||||| || ||||| |||
Sbjct 167 AGGCTATGCAGGAAGAGTTTGAAATGAGCTTGATGGGCGAATTAACTACTTCTCCTGGAC 226

Query 122 TGCAAATAAAGCAAAC 137
      | ||||| ||||| |||||
Sbjct 227 TTCAAATAAAGCAAAC 242
```

>gi|46454077|gb|CN448351.1| GUO_cDNA_13_09 Flower bud cDNA library from Lycoris longituba
Lycoris longituba cDNA clone GUO_cDNA_13_09.T3_005.ab1, mRNA sequence.
Length=601

Score = 114 bits (126), Expect = 3e-21
Identities = 102/128 (79%), Gaps = 0/128 (0%)
Strand=Plus/Plus

```
Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
```

```

Query 124  CAAATAAA 131
          |||| ||
Sbjct 549  TAAATCAA 556

```

Score = 114 bits (126), Expect = 3e-21
Identities = 136/184 (73%), Gaps = 3/184 (1%)
Strand=Plus/Minus

Query 64 TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCCTTGGACTG 123
| | | | | | | | | | | | | | | | | | | | | |
Sbjct 257 TCCATGCACGATGAGTTTGAGATGAGCATGATGGGAGAATAAATTCTTCCTTGGTTTT 198

Query	184	TTGA	187
Sbjct	140	TTGA	137

Score = 113 bits (124), Expect = 1e-20
Identities = 149/207 (71%), Gaps = 0/207 (0%)
Strand=Plus/Minus

Query	1926	TTATGTATGGATTATCAGGCTTTAAAGTAAGGCTACAGTCCCAGACAAGTTCTTGATTCCCT	1985
Subject	173	TTTTGCATAGACTATAGGCGCTTGAATAAGGCTACTGTGGCTGATAAAATTTCCAATACCC	114

```

Query    2046  AAGGCAAGGTATCACCAAATCAGAATG  2072
          |||||  |  |||||  |||||  |||
Sbjct    53    AAGGCAGGTTATCACCAAATCAGGATG  27

```

Score = 113 bits (124), Expect = 1e-20
Identities = 243/360 (67%), Gaps = 20/360 (5%)
Strand=Plus/Minus

Query	1953	AAGGCTACAGTCCCAGACAAGTTCTGTATTCCTGTCATGAAGAGTTGTTGGATGAGTTA	2012
Sbjct	247	AATGCTACCATCAAGAACACATTTCCAAATCCTTTAGTGGGAAGAAATGTTTGATGAATA	188

Query 2072 G-----CACAAACCTACCTTCAGAACTCACCAAGGCATTATGAATCTCC 2116
|
Sbjct 128 GTGTGAGGATGATGTTCTATAAACTGCTTTTCAGAACTCACCAAGGGTTATACGAATTCCT 69

Query 2117 AGTGATGCCATTGGATTAAACAAACACCCGACCACGTTCCAATGAGCATGAATGCCAC 2176
|||||
Sbjct 68 TGTAACTGCTATTTGGGCTTCAAAATGCTCCTGCTACATTCCAATCATTAAATGAATGACAC 9

Score = 111 bits (122), Expect = 4e-20
Identities = 236/344 (68%), Gaps = 14/344 (4%)
Strand=Plus/Plus

Query 136 ACACCCCAAGGCATTTACATTTCATCAGACCAAGTATGTGAAAAATTAGTTGAAGA-AGTT 194
|| ||| ||| | ||| | ||| ||| ||| ||| ||| ||| |||
Sbjct 79 ACTGAAGAAGGAATCTTTCATCAACCAGGCTAAGTATACTAAAGAACTTCTCAAGAGATTT 138

Query 195 CAACATAAGTGAT-GAAAAAGAGATGAAGACTTTTATGCATCCCACTACACATCTTGGAC 253
| | | | | | | | | | | | | | | | | | | | |
Sbjct 139 GGAATGGACTCATCGAAATCAAGAAGA--AATCCTATGAGTACAACACTACTCTCTTGATA 196

Query 254 TGGATGA----GGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATGATTGGATCA 309
||||| ||||| | || ||| ||| ||| ||| |||
Sbjct 197 AAGATGAAAATGGTAAAAATGTAGAT--ACTAAGCTC--TACAGAGGTATGATCGGATCT 252

Query 310 CTGCTCTATCTTAA-TGCTTCTAGGCCTTATATAATTTTGTAGTGTTTTATTATGTGCAAG 368

Score = 109 bits (120), Expect = 1e-19
Identities = 131/175 (74%), Gaps = 5/175 (2%)
Strand=Plus/Plus

```
>gi|46455763|gb|CN450037.1| GUO_cDNA_50_03 Flower bud cDNA library from Lycoris  
longituba  
Lycoris longituba cDNA clone GUO_cDNA_50_03.T3_002.ab1, mRNA
```

```

sequence.
Length=472

Score = 107 bits (118), Expect = 5e-19
Identities = 123/164 (75%), Gaps = 5/164 (3%)
Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
||||| ||||| || ||||| ||||| ||| ||||| ||||| |||
Sbjct 143 TATGTTGATGACATTATATTTGGCTATACTAACGAATCTCTTTGTCAAGATTTTCTGAA 202

Query 64 TTAATGCAAACTGAGTTTGAATGAGCATGATGGGAGAGCTAAATTCCTTGGACTG 123
|| ||||| | || ||||| ||||| ||||| || ||||| || ||||| ||
Sbjct 203 TTTATGCATAGGGAATTTGAGATGAGCATGATGGGTGAACATAAATTTATCCTTGGCCTT 262

Query 124 CAAATAAAGCAAACACCCCAAGGCATTTACATTCATCAGACCAA 167
||||| ||||| || ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct 263 CAAATCAAGCAAATA----AAGGAAGGAATATTTCATCA-ACCAA 301

>gi|46455762|gb|CN450036.1| GUO_cDNA_27_01 Flower bud cDNA library from Lycoris
longituba
Lycoris longituba cDNA clone GUO_cDNA_27_01.T3_001.ab1, mRNA
sequence.
Length=450

Score = 107 bits (118), Expect = 5e-19
Identities = 123/164 (75%), Gaps = 5/164 (3%)
Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
||||| ||||| || ||||| ||||| ||| ||||| ||||| |||
Sbjct 143 TATGTTGATGACATTATATTTGGCTATACTAACGAATCTCTTTGTCAAGATTTTCTGAA 202

Query 64 TTAATGCAAACTGAGTTTGAATGAGCATGATGGGAGAGCTAAATTCCTTGGACTG 123
|| ||||| | || ||||| ||||| ||||| || ||||| || ||||| ||
Sbjct 203 TTTATGCATAGGGAATTTGAGATGAGCATGATGGGTGAACATAAATTTATCCTTGGCCTT 262

Query 124 CAAATAAAGCAAACACCCCAAGGCATTTACATTCATCAGACCAA 167
||||| ||||| || ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct 263 CAAATCAAGCAAATA----AAGGAAGGAATATTTCATCA-ACCAA 301

>gi|46454834|gb|CN449108.1| Guo_cDNA_02_72 Flower bud cDNA library from Lycoris
longituba
Lycoris longituba cDNA clone Guo_cDNA_02_72.T7_076.ab1, mRNA
sequence.
Length=752

Score = 104 bits (114), Expect = 6e-18
Identities = 102/132 (77%), Gaps = 0/132 (0%)
Strand=Plus/Minus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
||| | ||||| || || ||||| ||||| ||||| ||| ||||| ||||| |||
Sbjct 741 TATATAGATGACATTATATTTGGTTCTACTAATGAGCTTCTTTGTCAAGAAATTTTCCAAG 682

Query 64 TTAATGCAAACTGAGTTTGAATGAGCATGATGGGAGAGCTAAATTCCTTGGACTG 123
|| ||||| | || ||||| ||||| ||||| ||||| || ||||| || ||||| ||
Sbjct 681 TTCATGCATAAGGAATTCGAAATGAGCATGATGGGTGAGTTAAATTCATTCTTGTCTT 622

Query 124 CAAATAAAGCAA 135

```

```
>gi|156641404|emb|AM791024.1| AM791024 COL, cold overnight library Nicotiana
tabacum cDNA clone
nt006087044, mRNA sequence.
Length=511
```

Score = 98.7 bits (108), Expect = 2e-16
Identities = 122/167 (73%), Gaps = 0/167 (0%)
Strand=Plus/Minus

```

Query 5      ATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAGT 64
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 216    ATGTAGATGATATTATTTTTGGTAGCCCTAACTCTGTTCTTTGTGAAGAATTGCTCTTT 157

```

Query 65 TAATGCAAAC T GAGTTT GAAAT GAGCAT GATGGG AGAGCT AAAA TTCTTC CTGGACTGC 124
||| || | | | | | | | | | | | | | | | | | | | | | |
Sbict 156 CCATGA AAGGAGA ATTTG AAAT GAGCAT GATG AGAGAA CTGACC TTCTTC CTGGGCTTC 97

Query	125	AAATAAAGCAAACACCCCAAGGCATTACATTCATCAGACCAAGTAT	171
Subject	96	AAATCAAGCAGTCCCCTAAAGGGATTTTCATTGCGAAACCAAGTAT	50

```
>gi|109856434|gb|DW485413.1| GH_RMIRS_052_G05_F Cotton Normalized Library random  
primed Gossypium  
hirsutum cDNA, mRNA sequence.  
Length=757
```

Score = 96.9 bits (106), Expect = 8e-16
Identities = 102/133 (76%), Gaps = 1/133 (0%)
Strand=Plus/Minus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbict 331 TATATFGATGATACTATTTTTGGTTCTACTGATGATCTTCTTTGTTAAGAATT-CAAAG 273

Query 64 TTAATGCAAAC TGAGTTTGAAATGAGCATGATGGGAGAGCTAAAAATTCTTCCTTGGACTG 123
| | | | | | | | | | | | | | | | | | | | | |
Sbjct 272 CTAATGCAAGGTGAATTGATATGAGCATGATAGGAGAATTAAACTTCTTTTTGAGACTC 213

```

Query    124    CAAATAAGCAAA    136
          |||| |||||
Sbjct    212    TAAATCAAGCAAA    200

```

>gi|109856433|gb|DW485412.1| GH_RMIRS_052_G05_035_R Cotton Normalized Library
random primed
Gossypium hirsutum cDNA, mRNA sequence.
Length=775

Score = 96.9 bits (106), Expect = 8e-16
Identities = 102/133 (76%), Gaps = 1/133 (0%)
Strand=Plus/Plus

```

Query 4      TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTTCTAAG 63
             ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 444    TATATTGATGATACTATTTTTGGTTCTACTGATGATCTTCTTGTAAAGAATTT-CAAAG 502

```

Query 64 TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCCTTGGACTG 123
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 503 CTAATGCAAGGTGAATTTGATATGAGCATGATAGGAGAATTAAACTTCTTTTGGACTC 562

Query 124 CAAATAAGCAAA 136

Sbjct 204 CTCATAGGAAGTGAGTTTGAAATGAATATGATGGGGAACTAAATGCCTTCCTGTCTTT 263

Query 124 CAAATAAGCA 134
 ||||| |||||

Sbjct 264 CAAATGAAGCA 274

>gi|46453545|gb|CN447819.1| GUO_cDNA_40_33 Flower bud cDNA library from Lycoris
 longituba
 Lycoris longituba cDNA clone GUO_cDNA_40_33.T3_033.ab1, mRNA
 sequence.
 Length=462

Score = 84.2 bits (92), Expect = 5e-12
 Identities = 99/133 (74%), Gaps = 1/133 (0%)
 Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
 ||||| ||||| || ||||| | ||||| ||||| || ||||| || ||

Sbjct 308 TATGTAGATGACATTATTTTAGATCTACTAATGAAATTTATTACAAAGACTTTGAAAAA 367

Query 64 TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAATTCCTTGGACTG 123
 | ||||| || ||||| ||||| ||||| || || || ||||| |

Sbjct 368 TCCATGCATGATGAATTTGAAAT-AGCATAATGGGAGAACTTAACATTTTCCCTTGGTTTT 426

Query 124 CAAATAAGCAAA 136
 ||| | |||||

Sbjct 427 CAAGTCAAGCAAA 439

>gi|34949210|gb|CA095903.1| SCACCL6007A10.g CL6 Saccharum officinarum cDNA clone
 SCACCL6007A10
 5', mRNA sequence.
 Length=645

Score = 82.4 bits (90), Expect = 2e-11
 Identities = 101/136 (74%), Gaps = 4/136 (2%)
 Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTA--TGAAGATTTTCTA 61
 ||||| ||||| ||||| ||||| || || ||||| ||||| |||||

Sbjct 333 TATGTGGATGATATCATTTTTGGTGCTCTCTCAC--GCTCTTGTTGCAAAGTTTCTG 390

Query 62 AGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAATTCCTTGGAC 121
 || ||| | || || || ||||| ||||| || || ||||| ||

Sbjct 391 AGACTATGAGCAGGGAATTCGAGATGAGCATGATGGGCGAGTTGACATTCCTCCTCGGGT 450

Query 122 TGCAAAATAAGCAAAAC 137
 ||||| |||||

Sbjct 451 TGCAAAATCAAGCAAAAC 466

>gi|195283410|gb|FG452295.1| 010603KAFB006601HT (KAFB) Actinidia deliciosa buds 3
 days after
 hydrogen cyanamide treatment Actinidia deliciosa cDNA clone
 KAFBB00660, mRNA sequence.
 Length=380

Score = 80.6 bits (88), Expect = 6e-11
 Identities = 61/72 (84%), Gaps = 0/72 (0%)
 Strand=Plus/Minus

Query 67 ATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAATTCCTTGGACTGCAA 126
 ||||| ||| ||||| ||||| ||||| ||||| || ||||| || |||||

Sbjct 379 ATGCAAGGTGAATTTGAAATGAGCATGATGGGGAGCTGAATTTCTTCCTTGGTCTTCAA 320

Query 127 ATAAAGCAAACA 138
 || || ||| ||

Sbjct 319 ATCAAACAATCA 308

>gi|88903506|dbj|CI089044.1| CI089044 Oryza sativa (japonica cultivar-group) Cd
 treated callus
 Oryza sativa Japonica Group cDNA clone 018-M055R-F09 3',
 mRNA sequence.
 Length=525

Score = 77.0 bits (84), Expect = 8e-10
 Identities = 90/122 (73%), Gaps = 0/122 (0%)
 Strand=Plus/Plus

Query 50 AAGATTTTCTAAGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAT 109
 ||||| || || ||||| | || ||||| ||||| ||||| || || ||

Sbjct 10 AAGATTTTGCTGAGACTATGCGCAGGGAATTTGAGATGAGCATGATGGATGAGTTATCGT 69

Query 110 TCTTCCTTGGACTGCAAAATAAGCAAACACCCCAAGGCATTACATTTCAGACCAAGT 169
 ||| | || ||||| ||||| ||||| || || ||||| || |||||

Sbjct 70 ACTTTTGGGATTGCAAATTAAGCAAACCTCAAGGTACTTTTGTGCATCAACGAAGT 129

Query 170 AT 171
 ||

Sbjct 130 AT 131

>gi|35262416|gb|CA214784.1| SCQGF1095H02.g FL1 Saccharum officinarum cDNA clone
 SCQGF1095H02
 5', mRNA sequence.
 Length=719

Score = 77.0 bits (84), Expect = 8e-10
 Identities = 74/95 (77%), Gaps = 0/95 (0%)
 Strand=Plus/Plus

Query 76 GAGTTTGAAATGAGCATGATGGGAGAGCTAAATTCCTTGGACTGCAAAATAAGCAA 135
 || || || ||||| ||||| ||||| || ||||| ||||| |||||

Sbjct 2 GAATTCGAGATGAGCATGATGGGGAGTTGACATTCCTTGGGCTGCAATCAAGCAA 61

Query 136 ACACCCCAAGGCATTACATTCATCAGACCAAGTA 170
 ||||| ||||| || ||||| || || |||||

Sbjct 62 ACACGTGAAGGAACATTCATGCACCAAGGCAAGTA 96

>gi|29637310|gb|CB642319.1| OSJNEb02H03.r OSJNEb Oryza sativa Japonica Group cDNA
 clone OSJNEb02H03
 3', mRNA sequence.
 Length=735

Score = 77.0 bits (84), Expect = 8e-10
 Identities = 90/122 (73%), Gaps = 0/122 (0%)
 Strand=Plus/Minus

Query 50 AAGATTTTCTAAGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAT 109
 ||||| || || ||||| | || ||||| ||||| ||||| || || ||

Sbjct 467 AAGATTTTGCTGAGACTATGCGCAGGGAATTTGAGATGAGCATGATGGATGAGTTATCGT 408

Query	170	AT	171
Sbjct	347	AT	346

Score = 75.2 bits (82), Expect = 3e-09
Identities = 77/101 (76%), Gaps = 0/101 (0%)
Strand=Plus/Plus

```

Query 64      TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCT 104
              |||||      ||||| || ||||| || ||||| ||
Sbjct 613     CTTATGCGGGGAGGTTTCGAGATGAGCATGGAGGGGAGAACT 653

```

Score = 75.2 bits (82), Expect = 3e-09
Identities = 61/73 (83%), Gaps = 2/73 (2%)
Strand=Plus/Plus

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Query    142  CAAGG--CATTTA  152
          |||  |||||
Sbjct    65   GAAGGGACATTTA  77

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Lambda	K	H
0.634	0.408	0.912

Gapped			
Lambda	K	H	
0.625	0.410	0.780	

Database: All GenBank+EMBL+DDBJ+PDB sequences from EST Divisions
Posted date: Dec 31, 2009 5:45 PM
Number of letters in database: 35,552,074,586
Number of sequences in database: 64,526,527

Sequences producing significant alignments:	Score (Bits)	E Value
gi 224775873 gb AC235056.1 Glycine max strain Williams 82 clone...	1485	0.0
gi 224922962 gb AC235198.1 Glycine max strain Williams 82 clone...	834	0.0
gi 224923197 gb AC235433.1 Glycine max strain Williams 82 clone...	672	0.0
gi 224923212 gb AC235448.1 Glycine max strain Williams 82 clone...	600	3e-
gi 224923188 gb AC235424.1 Glycine max strain Williams 82 clone...	600	3e-
gi 224923144 gb AC235380.1 Glycine max strain Williams 82 clone...	600	3e-
gi 224923077 gb AC235313.1 Glycine max strain Williams 82 clone...	556	3e-
gi 224923032 gb AC235268.1 Glycine max strain Williams 82 clone...	515	8e-
gi 224923157 gb AC235393.1 Glycine max strain Williams 82 clone...	389	8e-
gi 224922940 gb AC235176.1 Glycine max strain Williams 82 clone...	354	2e-9
gi 224922890 gb AC235126.1 Glycine max strain Williams 82 clone...	347	3e-9
gi 224923073 gb AC235309.1 Glycine max strain Williams 82 clone...	340	4e-8
gi 148372216 gb EF623860.1 Glycine max cultivar Williams 82 clo...	325	8e-8
gi 224923161 gb AC235397.1 Glycine max strain Williams 82 clone...	320	4e-8
gi 224923182 gb AC235418.1 Glycine max strain Williams 82 clone...	311	2e-8
gi 224775870 gb AC235053.1 Glycine max strain Williams 82 clone...	311	2e-8
gi 154816247 gb AC174437.28 Teramuss labialis clone t11-61f9, c...	306	8e-7
gi 224923121 gb AC235357.1 Glycine max strain Williams 82 clone...	304	3e-7
gi 224923162 gb AC235398.1 Glycine max strain Williams 82 clone...	280	3e-7
gi 224923123 gb AC235359.1 Glycine max strain Williams 82 clone...	280	3e-7
gi 224922956 gb AC235192.1 Glycine max strain Williams 82 clone...	268	2e-6
gi 224923017 gb AC235253.1 Glycine max strain Williams 82 clone...	262	8e-6
gi 227120316 gb AC235124.2 Glycine max strain Williams 82 clone...	235	1e-5
gi 224922977 gb AC235213.1 Glycine max strain Williams 82 clone...	235	1e-5
gi 229608992 gb AC236296.1 Glycine max strain Williams 82 clone...	219	9e-5
gi 224775861 gb AC235044.1 Glycine max strain Williams 82 clone...	219	9e-5
gi 189162478 dbj AP009701.1 Lotus japonicus genomic DNA, clone:...	219	9e-5
gi 258679636 gb AC236031.2 Glycine max clone GM_WBb0042E11, com...	206	6e-4
gi 224923196 gb AC235432.1 Glycine max strain Williams 82 clone...	206	6e-4

gi 123707045	emb AM484266.1	Vitis vinifera, whole genome shotgun...	152	1e-32
gi 123704339	emb AM474748.1	Vitis vinifera, whole genome shotgun...	152	1e-32
gi 123686155	emb AM437843.1	Vitis vinifera contig VV78X007838.1...	152	1e-32
gi 147838653	emb AM440565.2	Vitis vinifera contig VV78X201369.4...	150	4e-32
gi 147789676	emb AM443590.2	Vitis vinifera contig VV78X088606.9...	150	4e-32
gi 147785700	emb AM483478.2	Vitis vinifera contig VV78X234092.1...	150	4e-32
gi 123696077	emb AM423434.1	Vitis vinifera contig VV78X011484.8...	150	4e-32
gi 123692737	emb AM485799.1	Vitis vinifera, whole genome shotgun...	150	4e-32
gi 123684895	emb AM465346.1	Vitis vinifera contig VV78X020810.1...	150	4e-32
<p>>gi 224775873 gb AC235056.1 Glycine max strain Williams 82 clone GM_WBb0174F23, complete sequence Length=132479</p> <p>Score = 1485 bits (1646), Expect = 0.0 Identities = 1055/1203 (87%), Gaps = 20/1203 (1%) Strand=Plus/Plus</p>				
Query	2441	GGGTTTTTGGAACTTACAGGTTATTATAAAAGGTCCATTTCGAATTATGGGAAGATAGCT	2500	
Sbjct	123920	GGATTTTITAGACTGTAGGGTTATTACAGAAGGTTTCATTTCGAATTCTGGGAAGATAGCC	123979	
Query	2501	CGCCCATTGATGTGATCTATTAAAGTAAGGAAATTTTAAAGTGAATGAGGATAGATTAAAG	2560	
Sbjct	123980	CGCCCATTGACTGTGATCTATTAAACAAAGGAAATCTTAAAGTGAATGAGGATAGTAATAAG	124039	
Query	2561	GCTTCCATACAATTACAACAAGCTATTACCACAATACCAACACTATCCATGCTTGATTTT	2620	
Sbjct	124040	GCTTTCATACAATTACAGCAAGCTGTGTACCACAGCAACAGTACTATCCATGCTTAATTTT	124099	
Query	2621	TCAAACAATTTCTCCATAGAAATGTGATGCCTCGGGGAAGGGAATTGGAGTTGTTCTAACA	2680	
Sbjct	124100	TCAAACAATTTCTCCATAGAAATGTGATGCCTCGGAG--GGGAATTGGAGCTGTTCTAACA	124157	
Query	2681	CAAGATAGAAAGCAAATTGCTTATTTCAACAAGGCATTAAAGATTGACTCTTTCTAAA	2740	
Sbjct	124158	--AGACAGAAAGCCAATTGCTTATTTCAAGCAAGCATTTGGCAGATTCAAGTCTTTCTAAA	124215	
Query	2741	TCTATGTATGAAAAGGAATCAATGGCTCTTGTCTTAGCCATACAACATTGGAGGCCTTAT	2800	
Sbjct	124216	TCTGTGTATGAAAAGGAAGTATGGCTC--GTCTTAGCCATACAACATTGGAGGCCTTAT	124273	
Query	2801	CTTCCGGATTAGAAATTTACTATATACATTGACCAAAAAAGTTTGAGATATCTACTAGAT	2860	
Sbjct	124274	CTTCTGGGTCAGAAATTTACTGTATACACTGACCAAAAAAGTTTGAGATATCTACTTGAG	124333	
Query	2861	CAGCGAATTACAACCTCA--ACCAACAATATTGGGTAGCCAAGTTGCTGGGGTATGAGTTT	2918	
Sbjct	124334	CAGCGAATTACAACCTCAGAACTAACAAAATTTGGCTTGCCAAGTTGCTGG--TATGAGTTC	124391	
Query	2919	GACATTGTGTATAAGGTGGGGGCTTCAACAAGGTTGTTGATGCTCTATCT--AGAAGAG	2976	
Sbjct	124392	GACATTGTGTATAAGGTGGGGGCTTCAACATGTTGCTGATGCTCTATCTCTAGAAGAG	124451	
Query	2977	ATGAAGACAAAGAATTGCAGGGCATTCTAGACCTTTCTGGAAAGACATAACAAAAATTA	3036	
Sbjct	124452	ATGAAGACAAAGAATTGCAGGGCATTCTAGACCTTTCTAGCAAGACACAACAGAAATTG	124511	
Query	3037	ATGAAGAAGTTTCAGAAGGATCCCGCGTTGGCTAAAAATCCGAGAAGAATTGAAGGATAATC	3096	

Sbjct	124512	ATGACGAAGTTTAGAAGGATCCACGTTGGCTAAAACTGAGAAGAATTGAAGGAGAATC	124571
Query	3097	TAGATTACACCCCTCAGTACACCCTGGAGTGTGACATATTATACTTCAGAGGGAGGTTGG	3156
Sbjct	124572	CAGATTACAACTCAGTACACCCTGGAGCATGACAGATTATACTACAAAGGGAGGCTGG	124631
Query	3157	TCCTATTAGCTTCTTCATTGTGGATTCCAAAGTTACTACAAGAATTCAGACTTCTCTTA	3216
Sbjct	124632	TCCTGTGAGCTTCTTCATTGTGGATTCCAAAGTTACTACAGGAATTTTCATAGTTATCCTA	124691
Query	3217	TGGGAGGGCACTCGGGTATTACATAAATTATAGAAGAATCACTCAATCGCTTTATTGGA	3276
Sbjct	124692	TGGGAGGGCAGTCGGGTATATACAGAACTTATCGAAGAATCGCTCAATCGCTTTATTGGA	124751
Query	3277	TACCAATAAAGGGAGAAATCACTAAGTTTGTGGTTGCGTGTCTGTGGGCCAAGAAGTA	3336
Sbjct	124752	TAGGAATGAAGGGAGAAATCA--GAGTTTGTGGTTGCGTGTCTGTACCAAGAAGCA	124809
Query	3337	AATATCAAGCATCCTCTCCAGCAGGTTTACTACAACCTTTGCCAATTCCAAATGCTATTT	3396
Sbjct	124810	AATATCAAGCATCCTCTCTAGCAGGTTTACTGCAACCTTTGCCAATTCCAAGCGCTATTT	124869
Query	3397	GGGAAGAAATAGTATGAATTTTATTGTAGGTATGCTAAAAATCAAAGGGTTTGATGTTA	3456
Sbjct	124870	GGGAAGAAATCAACATGGATTTTATTGTAGGTTTGCCGAAGTCAACAGGGTTTGATGCTA	124929
Query	3457	TACTAGTAGAGGTCGACAAAGTTAAGCAAAATATAGATATTTTATTGTGATTAAGCACCCT	3516
Sbjct	124930	TACTAGTAGTGGTAGGTTAAGCAAAATATGGGCATTTTATTGTGATTAAGCACCCT	124989
Query	3517	ACTTTGCTAGGTCATTGTTGA-----TGTTAAAGAAATAATTGGTTGCTTGAGGTGC	3570
Sbjct	124990	AGTCTGCTAGGTCATAGCTGAAATTTTGTAAAGAAATAATTCGGTTGCATGGGTGC	125049
Query	3571	CTATATCTATTGTTAGCGACAGTGACCTTATTTTATGAGTCATTTTTCGAAGAATTAT	3630
Sbjct	125050	CTATATCTATTGTCAGTGACAGGGACCTACTTTTATGAGTCATTTTTCGAAGAATTAT	125109
Query	3631	TCA 3633	
Sbjct	125110	TCA 125112	

Score = 1168 bits (1294), Expect = 0.0
 Identities = 999/1234 (80%), Gaps = 91/1234 (7%)
 Strand=Plus/Plus

Query	639	AGCCATGGAGGTTACCTCGACATTGAAGACCCCAAGAAATAGGTTCAAAGTTTGGAAA	698
Sbjct	122776	AGCCATGGAGGTTGCCACACATTGAAGATTCGATGAACAGGTTCAAAGTTTGGAAA	122835
Query	699	TCCACAGGGTCAGAGCACAAGTGCAAGTTTCAAGTATCAAGGCAGCAACGAAGCTATATC	758
Sbjct	122836	TTTGCAGGGTTGGAGTACAAGTGTGGGTTTCAGATATCAAGGCCGCAACGGAGCTGTATC	122895
Query	759	GTAGGTAGGGGAGTTTGTGGTACCAATAATGCCCAACACCCACTGGTGGGACTCAAAA	818
Sbjct	122896	GCGGTTAGGGGCGTTTGTGGTACCAATAATGCCTGAACATTCCTGATGGGACTCGGAA	122955
Query	819	TCTACAAGGGGAGAGCAGAATGTCTTCTACATCATCAATATCCAAACCAAGATTCTCAAG	878
Sbjct	122956	TCTACAAGGAGAGAGCAAAATGTCTTCTACGCCCTTCGGTAGCCAAACAGGATTCTTGGG	123015

Query	879	ACCGTGAACAAAGGATCTCAAACCATTCTTTATGTTGAGTATGTCAAATGAAGAGACTC	938
Sbjct	123016	ACTGCGAAACAGAGGATCTCGAACCCCTTCGCTATGCTGAGTATGTCAAATCAAGGACTT	123075
Query	939	AGGGTGTGTGTATCACTCGCGTTTGGCCCTTTGGGCCAAGGCACCGTTGTCTCTGAAAAAA	998
Sbjct	123076	AGGGCGCTGTGTATCACTGTGGTTTGGCCCTTTGGGCCAGGGGACCGTTGTCTCTGAAAAAA	123135
Query	999	TATGAGAGTTGTAATACTCGCTAAGGATGAGTAGATTAATGAAGACGGGGAGATCATAGG	1058
Sbjct	123136	T----GAGTTGTAATACTGGCTGAGGATGAGCAGATTAATGAAGACGGGGAGATTACAAG	123191
Query	1059	ATTAAAAATGA-----GAATGAGGAAGAATGTGAGGAAGTTTGGAGATGGTTTGCTA	1112
Sbjct	123192	ATTAGAAAAAGAAATGGGAATGAGGAAGA---TGAGGAAGTTTGGAGACGGTTTGCCA	123248
Query	1113	GCGGATGGATTGTGTCAGTTTGTTCGCGAGGTGGGCTAACCC-AGCCTCAAGC-ATGAAGC	1170
Sbjct	123249	GTGGATGGATTGTGCC-TTGTTCGCGAGGTGGGCTAACCCAGCCTCAAACCATGAAGC	123307
Query	1171	TTAGGTGAGAATTATAGGGGCAAGAGGTGATAATCTTGATTGACAATAGGGCAAGCCACA	1230
Sbjct	123308	TTAG-----GGG-AGA-----ATT-----ACAGGG-----ACA	123329
Query	1231	ACTTTATATCCAACAAATTTGGTACATAAATTTGGGACTCAGCATAGATCCACAAAGCCCT	1290
Sbjct	123330	A-----ACAAAT-----ATTGGGACTCAGCACAGATCCACAAAG----	123364
Query	1291	ATTATATGAGATTGGGGGATAGTAACCGCAAAATCCACTCAAGGATGTTGTGAAGAACTTAA	1350
Sbjct	123365	-----TGAGATTGGGAGATGGTAATCACAATCCACTCAAGGATGCTGTGAAGAACTTAA	123418
Query	1351	AAA-ATAGTTGGGAGCTTATACCATGGTAGGATATTTCTATCTATTTAAGTTGGGAGGAG	1409
Sbjct	123419	AAATACAGTTGGGAGCTTATACTATGGTAGGAGACTTCTTTCTATTGAGTTGGGAGGAG	123478
Query	1410	TGGACCTAATTATTGGAGTTGCTTAGTTGGAACATTGGGAGAAATTAAGGTGAATTGGA	1469
Sbjct	123479	TGGACCTAATTCTGGGAGTTGCTTGACTGGAACATTGGGAGAAATTAAGGTGAATTGGA	123538
Query	1470	GGACCCTAAGTATGTCTTTTGTCCACCAAGATCAGAATATGGTGA-TCAAGGAGATCTTG	1528
Sbjct	123539	GGACCCTAAGTATGTCTTTTGTCCATCAAGATCAGAATGTGTTGATTTCAGGGAGTTCTTG	123598
Query	1529	GTTTATTGAAGACAATGATCATTTTGAGAACATTGCAAAAAATAGTTAGCAAGGAAGTTG	1588
Sbjct	123599	GTTTGTCTAAGACAATGATCATTTTGAGAACACAGCAGAAAAATAGCTAGCCAGGAGGTTG	123658
Query	1589	AGATGATGTTTATGTTGTGGGTAATTGAAAGCAACTATGTGGAACAAATGATTTAACAA	1648
Sbjct	123659	AGATGATGTTTATGCTGTGGGTAAGTAAAGCAACACCGTGGAAACAAATGATTTAAC--	123716
Query	1649	AGAACCAAGAAAATAGTTGTAGCAAGTACTGATAGAGTTTGCTACAGTTTTCAGG-AC	1707
Sbjct	123717	-GAACCAAGAAAGTCTGTTGAGCAGGTGCTGACAGGGCTCGCTACAATTTTTCAGGAAC	123775
Query	1708	CTAAGGGTTTACCACCCTCTAGAGAGTTGATCACAAGATTGCAATTAAGTCCGGGGCAT	1767
Sbjct	123776	CTAAGGGTTTACCACCGTCTAGAGAGTTGATCATTGAATTCGAATTAAGTCTGGCACAG	123835
Query	1768	ATCCAGATAATGTTAGGCCTTATCGTTACCCCCACTTACAGAAGAATGAGATAAAAACTC	1827

Sbjct	114109	GCCAGATTTCTCAAAAAAATTCCTCATAGAAATGTGATGCATTGGGAAAGGGAGTAGAGGC	114050
Query	2671	TGTCTCAACACAAGATAGAAAGCAAAATGCTTATTTCAACAAGGCATTAAGATTGAC	2730
Sbjct	114049	TGTGTTAACTCAAGAAAAAGGCCCTTTGTGTTTTTTAGCAAGGCTTTGGAAAATTC AAC	113990
Query	2731	TCTTTCTAAATCTATGTATGAAAAGGAATCAATGGCTCTTGTCTTAGCCATACAACATTG	2790
Sbjct	113989	ACTCACTAAATTCGTTTATGAAAAGGAATTGACGGCCCTAGTTCTAGCAATCCAACACTG	113930
Query	2791	GAGGCCCTATCTCCGGATTAGAAATTTACTATATACATTGACCAAAAAAGTTTGAGATA	2850
Sbjct	113929	GAGGCCCTATCTCTTAGGTA AAAAATTCATTGTGTTAAATGATTAGAAGAGTCTAAGGTA	113870
Query	2851	TCTACTAGATCAGCGAATTACAACCTCAAC--CAACAATATTGGGTAGCCAAGTTGCTGGG	2908
Sbjct	113869	CCTCTTGGAGAAAAAGATAGCAACTCAAAATCAAAAAAATCGTTGGCCAAATTTGTTGGG	113810
Query	2909	GTATGAGTTTGACATTGTGTATAAGGTGGGGGCTTCAACAAGGTTGTTGATGCTCTATC	2968
Sbjct	113809	-TATAAGTTTGA AATTTGTGTAC AAGGCTGGAGCTTCAAAATAGAGTTGCTTATGCATTGTC	113751
Query	2969	TAGAAGAGATGAAGACAAAGAATTGCAGGGCATTCTAGACCTTTCTGGAAGACATAAC	3028
Sbjct	113750	TAAGAGGGATTAAGATAAGGATATGCAAGGAATATGAAGGCCCTTCTGCGCTAACATTGT	113691
Query	3029	AAAAATTAATGAAGAAGTTTCAAGAGATCCCGCTTGGCTAA AATCCGAGAAGAAATTGAA	3088
Sbjct	113690	TGAATTTGATGAAAAAGTTAAGAAGGATCTTGCTCAAGCCAAAATTTCTTGAGGACTTAAA	113631
Query	3089	GGATAATCTAGATTCACACCTCAGTACACCTGGAGTGTGACATATTACTTTCAGAGG	3148
Sbjct	113630	AATAAACCCCTGATTCACATCCTCAATATACCTTCGAGCAAGATAGACTATACTATAAAGG	113571
Query	3149	GAGGTTGGTCCTATTAGCTTCTTTCATTGTGGATTCCAAGTTACTACAAGAATTCAGAC	3208
Sbjct	113570	CAGGTTAGTTTTGTGAACAAATTCACATGGATCCCTAAACTTCTCCAGGAATTCACATAC	113511
Query	3209	TTCTCTTATGGGAGGGCACTCGGTTATTTACATAACTTATAGAAGAACTCACTCAATCGCT	3268
Sbjct	113510	TTCTCCTATAGGTGGGCATTTAGGTATCTACAAAACTCATAGAAGGATGGCTCAATCCCT	113451
Query	3269	TTATTGGATACCAAT-AAAGGGAGAAATCACTAAGTTTGTGGTTGCGTGTGCTGTTGGGCC	3327
Sbjct	113450	TTTCTGGATTGGCATGAAAGGGACCA-TCACTAATTTGTAGCAGCCTGTCTGTTGTGCC	113392
Query	3328	AAAGAAGTAAATATCAAGCATCCTCTCCAGCAGGTTTACTACAACCTTTGCCAATTCCAA	3387
Sbjct	113391	AACGGAGTAAATATCAGGCTTCTTCTCCAGCAGGTTACTGTAACTTTACCCATTCTTA	113332
Query	3388	ATGCTATTTTGGGAAGAAAT	3406
Sbjct	113331	AGGCCATATGGGAAGAAAT	113313

Score = 306 bits (338), Expect = 8e-79
 Identities = 477/676 (70%), Gaps = 17/676 (2%)
 Strand=Plus/Minus

Query	860	CCAAACCAAGATTCTCAAGACCGTGAAACAAAGGATCTCAAACCATTTCTTTATGTTGAGT	919
Sbjct	139403	CCAAACCAAGTTTCTTAGA-----AGCAGGGGAACTCAAAACATTCCTTATGCTAAGT	139350

Query	920	ATGTCAAATGAAGAGACTCAGGGTGTGTTTATCACTGCGGTTTGGCCTTTGGGCCAAGGC	979
Sbjct	139349	ATGTCAAGAGGAGAGATGAAGGAAGGTGTTATCATTGTGGAATGCTTTTGGACCAGGTC	139290
Query	980	ACCGTTGTCTCGAAAAAATATGAGAGTTGTAATACTCGCTAAGGATGAGTAGATTAATG	1039
Sbjct	139289	ACCGTTGTCTCAAAAAAGCCATGAGGGTGTTAATCATGGCCGAGGATGAGCAGATAGATG	139230
Query	1040	AAGACGGGGAGATCATAGGATTAAAAATGAGA-----ATGAGGAAGAATGTGAGGAAG	1093
Sbjct	139229	ATAATAGAGAGATTTCAGAATGGAAAAGGAGAGCGAACATGAGGAAAAGAGAGAGGAAG	139170
Query	1094	TTTTGGAGATGGTTTGTAGCGGATGGATTGTGTCAGTTTGTTCGCGAGGTGGGCTAACCC	1153
Sbjct	139169	CTCCTGATGTGAAATGTCAGTGGATGGATCTTTTAGTATGTTTAGTAGGAGGATTGACAA	139110
Query	1154	AGCCTCAAGC-ATGAAGCTTAGGTGAGAATTATAGGGG-CAAGAGGTGATAATCTTGATT	1211
Sbjct	139109	AACCTCAAACTATGAAGTTAAAAGGTGAATTGCAGGGGGCAAGAAGTGTGATCTTGATA	139050
Query	1212	GACAATAGGGCAAGCCACAACCTTTATATCCAACAAATTTGGTACATAAATTTGGGACTCAGC	1271
Sbjct	139049	GACAATGGAGCAAGTCACAATTTGTATCCAGCAAAATTGATACAAAATTTGGGACTCAAG	138990
Query	1272	ATAGATCCCAACAAGCCCTATTATATGAGATTGGGGGATAGTAACCGCAAAATCCACTCAA	1331
Sbjct	138989	CTCGAATCAACCAACCCCTATTATGTAAGATTAGGGGATGGGAATAGAAAATTAACCCAA	138930
Query	1332	GGATGTTGTAAGAA-CTTAAAAAATAGTTGGGAGCTTATACCATTGGTAGGATATTTCTAT	1390
Sbjct	138929	GGTTGCTACAAGAACCCTGAAGGTGTAGCTGGG-GGGTATATGATGGAAGGAGATTCTTT	138871
Query	1391	CTATTTAAGTTGGGAGGAGTGGACCTAATTATTGGAGTTGCTTAGTTGGAAACATTGGGA	1450
Sbjct	138870	TTGTTTGACTTAGGATGAGTTGACTTGATTCTTGGTGTGGCCTGGCTAGCCACTTTGGGG	138811
Query	1451	GAAATTAAGGTGAATTTGGAGGACCTAAGTATGCTTTTGTCCACCAAGATCAGAATATG	1510
Sbjct	138810	GAAATTAAGGCAAAATTTGAAGACCTAAGCATGTCCCTTCATTTCATCAAGGATAGAATATG	138751
Query	1511	GTGAT-CAAGGAGATC	1525
Sbjct	138750	ATCATACAAAGAGATC	138735

Score = 105 bits (116), Expect = 1e-18
 Identities = 134/183 (73%), Gaps = 1/183 (0%)
 Strand=Plus/Minus

Query	4	TATGTGGATGATATCATTTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTTCTAAG	63
Sbjct	48834	TATGTTGATGATATTATCTTTGGATCTACTAATGAATTATTGTGCAAGGAATTCCTCAT	48775
Query	64	TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTTCTTCTTGGACTG	123
Sbjct	48774	GACATGCAAAAGTGAGTTTGAAATGTCAATGATGGGAGAACTTAATTTCTTTCTGGATTA	48715
Query	124	CAAAATAAGCAAAACCCCCAAGGCATTTACATTCATCAGACCAAGTA-TGTGAAAAATTA	182
Sbjct	48714	CAAAATAAACCAACCAAGGATGGTATTTTGTTAATCAAACCAAGTACTGCAAAAAGTTA	48655

>gi|224923188|gb|AC235424.1| Glycine max strain Williams 82 clone GM_WBb0138C22,
complete
sequence
Length=196178

Score = 600 bits (664), Expect = 3e-167
Identities = 515/634 (81%), Gaps = 2/634 (0%)
Strand=Plus/Minus

Query	4	TATGTGGATGATATCATTTTTGGTGTCTACTAATGAAATGCTCTATGAAGATTTTTCTAAG	63
Sbjct	54765	TATGTGGATGATATCATTTTTG-TGCTACTAATGAAATGCGTTGCGAAGATTTTTCTAAG	54707
Query	64	TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCTTGGACTG	123
Sbjct	54706	CTGGTGCAGATAGAATTTGAAATGAGCATGATGGGAGAACTAAAATTCTTCTCGGATTA	54647
Query	124	CAAAATAAGCAAAACACCCCAAGGCATTTACATTCATCAGACCAAGTATGTGAAAAATTAG	183
Sbjct	54646	CAAAAAAAGCAAAACACCCCAAGGCATCTACATTCATCAGACCATGTATATGAAGAATTTC	54587
Query	184	TTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGACTTTTATGCATCCCACTACA	243
Sbjct	54586	T-GAAGAAATTCACATGGGCGATGCAAAAGTAATGAAGACTCCAATGCACCCACCATA	54528
Query	244	CATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATGATT	303
Sbjct	54527	TACCTTAGACTAGATGAGGAATCAACGATGGTGGACAGGACTTAGTACAAAGCAATGATT	54468
Query	304	GGATCACTGCTCTATCTTAATGCTTCTAGGCCTTATATAATTTTATGTTTTATTATGT	363
Sbjct	54467	GGTTCGTTGTTTTATCTCACTGTGTCCAGGCCTGATATCATTTTATGTTTTCTCTACAT	54408
Query	364	GCAAGATTCCAAAAGGAACCAAGGGAAGTTCAATTAAGTGCAGTTAAACCTATATTCTAA	423
Sbjct	54407	GCAAGATTTCAAAAGGAACCAAGGAGAGTTCACTTAAGTGTAGTCAACATATATTAGA	54348
Query	424	TATTTAATTAGAACTCATAACCTTGGTCTTATGCTTAAAGAGAAGAGATAGTTTCAGACTC	483
Sbjct	54347	TATCTAATGGGAATTTCTAATCTTGGTCTTATGTTCAAAGAAGAGAAAGTTTCAGACTT	54288
Query	484	ATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAGAAAAAGTACAAGTGA	543
Sbjct	54287	ATAAGCTATTGTGATGTTGACTATGTTGGTGATAAAGTTGAAAGAAAAATACAAAAGGA	54228
Query	544	AGTTGTCACTTTATAGGTGGCAACTTAGTCACTTGGATATGGAAGAAGTAGGGATCAACT	603
Sbjct	54227	AGTTGTCACTTTCATAGGTGATAATTTAGTAACATGGATATGCAAGAAGCAAGGCTTAATT	54168
Query	604	ACATTGTTCACTGCTGAAGTAGAATGCGTGTGAC	637
Sbjct	54167	GCATTGTCCACTTCTTAAGCTGAATATATGTGAC	54134

>gi|224923144|gb|AC235380.1| Glycine max strain Williams 82 clone GM_WBb0111E02,
complete
sequence
Length=123474

Score = 600 bits (664), Expect = 3e-167

Identities = 515/634 (81%), Gaps = 2/634 (0%)
Strand=Plus/Plus

Query	4	TATGTGGATGATATCATTTTTGGTGTCTACTAATGAAATGCTCTATGAAGATTTTTCTAAG	63
Sbjct	31945	TATGTGGATGATATCATTTTTG-TGCTACTAATGAAATGCGTTGCGAAGATTTTTCTAAG	32003
Query	64	TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCTTGGACTG	123
Sbjct	32004	CTGGTGCAGATAGAATTTGAAATGAGCATGATGGGAGAACTAAAATTCTTCTCGGATTA	32063
Query	124	CAAAATAAGCAAAACACCCCAAGGCATTTACATTCATCAGACCAAGTATGTGAAAAATTAG	183
Sbjct	32064	CAAAAAAAGCAAAACACCCCAAGGCATCTACATTCATCAGACCATGTATATGAAGAATTTC	32123
Query	184	TTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGACTTTTATGCATCCCACTACA	243
Sbjct	32124	T-GAAGAAATTCACATGGGCGATGCAAAAGTAATGAAGACTCCAATGCACCCACCATA	32182
Query	244	CATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATGATT	303
Sbjct	32183	TACCTTAGACTAGATGAGGAATCAACGATGGTGGACAGGACTTAGTACAAAGCAATGATT	32242
Query	304	GGATCACTGCTCTATCTTAATGCTTCTAGGCCTTATATAATTTTATGTTTTATTATGT	363
Sbjct	32243	GGTTCGTTGTTTTATCTCACTGTGTCCAGGCCTGATATCATTTTATGTTTTCTCTACAT	32302
Query	364	GCAAGATTCCAAAAGGAACCAAGGGAAGTTCAATTAAGTGCAGTTAAACCTATATTCTAA	423
Sbjct	32303	GCAAGATTTCAAAAGGAACCAAGGAGAGTTCACTTAAGTGTAGTCAACATATATTAGA	32362
Query	424	TATTTAATTAGAACTCATAACCTTGGTCTTATGCTTAAAGAGAAGAGATAGTTTCAGACTC	483
Sbjct	32363	TATCTAATGGGAATTTCTAATCTTGGTCTTATGTTCAAAGAAGAGAAAGTTTCAGACTT	32422
Query	484	ATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAGAAAAAGTACAAGTGA	543
Sbjct	32423	ATAAGCTATTGTGATGTTGACTATGTTGGTGATAAAGTTGAAAGAAAAATACAAAAGGA	32482
Query	544	AGTTGTCACTTTATAGGTGGCAACTTAGTCACTTGGATATGGAAGAAGTAGGGATCAACT	603
Sbjct	32483	AGTTGTCACTTTCATAGGTGATAATTTAGTAACATGGATATGCAAGAAGCAAGGCTTAATT	32542
Query	604	ACATTGTTCACTGCTGAAGTAGAATGCGTGTGAC	637
Sbjct	32543	GCATTGTCCACTTCTTAAGCTGAATATATGTGAC	32576

>gi|224923077|gb|AC235313.1| Glycine max strain Williams 82 clone GM_WBb0072N12,
complete
sequence
Length=145518

Score = 556 bits (616), Expect = 3e-154
Identities = 501/628 (79%), Gaps = 1/628 (0%)
Strand=Plus/Plus

Query	1	GTGTATGTGGATGATATCATTTTTGGTGTCTACTAATGAAATGCTCTATGAAGATTTTTCT	60
Sbjct	9072	GTATATGTGGATGACATCATTTTTGGTGTCTACTAATGAAATACCTTTATGAAGATTTTTCT	9131
Query	61	AAGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCTTGGGA	120

>gi|224922890|gb|AC235126.1| Glycine max strain Williams 82 clone GM_WBa0043I07,
complete
sequence
Length=115742

Score = 347 bits (384), Expect = 3e-91
Identities = 368/479 (76%), Gaps = 6/479 (1%)
Strand=Plus/Minus

Query 165 CAAGTATGTGAAA-AATTAGTTGAAGAAGTTCACATAAGTGATGAAAAAGAGATGAAGA 223
Sbjct 9169 CATGTATGTGAAAGAACTA-TTGAAGAAATTCACATAAAAGATGCAAAACAAATAAAGA 9111
Query 224 CTTTTATGCATCCCACTACACATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGA 283
Sbjct 9110 CACCCATGCATCTTACAACAGATCTTGGATTAGACATAGAATCAACAAAGGTGGATGGGA 9051
Query 284 CTCAATACAAAGCAATGATTGGATCACTGCTCTATCTTAATGCTTCTAGGCCCTTATATAA 343
Sbjct 9050 CTCAATACAAAGTAATGATTGATCATTGTTTTATCTCACAACATCCATACCTGATATCA 8991
Query 344 TTTTATAGTGTTTATTATGTGCAAGATTCCAAAAGGAACCAAGGGAAGTTCATTTAACTG 403
Sbjct 8990 TGTTTAACGTTTGATTATGTGCGAGATTTCACAAGAAGCAAGGGAAGTTCATCTAACTA 8931
Query 404 CAGTTAAACCTATATTCTA-ATATTTAATTAGAAGTTCATAACCTTGGTCTTATGCTTAAG 462
Sbjct 8930 TAGTTAAAC--ATATTTAGATATTTAATTGGAAGTTCATCTTGGCCTTCTATTAGA 8873
Query 463 AGAAGAGATAGTTTCAGACTCATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTC 522
Sbjct 8872 AGAAGAGA-AAATTCAGGCTCAAGCTTTTATGATGCTGACTATGTCGGGGACAAAGTA 8814
Query 523 GAAAGAAAAGTACAAGTGAAGTTGTCACTTTATAGGTGGCAACTTAGTCACTTGGATA 582
Sbjct 8813 GAAAGAAAAGAGCAAAAACAAAAGTTTCCACTTTATAGTGGCAACCTAGTTACATGGATA 8754
Query 583 TGGAAGAAGTAGGGATCAACTACATTGTTCACTGCTGAAGTAGAATGCGTGTCACTAGC 641
Sbjct 8753 TGCAAGAAGTAAGGCTCAACTGCATTGTCCACTATTGAATTAGAGTACATGTTAGTAGC 8695

Score = 87.8 bits (96), Expect = 4e-13
Identities = 102/136 (75%), Gaps = 4/136 (2%)
Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATG--AAGATTTTCTA 61
Sbjct 97117 TATGTTGATGATATTATCTTTGGATCCACTTATGACT--CTTTATGCAAGAATTCTCTC 97174
Query 62 AGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCCCTGGAC 121
Sbjct 97175 AAGACATGTAAAGTGAAGTTTGAAATGTCAATGATAGGAGAAGTAAATTCTTCTTGGGT 97234
Query 122 TGCAAAATAAGCAAAC 137
Sbjct 97235 TGCAAAATCAAGCAAAC 97250

>gi|224923073|gb|AC235309.1| Glycine max strain Williams 82 clone GM_WBb0069M12,
complete

sequence
Length=115765

Score = 340 bits (376), Expect = 4e-89
Identities = 436/592 (73%), Gaps = 12/592 (2%)
Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTCTAAG 63
Sbjct 5670 TAAGTGGACGACATTATATTGGTGTACTAATGAACCTCTCTGGGAGGAATTTTCTAAG 5729
Query 64 TTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAAATCTTCCCTGGACTG 123
Sbjct 5730 CTAATCCAGGTTGAATTCGAAATGAGTATGATAGGAGAGCTAAAGTTCTTCTTAGGACTA 5789
Query 124 CAAATAAAGCAAAC-ACCCCAAGGCATTTACATTCATCAGACCAAGTATGTGAA--AAAT 180
Sbjct 5790 CAGATAAAAATAAACCAACACTAGGG-TCTATATCCATCAAATCAAGTATGTCAAGGAAC 5848
Query 181 TAGTTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGACTTTTATGCATCCCACT 240
Sbjct 5849 TC--TCAAGAAGTTTATATAGAAGATGTAAAAGAAATGAAGACTTATATGCATCCAAC- 5905
Query 241 ACACATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATG 300
Sbjct 5906 --ATGCTTGGACTTGACGAGGAATCCAACAAAGTGGACAACCTACAATACAGAGCGATG 5963
Query 301 ATTGGATCACTGCTCTATCTTAATGCTTCTAGGCCCTATATAATTTTATAGTGTTTTATTA 360
Sbjct 5964 AATGGATCCTTACTATATATAATTGCATCTAGACCTGACATATTCTTCAGTGTGGACTA 6023
Query 361 TGTGCAAGATTCCAAAAGGAACCAAGGGAAGTTCATTTAACTGCAGTTAAACCTATATTC 420
Sbjct 6024 TGTGCTAGATTCCAATAAGACCCAAGGGAAGTTCACCTTAATTGTTGTCAAAAGAATATT- 6082
Query 421 TAATATTTAATTAGAAGTCAACCTTGGTCTTATGCTTAAG-AGAAGAGATAGTTTCAG 479
Sbjct 6083 TAGAATTTAATTGGAAGTCCAACTCTTGGTCTTACTTTAAGCAAAATAAGGAATTT-AG 6141
Query 480 ACTCATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAGAAAAAGTACAAG 539
Sbjct 6142 ATTGATCAATTGATGTGATGCCAACTATTCTGGTGACAAACTTGAAAGAAGAAGCACTAG 6201
Query 540 TGGAAGTTGTCACTTTATAGGTGGCAACTTAGTCACTTGGATATGGAAGAAG 591
Sbjct 6202 TCAAAGTTGTCACTCTATTGGTGGAAACCTAGTCACTTAGATCAGCAAGAAG 6253

Score = 77.0 bits (84), Expect = 7e-10
Identities = 99/133 (74%), Gaps = 4/133 (3%)
Strand=Plus/Minus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATGAA--GATTTTCTA 61
Sbjct 43060 TATGTAGATGATATTATTTCTGAGTTACCAATGAA-TCCT-TGTGCAAGGATTTCTCCG 43003
Query 62 AGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCCCTGGAC 121
Sbjct 43002 ATATGATGAAGAGTGAAGTTTGAAATAAGCATGATAGGAGAATTAAGTTCTTCTTAGGGC 42943
Query 122 TGCAAAATAAGCA 134
Sbjct 43002 TGCAAAATAAGCA 134

Sbjct 124857 CTTATGCAGACAAAGTTTGAGATAAGTATGATGGGAGAAATTAAAGTTCTTCCTTGGACTC 124798

Query 124 CAAATAAAGCAAAACACCCCAAGGCATTACATTCATCAGACCAAGTATGTGAAAAATTAG 183

Sbjct 124797 CAAATCAAGCAAAACAAATGAAGGCATATACATACACCAATCTAAGTACATGAAAGAACTC 124738

Query 184 TTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGACTTTTATGCATCCCACTACA 243

Sbjct 124737 TTGAAGAAGTTCAAGAGGGACGATGCAAGCTGATGAAAACCTTCTATGCATCCAACCACT 124678

Query 244 CATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATGATT 303

Sbjct 124677 GTACTTGGACTGGACAATGA---ACTAAAGGTGGACGAAAAGACATACAAAGGAATGATA 124621

Query 304 GGATCACTGCTCTATCTTAATGCTTCTAGGCCTTATATAATTTTATGTTTTATTATGT 363

Sbjct 124620 GGATCTCTTCTGTATCTCATTGCGTCCATACATTGATGTTTATGTTTCACTGTATGCCGCTAT 124561

Query 364 GCAAGATTCCAAAAGGAACCAAGGGAAGTTCATTAACTGCAGTTAAACCTATATTCTAA 423

Sbjct 124560 TCCAGATTCCGAAAGGAACCAAGGGAAGTTCATTATCTGTTGTCAAACGAATATTCAA 124501

Query 424 TATTTAATTAGAACTCATAACCTTGGTCTTATGC-TTAAGAGAAGAGATAGTTTCAGACT 482

Sbjct 124500 TATCTAATTGGAACCTCCTAACCTTGGT-GTGTGCAATAAGAGAGAAAAGGAATACAGGTT 124442

Query 483 CATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAGAAAAGTACAAGTGG 542

Sbjct 124441 TCTTGGTTATTGTGATGCCGATTTCAGTGGAGATAAAGTGGAAACAAAAGCACTAGTGG 124382

Query 543 AAGTTGTCACTTTAT 557

Sbjct 124381 AGGCTTTCACCTTTAT 124367

>gi|224775870|gb|AC235053.1| Glycine max strain Williams 82 clone GM_WBb0148022, complete sequence
Length=135915

Score = 311 bits (344), Expect = 2e-80
Identities = 404/555 (72%), Gaps = 5/555 (0%)
Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTTCTAAG 63

Sbjct 10871 TATGTGGACAATATCATATTCGGTGCTACTAATGAATCTTTATGTGAGGGCCTTTCCAAG 10930

Query 64 TTAATGCAAACTGAGTTTGAATGAGCATGATGGGAGAGCTAAAATCTCTCTGGACTG 123

Sbjct 10931 CTTATGCAGACAAAGTTTGAAGATAAGTATGATGGGAGAAATTAAAGTTCTCTCTGGACTC 10990

Query 124 CAAATAAAGCAAAACACCCCAAGGCATTACATTCATCAGACCAAGTATGTGAAAAATTAG 183

Sbjct 10991 CAAATCAAGCAAAACAAATGAAGGCATATACATACACCAATCTAAGTACATGAAAGAACTC 11050

Query 184 TTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGACTTTTATGCATCCCACTACA 243

Sbjct 11051 TTGAAGAAGTTCAAGAGGGACGATGCAAGCTGATGAAAACCTTCTATGCATCCAACCACT 11110

Query 244 CATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATGATT 303

Sbjct 11111 GTACTTGGACTGGACAATGA---ACTAAAGGTGGACGAAAAGACATACAAAGGAATGATA 11167

Query 304 GGATCACTGCTCTATCTTAATGCTTCTAGGCCTTATATAATTTTATGTTTTATTATGT 363

Sbjct 11168 GGATCTCTTCTGTATCTCATTGCGTCCATACCTGATGTTATGTTTCACTGTATGCCGCTAT 11227

Query 364 GCAAGATTCCAAAAGGAACCAAGGGAAGTTCATTAACTGCAGTTAAACCTATATTCTAA 423

Sbjct 11228 TCCAGATTCCGAAAGGAACCAAGGGAAGTTCATTATCTGTTGTCAAACGAATATTCAA 11287

Query 424 TATTTAATTAGAACTCATAACCTTGGTCTTATGC-TTAAGAGAAGAGATAGTTTCAGACT 482

Sbjct 11288 TATCTAATTGGAACCTCCTAACCTTGGT-GTGTGCAATAAGAGAGAAAAGGAATACAGGTT 11346

Query 483 CATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAGAAAAGTACAAGTGG 542

Sbjct 11347 TCTTGGTTATTGTGATGCCGATTTCAGTGGAGATAAAGTGGAAACAAAAGCACTAGTGG 11406

Query 543 AAGTTGTCACTTTAT 557

Sbjct 11407 AGGCTTTCACCTTTAT 11421

>gi|154816247|gb|AC174437.28| Teramnus labialis clone t11-61f9, complete sequence
Length=155779

Score = 306 bits (338), Expect = 8e-79
Identities = 447/627 (71%), Gaps = 4/627 (0%)
Strand=Plus/Plus

Query 4 TATGTGGATGATATCATTTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTTCTAAG 63

Sbjct 17364 TATGTGTGATGATATCATTTTTTGGTGCTACTAATGAATCCTTGTGAAGGAATCTCTGAG 17423

Query 64 TTAATGCAAACTGAGTTTGAATGAGCATGATGGGAGAGCTAAAATCTCTCTGGACTG 123

Sbjct 17424 CTGATGCAGGAAGAATTGAAATGAGCATGATGGGTGAGCTAAAGTCTCTCTGGACTC 17483

Query 124 CAAATAAAGCAAAACACCCCAAGGCATTACATTCATCAGACCAAGTATGTGAAAAATTAG 183

Sbjct 17484 CAAATAAAGCAAAACCAAGAAGGGATCTACGTCCATCAGACCAAGTACGTGAAAGAACTT 17543

Query 184 TTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGACTTTTATGCATCCCACTACA 243

Sbjct 17544 CTCAAGAAGTTTAACATGCTGGACGCCAAATCTATGAAGACTCCTATGCATCCAGCAAC 17603

Query 244 CATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATGATT 303

Sbjct 17604 TATCTATCAATGGACGAGTCCTCGAACAAGATGGACGTAATGCTATACAAGAAAATGATA 17663

Query 304 GGATCACTGCTCTATCTTAATGCTTCTAGGCCTTATATAATTTTATGTTTTATTATGT 363

Sbjct 17664 GGTCTCTAATGTACCTAACAGCGTCCAGACCTGCATCCTGTTTCACTGTCAACCTATGC 17723

Query 364 GCAAGATTCCAAAAGGAACCAAGGGAAGTTCATTAACTGCAGTTAAACCTATATTCTAA 423

Sbjct 17724 TCCAGATTCCAAAGTGATCCAAGGGAGGTACATTGTGTCAGCGGTTAAATGCATTTTCAGA 17783

Query 424 TATTTAATT-AGAAGTCAATACCTTGGTCTTATGCTTAAAGAGAAGAGA-TAGTTTCAGAC 481

Sbjct 17784 TATTTAATTGACAGCAC-TAACCTTGGTCTTCTG-TACAAAGGAGAAAGTCAATTCAGGC 17841

Score = 224 bits (248), Expect = 2e-54
Identities = 413/602 (68%), Gaps = 4/602 (0%)
Strand=Plus/Minus

Monsanto Company

Score = 132 bits (146), Expect = 1e-26
Identities = 223/321 (69%), Gaps = 4/321 (1%)
Strand=Plus/Minus

Characterization Center
0-071


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Query    601      ACTACATTGTTCACTGCTGAA    621
          ||| ||| ||||| |||
Sbjct   79144    GTAGCACTATCCACTGCAGAA    79124

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Query 2480 TGCAATTATGGGAAGATAGCTCGCCCATTTGATTGATCTATTAAAGTAAGGAAATTTTAAG 2539

Monsanto Company

Regulatory Product Characterization Center
RAR-10-071

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Strand=Plus/Plus

Query	106	AAATTCCTCCCTGGACTGCAAAATAAAGCAAACACCCCAAGGCATTTACATTCATCAGACC	165
Sbjct	18364	AAGTTCCTCTTAGGACTACAGATAAAATATACCAACAATGAAATCTATATCCATAAAACC	18423
Query	166	AAGTATGTGAAAAA--TAGTTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGA	223
Sbjct	18424	AAGTATGTCAAAGAACTTA--TCAAGAAAGTTCAAGTTGGAAGGTGCAAAAGAAATTGAGA	18481
Query	224	CT--TTTATGCATCCCACTACACATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGT	281
Sbjct	18482	CTCCTCTATGCATCCAACGACAGTCTTGGACTGGACGAGGAATCCAATAAAATACACAA	18541
Query	282	GACTCAATACAAAGCAATGATTGGATCACTGCTCTATCTTAATGCTTCTAGGCCTTATAT	341
Sbjct	18542	CTCTTAATAGAGAACTATCATTGGATCCCTACTATATCTAACTACGTCAGACCATGAT	18601
Query	342	AATTTTATAGTGTATTATATGTGCAAGATTCACAAAGGAACCAAGGGAAGTTCATTTAAC	401
Sbjct	18602	ATTGTTCAAGTGTGGAATATGTCTAGATTTTAAACAAGACCAAGGGAAGTTCATTTAAC	18661
Query	402	TGCAGTTAAACCTATATTTCTAATATTTAATTAGAACTCATAACCTTGGTCTTATGCTTAA	461
Sbjct	18662	TACCGTTAAAAGGATATTTAGATATTTATTAGAACTCTCTAATCTTGGTCTTACTTTAA	18721
Query	462	G-AGAAGAGATAGTTTCAGACTCATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAG	520
Sbjct	18722	GTATAACA-AGGAATTCAGGTTGATTAGTTACTGTGATGCTAATTATGTTGGTGACAAA	18780
Query	521	TCGAAAGAAAAAGTACAAGTGAAGTTGTCACTTTATAGGTGGCAACTAGTCACTTGGGA	580
Sbjct	18781	TTGAAAGAAAGCACTAGTGAAAGTTGTCAATCATTATTTGGATACCTAGTCACTTGGGA	18840
Query	581	T 581	
Sbjct	18841	T 18841	

>gi|229608992|gb|AC236296.1| Glycine max strain Williams 82 clone GM_WBb0094F23, complete sequence
Length=189943

Score = 219 bits (242), Expect = 9e-53
Identities = 257/345 (74%), Gaps = 2/345 (0%)
Strand=Plus/Minus

Query	1	GTGTATGTGGATGATATCATTTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTTCT	60
Sbjct	141185	GTATATGTGGATGACATCATATTTGGTGCTACGAATGAGCCTCTATGTGAGGATATTTCT	141126
Query	61	AAGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCCTTGGA	120
Sbjct	141125	AAGCTAATGCAAACTCGAGTTTGAAATGAGCATGACGAGAGAACTAAAGTTCTTCTTAGGA	141066
Query	121	CTGCAAAATAAGCAAAACACCCCAAGGCATTTACATTCATCAGACCAAGTATGTGAAAAAT	180
Sbjct	141065	CTACAAATCAAAACAGACTAACAATGGAATCTACATCCATCAAAACCAAGTATGTGAAAGAA	141006
Query	181	TAGTTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGACTTTTATGCATCCCACT	240

Sbjct	141005	CTTCTGAAAAAGTTCAACCTAGAAAACCCCTAAGGAGATTAACACACCCATGCATCCAACA	140946
Query	241	ACACATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATG	300
Sbjct	140945	ATGTATCTTGGATTGGACAAAGAATCCAAGAAGGTGGATAACACTCAATTTAGTGCAATG	140886
Query	301	ATTGGATCACTGCTCTATCTTAAT-GCTTCTAGGCCTTATATAAT	344
Sbjct	140885	ATTGGCTCATTATTGTA-CTTGATCGCGTCTAGACCTGACATAAT	140842

>gi|224775861|gb|AC235044.1| Glycine max strain Williams 82 clone GM_WBb0005G15, complete sequence
Length=148301

Score = 219 bits (242), Expect = 9e-53
Identities = 257/345 (74%), Gaps = 2/345 (0%)
Strand=Plus/Minus

Query	1	GTGTATGTGGATGATATCATTTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTTCT	60
Sbjct	82886	GTATATGTGGATGACATCATATTTGGTGCTACGAATGAGCCTCTATGTGAGGATATTTCT	82827
Query	61	AAGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCCTTGGA	120
Sbjct	82826	AAGCTAATGCAAACTCGAGTTTGAAATGAGCATGACGAGAGAACTAAAGTTCTTCTTAGGA	82767
Query	121	CTGCAAAATAAGCAAAACACCCCAAGGCATTTACATTCATCAGACCAAGTATGTGAAAAAT	180
Sbjct	82766	CTACAAATCAAAACAGACTAACAATGGAATCTACATCCATCAAAACCAAGTATGTGAAAGAA	82707
Query	181	TAGTTGAAGAAGTTCAACATAAGTGATGAAAAAGAGATGAAGACTTTTATGCATCCCACT	240
Sbjct	82706	CTTCTGAAAAAGTTCAACCTAGAAAACCCCTAAGGAGATTAACACACCCATGCATCCAACA	82647
Query	241	ACACATCTTGGACTGGATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAGCAATG	300
Sbjct	82646	ATGTATCTTGGATTGGACAAAGAATCCAAGAAGGTGGATAACACTCAATTTAGTGCAATG	82587
Query	301	ATTGGATCACTGCTCTATCTTAAT-GCTTCTAGGCCTTATATAAT	344
Sbjct	82586	ATTGGCTCATTATTGTA-CTTGATCGCGTCTAGACCTGACATAAT	82543

>gi|189162478|dbj|AP009701.1| Lotus japonicus genomic DNA, clone: LjT31G10, TM1742, complete sequence
Length=107618

Score = 219 bits (242), Expect = 9e-53
Identities = 398/574 (69%), Gaps = 30/574 (5%)
Strand=Plus/Minus

Query	2	TGTATGTGGATGATATCATTTTTTGGTGCTACTAATGAAATGCTCTATGAAGATTTTTCTA	61
Sbjct	105308	TGTATGTGCGATGATATCATCTTCGGTGCAACTAGCGATAAACTGTGTAAAGAATTTTCTA	105249
Query	62	AGTTAATGCAAACTGAGTTTGAAATGAGCATGATGGGAGAGCTAAAATTCTTCCTTGGA	121
Sbjct	105248	CTCTCATGCAAAAGTGAATTTGAAATGAGTATGATGGGAGAACTGAAATCTTCTTAGGAC	105189

Query 297 AATGATTGGATCACTGCTCTATCTTAATGCTTCTAGGCCCTATATAATTTTGTGTTTT 356
 Sbjct 102209 CATGATAGGATCATTATTGTATTTAACTGCTAGCAGACCTGACATAGTGTTCGAGTAGG 102150

Query 357 ATTATGTGCAAGATTCCAAAAGGAACCAAGGGAAGTTTCATTTAACTGCAGTTAAACCTAT 416
 Sbjct 102149 TTTGTGTGCTAGATTTCAAACCTGTGCAAAAGAAATCTCATTTAACTGCAGTTAAAGGAT 102090

Query 417 ATTCTAATATTTAATTAGAAGCTCATAACCTTGGTCTTATGCTTAAGAGAA-GAGATAGTT 475
 Sbjct 102089 TTTTAGATATCTAGTAGGTACTACTGATCTTGGCCTT-TGGTATAGAAAAGGTTCTAGTT 102031

Query 476 TCAGACTCATG-AGC-TATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAGAAAAAG 533
 Sbjct 102030 T-TGA-TCTGTAGCTTATTGTGATGCTGATTATGCTGGAGACAAAGTTGAGAGGAAGAG 101973

Query 534 TACAAGTGGAAGTTGTCACTT 554
 Sbjct 101972 TACAAGTGGCACCTGTCAATT 101952

>gi|257900566|gb|AC134823.43| Medicago truncatula chromosome 6 clone mth2-20d18, complete sequence
 Length=119033

Score = 197 bits (218), Expect = 3e-46
 Identities = 385/560 (68%), Gaps = 18/560 (3%)
 Strand=Plus/Minus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATG--AAGATTTTCTA 61
 Sbjct 79784 TATGTTGATGATATAATATTTGGTTCTACTAATGCAT--CTCTTGCAAAGAATTTTCTA 79727

Query 62 AGTTAATGCAAACTGAGTTTGAATGAGCATGATGGGAGAGCTAAAATCTTCTTGGAC 121
 Sbjct 79726 AGTTAATGCAGGATGAATTTGAATGAGTATGATGGGAGAATTGAAATCTTCTTGGAA 79667

Query 122 TGCAAAATAAGCAAAACACCCCAAGGCATTACATTCATCAGACCAAGTATGTGAAAAATT 181
 Sbjct 79666 TTCAAATCAACCAAGTAAAGAAGGAGTATATGTTTCATCAAAACAAATAT---ACAAAGG 79610

Query 182 AG---TTGAAGAAGTTCAACATAAGTGATGAAAAGAGATGAAGACTTTTATGCATCCCA 238
 Sbjct 79609 AGCTTCTGAAGAAGTTCAAGCTAGAAGATTGTAAGTGATGAACACTCCAATGCATCCAA 79550

Query 239 C-TACACATCTTGGACTG--GATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAG 295
 Sbjct 79549 CTTGCACCTTAAGCAAGAAGATACTGGAAACAGT---AGTAGACCAGAAGCTATACAGAG 79493

Query 296 CAATGATTGGATCACTGCTCTATCTTAATGCTTCTAGGCCCTATATAATTTTGTGTTT 355
 Sbjct 79492 GTATGATTGGTTCTCTGTATACCTCACTGCATCTAGACCTGATATTTTATTCAGTGTAT 79433

Query 356 TATTATGTGCAAGATTCCAAAAGGAACCAAGGGAAGTTTCATTTAACTGCAGTTAAACCTA 415
 Sbjct 79432 GCTTGTGTGCAAGATTTCATCAGATCCTAGAGAATCTCATTTAACTGCAGTTAAGAGAA 79373

Query 416 TATTCTAATATTTAATTAGAAGCTCATAACCTTGGTCTTATGCTTAAGAGAAGAGATAG-T 474
 Sbjct 79372 TCTTCAGGTATCTGAAAGGAACAACTAATCTTGGACTCCTGTATAGGA-AATCCCTAGAT 79314

Query 475 TTCAGACTCATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAGAAAAAGT 534
 Sbjct 79313 TATAAGTTGATTGGATTCTGTGATGCTGATTATGCTGGTGATAGGATTGAAAGAAAAATCA 79254

Query 535 ACAAGTGGGAAGTTGTCACTT 554
 Sbjct 79253 ACCAGTGGAAATTGTCAATT 79234

>gi|212290237|gb|AC225483.5| Medicago truncatula clone mth2-25o13, complete sequence
 Length=116665

Score = 197 bits (218), Expect = 3e-46
 Identities = 385/560 (68%), Gaps = 18/560 (3%)
 Strand=Plus/Minus

Query 4 TATGTGGATGATATCATTTTTGGTGCTACTAATGAAATGCTCTATG--AAGATTTTCTA 61
 Sbjct 60766 TATGTTGATGATATAATATTTGGTTCTACTAATGCAT--CTCTTGCAAAGAATTTTCTA 60709

Query 62 AGTTAATGCAAACTGAGTTTGAATGAGCATGATGGGAGAGCTAAAATCTTCTTGGAC 121
 Sbjct 60708 AGTTAATGCAGGATGAATTTGAATGAGTATGATGGGAGAATTGAAATCTTCTTGGAA 60649

Query 122 TGCAAAATAAGCAAAACACCCCAAGGCATTACATTCATCAGACCAAGTATGTGAAAAATT 181
 Sbjct 60648 TTCAAATCAACCAAGTAAAGAAGGAGTATATGTTTCATCAACAAATAT---ACAAAGG 60592

Query 182 AG---TTGAAGAAGTTCAACATAAGTGATGAAAAGAGATGAAGACTTTTATGCATCCCA 238
 Sbjct 60591 AGCTTCTGAAGAAGTTCAAGCTAGAAGATTGTAAAGTGATGAACACTCCAATGCATCCAA 60532

Query 239 C-TACACATCTTGGACTG--GATGAGGAATCAATGAAGGTGGACGTGACTCAATACAAAG 295
 Sbjct 60531 CTTGCACCTTAAGCAAGAAGATACTGGAACAGT---AGTAGACCAGAAGCTATACAGAG 60475

Query 296 CAATGATTGGATCACTGCTCTATCTTAATGCTTCTAGGCCCTATATAATTTTGTGTTT 355
 Sbjct 60474 GTATGATTGGTTCTCTGTATACCTCACTGCATCTAGACCTGATATTTTATTCAGTGTAT 60415

Query 356 TATTATGTGCAAGATTCCAAAAGGAACCAAGGGAAGTTTCATTTAACTGCAGTTAAACCTA 415
 Sbjct 60414 GCTTGTGTGCAAGATTTCATCAGATCCTAGAGAATCTCATTTAACTGCAGTTAAGAGAA 60355

Query 416 TATTCTAATATTTAATTAGAAGCTCATAACCTTGGTCTTATGCTTAAGAGAAGAGATAG-T 474
 Sbjct 60354 TCTTCAGGTATCTGAAAGGAACAACTAATCTTGGACTCCTGTATAGGA-AATCCCTAGAT 60296

Query 475 TTCAGACTCATGAGCTATTGAGATGTGGACTATGTTGGTGATAAAGTCGAAAGAAAAAGT 534
 Sbjct 60295 TATAAGTTGATTGGATTCTGTGATGCTGATTATGCTGGTGATAGGATTGAAAGAAAAATCA 60236

Query 535 ACAAGTGGGAAGTTGTCACTT 554
 Sbjct 60235 ACCAGTGGAAATTGTCAATT 60216

>gi|62909806|emb|CR932957.2| Medicago truncatula chromosome 5 clone mth2-58c3, COMPLETE SEQUENCE
 Length=136080

Reference:

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
10,272,453 sequences; 3,505,279,183 total letters

Query= OmniSoy_seq
Length=3635

	Score (Bits)	E Value
Sequences producing significant alignments:		
gi 124359710 gb ABN06064.1 RNA-directed DNA polymerase (Reverse...	266	0.0
gi 208609065 dbj BAG72154.1 hypothetical protein [Lotus japonicus]	271	9e-
gi 208609057 dbj BAG72151.1 hypothetical protein [Lotus japonicus]	271	9e-
gi 208609055 dbj BAG72150.1 hypothetical protein [Lotus japonicus]	271	9e-
gi 208609060 dbj BAG72152.1 hypothetical protein [Lotus japonicus]	271	9e-
gi 208609051 dbj BAG72148.1 hypothetical protein [Lotus japonic...	271	1e-
gi 208609049 dbj BAG72147.1 hypothetical protein [Lotus japonic...	267	6e-
gi 170660047 gb ACB28472.1 polyprotein [Ananas comosus]	266	6e-
gi 225465489 ref XP_002271052.1 PREDICTED: hypothetical protein...	256	1e-
gi 225462616 ref XP_002263623.1 PREDICTED: hypothetical protein...	251	1e-
gi 227438239 gb ACP30609.1 disease resistance protein [Brassica...	255	7e-
gi 225443027 ref XP_002267560.1 PREDICTED: hypothetical protein...	248	6e-
gi 89887334 gb ABD78322.1 polyprotein [Primula vulgaris]	255	3e-
gi 147854459 emb CAN78588.1 hypothetical protein [Vitis vinifera]	256	9e-
gi 225455084 ref XP_002267679.1 PREDICTED: hypothetical protein...	252	8e-
gi 116309032 emb CAH66146.1 OSIGBa0114M03.4 [Oryza sativa (indi...	253	1e-
gi 225443419 ref XP_002267647.1 PREDICTED: hypothetical protein...	246	2e-
gi 225463073 ref XP_002269644.1 PREDICTED: hypothetical protein...	250	5e-
gi 15451607 gb AAK98731.1 AC090485_10 Putative retroelement [Ory...	244	3e-
gi 27764548 gb AAO23078.1 polyprotein [Glycine max]	246	6e-
gi 242070717 ref XP_002450635.1 hypothetical protein SORBIDRAFT...	251	5e-
gi 242095940 ref XP_002438460.1 hypothetical protein SORBIDRAFT...	243	1e-

gi 242065034 ref XP_002453806.1 hypothetical protein SORBIDRAFT...	243	2e-
gi 225432842 ref XP_002279912.1 PREDICTED: similar to polyprote...	259	7e-
gi 115457692 ref NP_001052446.1 Os04g0316700 [Oryza sativa (jap...	250	2e-
gi 32492359 emb CAE05990.1 OSJNBa0004L19.22 [Oryza sativa (japo...	250	2e-
gi 115438795 ref NP_001043677.1 Os01g0640000 [Oryza sativa (jap...	241	2e-
gi 115481476 ref NP_001064331.1 Os10g0317000 [Oryza sativa (jap...	232	1e-
gi 115462807 ref NP_001055003.1 Os05g0241900 [Oryza sativa (jap...	253	2e-
gi 115457202 ref NP_001052201.1 Os04g0191000 [Oryza sativa (jap...	236	4e-
gi 147772855 emb CAN73669.1 hypothetical protein [Vitis vinifera]	247	4e-
gi 115468162 ref NP_001057680.1 Os06g0493000 [Oryza sativa (jap...	235	1e-
gi 147852240 emb CAN80132.1 hypothetical protein [Vitis vinifera]	252	2e-
gi 147837833 emb CAN62821.1 hypothetical protein [Vitis vinifera]	249	3e-
gi 18568267 gb AAL75999.1 AF466646_7 putative polyprotein [Zea m...	254	1e-
gi 242093834 ref XP_002437407.1 hypothetical protein SORBIDRAFT...	246	1e-
gi 38346992 emb CAD40278.2 OSJNBb0062H02.17 [Oryza sativa (japo...	248	2e-
gi 242085372 ref XP_002443111.1 hypothetical protein SORBIDRAFT...	249	3e-
gi 62733109 gb AAK95226.1 retrotransposon protein, putative, un...	243	6e-
gi 108864085 gb ABA91843.2 retrotransposon protein, putative, u...	243	6e-
gi 10140673 gb AAG13508.1 AC068924_13 putative gag-pol polyprote...	231	8e-
gi 115486613 ref NP_001068450.1 Os11g0677100 [Oryza sativa (jap...	229	2e-
gi 242085414 ref XP_002443132.1 hypothetical protein SORBIDRAFT...	223	2e-
gi 116309424 emb CAH66499.1 H0321H01.8 [Oryza sativa (indica cu...	225	6e-
gi 78183243 emb CAJ00274.1 hypothetical protein [Lotus japonicus]	232	2e-
gi 77555174 gb ABA97970.1 retrotransposon protein, putative, un...	222	3e-
gi 78183241 emb CAJ00278.1 hypothetical protein [Lotus japonicus]	232	3e-
gi 115482042 ref NP_001064614.1 Os10g0419000 [Oryza sativa (jap...	238	1e-
gi 77554308 gb ABA97104.1 retrotransposon protein, putative, un...	236	4e-
gi 147775005 emb CAN70471.1 hypothetical protein [Vitis vinifera]	246	7e-
gi 78708062 gb ABB47037.1 retrotransposon protein, putative, un...	231	1e-
gi 18958673 gb AAL82656.1 AC092387_4 retrotransposon protein, pu...	231	1e-
gi 77552522 gb ABA95319.1 retrotransposon protein, putative, un...	233	1e-

gi 78183249 emb CAJ00277.1	hypothetical protein [Lotus japonicus]	230	1e-	gi 32483242 emb CAE02543.1	OSJNBb0069N01.1 [Oryza sativa (japon...	184	1e-
130				102			
gi 12322008 gb AAG51046.1 AC069473_8	gypsy/Ty-3 retroelement pol...	228	2e-	gi 253761750 ref XP_002489250.1	hypothetical protein SORBIDRAFT...	236	2e-
129				102			
gi 15451608 gb AAK98732.1 AC090485_11	Putative retroelement [Ory...	231	6e-	gi 115474951 ref NP_001061072.1	Os08g0164800 [Oryza sativa (jap...	251	2e-
129				101			
gi 108706171 gb ABF93966.1	retrotransposon protein, putative, u...	231	6e-	gi 22296822 gb AAM94350.1	gag-pol polyprotein [Zea mays]	187	1e-
129				100			
gi 14165316 gb AAK55448.1 AC069300_3	putative polyprotein [Oryza...	239	1e-	gi 13992688 gb AAK51582.1 AC022352_18	Putative retroelement [Ory...	187	5e-
128				100			
gi 242033109 ref XP_002463949.1	hypothetical protein SORBIDRAFT...	193	2e-	gi 108864644 gb ABA95339.2	retrotransposon protein, putative, u...	229	8e-
128				100			
gi 18568269 gb AAL76001.1 AF466646_9	putative gag-pol polyprotei...	227	4e-	gi 147816473 emb CAN64046.1	hypothetical protein [Vitis vinifera]	236	3e-99
128				gi 15340827 gb AAK94516.1	gag-pol polyprotein [Hordeum vulgare]	186	7e-99
gi 90399077 emb CAJ86299.1	H0124B04.16 [Oryza sativa (indica cu...	235	5e-	gi 115392332 gb ABI96971.1	putative gag-pol polyprotein [Tritic...	185	7e-99
128				gi 15340828 gb AAK94517.1	gag-pol polyprotein [Hordeum vulgare]	186	1e-98
gi 77557165 gb ABA99961.1	retrotransposon protein, putative, un...	205	3e-	gi 15187182 gb AAK91332.1 AC090441_14	Putative gag-pol polyprote...	183	3e-98
126				gi 34015213 gb AAQ56407.1	putative gag-pol polyprotein [Oryza s...	182	4e-98
gi 255677065 dbj BAF19594.2	Os06g0493000 [Oryza sativa Japonica...	190	4e-	gi 8778340 gb AAF79348.1 AC007887_7	F1504.13 [Arabidopsis thaliana]	190	6e-98
124				gi 34015141 gb AAQ56338.1	putative gag-pol polyprotein [Oryza s...	183	1e-97
gi 12322948 gb AAG51464.1 AC069160_10	gypsy/Ty3 element polyprot...	213	8e-	gi 34015193 gb AAQ56388.1	putative gag-pol polyprotein [Oryza s...	181	1e-97
123				gi 62733754 gb AAX95863.1	retrotransposon protein, putative, un...	213	5e-97
gi 108707050 gb ABF94845.1	retrotransposon protein, putative, u...	210	3e-				
121							
gi 77551464 gb ABA94261.1	retrotransposon protein, putative, un...	227	1e-	>gi 124359710 gb ABN06064.1	RNA-directed DNA polymerase (Reverse transcriptase);		
120				Chromo;			
gi 147810501 emb CAN60890.1	hypothetical protein [Vitis vinifera]	169	1e-	Zinc finger, CCHC-type; Peptidase aspartic, active site; Polynucleotidyl			
119				transferase, Ribonuclease H fold [Medicago truncatula]			
gi 242085390 ref XP_002443120.1	hypothetical protein SORBIDRAFT...	247	2e-	Length=1297			
118							
gi 242085388 ref XP_002443119.1	hypothetical protein SORBIDRAFT...	244	4e-	Score = 266 bits (680), Expect (3) = 0.0			
118				Identities = 138/239 (57%), Positives = 169/239 (70%), Gaps = 7/239 (2%)			
gi 115472395 ref NP_001059796.1	Os07g0518300 [Oryza sativa (jap...	211	1e-	Frame = +3			
116							
gi 110289541 gb AAP54937.2	retrotransposon protein, putative, u...	216	8e-	Query 1698	FSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRYPHLQKNEIKTLVVEML*LGIIRLSNSS	1877	
116					F P GLPP R+ +H I +K G NVRPYRYPH KNEI+ V EML GIIR S SS		
gi 18378613 gb AAL68644.1 AF458768_1	polyprotein [Oryza sativa J...	182	8e-	Sbjct 358	FQEP TGLPPKRKKEHVITLKEGEGAVNVRPYRYPHHKNEIEKQVREMIQAGIIRHSTSS	417	
114							
gi 147774273 emb CAN76793.1	hypothetical protein [Vitis vinifera]	414	5e-	Query 1878	YSSPVILVKRKDG+SRLCMDYQALSKATVPDKFLIPVMKELLDENGLPIHFSKIDLKARY	2057	
113					+SSPVILVK KD S R+C+DY+AL+KATVPDKF IPV++ELLDEL+G +SK+DLK+ Y		
gi 18378611 gb AAL68643.1 AF458767_1	polyprotein [Oryza sativa J...	235	1e-	Sbjct 418	FSSPVILVKEKDNSWRMCIDYRNLKATVPDKFPIPVIEELDELHGARYFSKLDLKSgy	477	
112							
gi 38346427 emb CAD40214.2	OSJNBa0019J05.12 [Oryza sativa (japo...	225	3e-	Query 2058	HQIR-----MHKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD	2222	
112					HQ+R +HK FRTH+ HYE VMPFGL N P+TFQ MN + LR++V+VFFDD		
gi 38605839 emb CAE02919.3	OSJNBb0108J11.11 [Oryza sativa (japo...	235	5e-	Sbjct 478	HQVRVKEEDIHKTAFRTHEDHYEYLVMPFGLMNPSTFQSLMNDVFRLLLRKFVLFVFFDD	537	
112							
gi 225443314 ref XP_002275129.1	PREDICTED: hypothetical protein...	410	6e-	Query 2223	ILVYSKSWEAHLHDLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMRP	2399	
112					ILVYS+ W+ H++H+ VL + H N KKKC FGQ LGH+ISKEGV + P		
gi 115470911 ref NP_001059054.1	Os07g0184000 [Oryza sativa (jap...	238	7e-	Sbjct 538	ILVYSQDWKTHMEHVEEVLRLIMQTHGLVAN--KKKCYFGQETVEYLGHLISKEGVAVD	594	
111							
gi 32489310 emb CAE03706.1	OSJNBa0060B20.14 [Oryza sativa (japo...	201	1e-				
107							
gi 57863925 gb AAS55774.2	putative polyprotein [Oryza sativa Ja...	178	1e-	Score = 264 bits (675), Expect (3) = 0.0			
105				Identities = 133/255 (52%), Positives = 182/255 (71%), Gaps = 3/255 (1%)			
gi 78183245 emb CAJ00275.1	hypothetical protein [Lotus japonicus]	232	3e-	Frame = +3			
105							
gi 6466937 gb AAF13073.1 AC011621_1	putative retroelement pol po...	256	4e-	Query 2880	QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKEL-QGISRPFWKDITKINEEVQKD	3056	
105					QQ W AKLLGY+F+I+YK G NK DALSR ED EL QGI+ WKD + EE+ +D		
gi 147843077 emb CAN83300.1	hypothetical protein [Vitis vinifera]	385	2e-	Sbjct 761	QQNWAAKLLGYDFEIIYKPKGLNKGDALSRVREDGELCQGITSVQWKDEKLLREELSRD	820	
104							
gi 115457464 ref NP_001052332.1	Os04g0262800 [Oryza sativa (jap...	174	3e-	Query 3057	PALAKIREELKDNLDSPQYTLECDILYFRGLVLLASSLWIPKLLQEFQTSLMGGHSGI	3236	
103					L KI +L+ + S P Y L+ +L + GRLV+ + S+ IP LL EF ++ GGHS		
				Sbjct 821	SQQLKIIGDLQRDASSRPGYMLKQGVLLYEGRLVSVSSKVMIPITLLAEFSTPQGGHSGF	880	

Query 3237 YITYRRITQSLYWIPIKGEITKFFVACHVGQRSKYQASSPAGLLQPLIPNAIWEEISMN 3416
 Y TYRR+ ++YW+ +K + ++V +C QR KY ASSP GLLQPLP+P+ IWE++SM+
 Sbjct 881 YRTYRRLLAANVYVWGMKNVTQVEYVRSCDTCQQRKYLASSPGGLLQPLPVPDRIWEDLSMD 940

Query 3417 FIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLVPIISIVSD 3590
 FI+G+ KSKG++ +LV VD+LSKY +FI++KHPY A+ I DV +E++ L +P+SIVSD
 Sbjct 941 FTMGLPKSKGYEAVLVVVDRLSKYSHFILLKHPYTAKVADVFIREVVRLHGFIPLSIVSD 1000

Query 3591 SDLIFMSHFLQELFK 3635
 D IFMS+F +ELFK
 Sbjct 1001 RDPFIFMSNFWKELFK 1015

Score = 179 bits (455), Expect (3) = 0.0
 Identities = 89/156 (57%), Positives = 114/156 (73%), Gaps = 0/156 (0%)
 Frame = +2

Query 2408 WPMPTKPTKTLRGFLELTGYIKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQLQAI 2587
 WP+PK K +RGFL LT YY++ I +YGKIA+PL +L K F WNE + A QL++ +
 Sbjct 603 WPIPKNVKGVRGFLGLTDYYRKFIKDYGKIAKPLTELTKDAFMWNEKTQDAFDQLKRRL 662

Query 2588 TTIPTLSMLDFSQFSIECDASGKIGVVLTDQRKQIAYFNKALKDLTSLKSMEYKESMA 2767
 TT P L++ DF+K+F IECNASG GIG +L QDRK +AY++KAL L+KS YEKE MA
 Sbjct 663 TTSPLVALPDFNKEFVIECDASGGGIGAILMQDRKPVAYYSKALGVRNLTAKSAYEKELMA 722

Query 2768 LVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 +VLAIQHWRPYL +F + DQKSL+ LL QR+ T
 Sbjct 723 VVLAIQHWRPYLLGRRFVVDQKSLKQLLQQRVVT 758

Score = 51.6 bits (122), Expect (3) = 7e-21
 Identities = 28/85 (32%), Positives = 48/85 (56%), Gaps = 2/85 (2%)
 Frame = +3

Query 1098 GDGLLADGVFSLFRRWANPASSMKLR*EL*GQEVIIIDNRASHNFIISNKLVLKGLSID 1277
 GDG + + F + S+KL + V++L+D+ A+HNFIS +LVHK+ ++
 Sbjct 159 GDGEMC--MMEFFHLGHSRPSIKLMGVIVEFVVVLVDGATHNFISQQLVHKMNWAVV 216

Query 1278 PTKPYMRLGDSNRKSTQGCCNKL 1352
 T ++LGD + T+G C+ L+
 Sbjct 217 DTPCMSIKLGDGYSYKTKGTCEGLE 241

Score = 50.4 bits (119), Expect (3) = 7e-21
 Identities = 29/110 (26%), Positives = 53/110 (48%), Gaps = 1/110 (0%)
 Frame = +1

Query 736 QGSNEAIS*VGEFSGTNNATPTGGTONLQGESRMSSTSSISKPRFSRP+NKGSQTILYV 915
 QGSN S N GG++ + + K + S P ++ + Y
 Sbjct 44 QGSNRGNSTDWVMVKNGKEHGSAGGSKGTGFGPKGEKQAQYDKKK-SGPRDRSFTHLSYN 102

Query 916 EYVK*RDSGCCYHCGLAFGRHRCPEKNMRVVILAKDE*INEDGEIIGLK 1065
 E ++ + G C+ CG F P H+CP+K +RV++L +DE +G+++ ++
 Sbjct 103 ELMERKQKGLCFKCGGPFHPMHQCPDKQLRVLVLEDEEGEPEGKLLAVE 152

Score = 46.6 bits (109), Expect (3) = 7e-21
 Identities = 20/43 (46%), Positives = 30/43 (69%), Gaps = 0/43 (0%)
 Frame = +2

Query 1391 LFKLGGVDLIIGVA*LETIGEIKVNWRTLSMSFVHQDQNMVIK 1519

Sbjct 255 LFDLGGVDMVLGIEWLRTLGLDMIVNWNKQTMFSFWHNKKWVTVK 297

>gi|208609065|dbj|BAG72154.1| hypothetical protein [Lotus japonicus]
 Length=1558

Score = 271 bits (694), Expect (3) = 9e-170
 Identities = 141/239 (58%), Positives = 171/239 (71%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRYPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F PKGLPP R DH I ++ GA N+RPYRYP QKNEI+ LV EML GIIR S S
 Sbjct 601 FQEPKGLPPRRRTTDHAIQLQEGASIPNIRPYRYPFYQKNEIEKLVKEMLSNGIIRHSTSP 660

Query 1878 YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELDELNGPIHFSKIDLKARY 2057
 +SSP ILVK+KDG R C+DY+AL+KAT+PDKF IP++ ELLDE+ + FSK+DLK+ Y
 Sbjct 661 FSSPAILVKKKDGGRFCVDYRALNKATIPDKFPIPIIDELLDEIGAAVVFSKLDLKSgy 720

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLLRYVVVFDD 2222
 HQIRM K FRTH+GHYE V+PFGLTN P+TFQ MN L+P+LR++V+VFFDD
 Sbjct 721 HQIRMKEEDIPKTAFRTHGHEHYELVLPFGLTNAPSTFQALMNQVLRPYLRKFVLFVFFDD 780

Query 2223 ILVYSKSWEAHLHLS*VLARLLEHYFFTNVFKKCSFGQIKACGLGHVISKEGVLMRP 2399
 IL+YSK+ E H DHL VL L E+ N +KKCSFGQ+ LGHVIS+ GV P
 Sbjct 781 ILIYSKNEELHKDHLRIVLQVLKENNLVAN--QKKCSFGQPEI IYLGHVISQAGVAADP 837

Score = 207 bits (526), Expect (3) = 9e-170
 Identities = 110/254 (43%), Positives = 159/254 (62%), Gaps = 5/254 (1%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDEKELQGISRPFWKDITKINEEVQKDP 3059
 QQ W++KL+GY+F+I YK G NK DALSR+ + + + W D+ E+ +D
 Sbjct 1004 QQKWSKLMGYDFEIKYKPGIENKAADALSRLKQFSAISSVQCAEWADL---EAEILEDE 1060

Query 3060 ALAKIREELKDNLDSDHPQYTLECDILYFRGRVLASSLWIPKLLQEQFQTSMLGGHSGIY 3239
 K+ +EL +S Y L+ L ++ R+VL S I +L+EF + +GGH+GI+
 Sbjct 1061 RYRKVLQELATQGSNAVGYQLKRGRLLYKDRIVLPKGSTKILTVLKEFHDTALGGHAGIF 1120

Query 3240 IITYRRITQSLYWIPIKGEITKFFVACHVGQRSKYQASSPAGLLQPLIPNAIWEEISMNF 3419
 TY+RI+ YW +K +I +V C V QR+KY+A +PAG LQPLPIP+ W +ISM+F
 Sbjct 1121 RTYKRISALFYWEGMKLDIQNYVQKCEVCQRNKYEALNPAGFLQPLP IPSQGWTDISMDF 1180

Query 3420 IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLVPIISIVSDS 3593
 I G+ K+ G D ILV VD+ +KY +FI + HPY A+ I +V KE++ L P SIVSD
 Sbjct 1181 IGGLPKAMGKDTILVVVDREFTKYAHFIALSHPYNAKEIAEVFIKEVVRLHGFPSTIVSDR 1240

Query 3594 DLIFMSHFLQELFK 3635
 D +F+S F E+FK
 Sbjct 1241 DRVFLSTFWSEMFK 1254

Score = 169 bits (427), Expect (3) = 9e-170
 Identities = 82/157 (52%), Positives = 113/157 (71%), Gaps = 0/157 (0%)
 Frame = +2

Query 2399 IL*WPMPTKPTKTLRGFLELTGYIKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQLQ 2578
 +L WP+PK K LRGL LTGY+R + NY K+A+PL LLK +F+W E + +A ++L+
 Sbjct 843 MLDWPIPKEVKGLRGLGLTGYRRFVKNYSKLAQPLNQLLKNNSFQWTEGATQAFVKLK 902

Query 2579 QAITTIPTLSMLDFSQFSIECDASGKIGVVLTDQRKQIAYFNKALKDLTSLKSMEYE 2758

+ +TT+P L +F K F +E DASGKG+G VL Q+ + +AY +K L D +KS+YE+E
 Sbjct 903 EVMTTVPVLPVPNFDKPFIFLETASGKGLGAVLMDQEGRPVAYMSKTLSDRAQAKSVYERE 962
 Query 2759 SMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
 MA+VLA+Q WR YL KF I+ DQ+SLR+L DQRI
 Sbjct 963 LMAVVLAVQKWRHYLLGSKFVIHTDQSRSLRFLADQRI 999

>gi|208609057|dbj|BAG72151.1| hypothetical protein [Lotus japonicus]
 Length=1558

Score = 271 bits (694), Expect(3) = 9e-170
 Identities = 141/239 (58%), Positives = 171/239 (71%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F PKGLPP R DH I ++ GA N+RPYRYP QKNEI+ LV EML GIIR S S
 Sbjct 601 FQEPKGLPPRRRTTDHAIQLQEGASIPNIRPYRYPFYQKNEIEKLVKEMLNSGIIRHSTSP 660
 Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSP ILVK+KDG R C+DY+AL+KAT+PDKF IP++ ELLDE+ + FSK+DLK+ Y
 Sbjct 661 FSSPAILVKKKDGGRFCVDYRALNKATIPDKFPIPIIDELLDEIGA AVVFSKLDLKS GY 720
 Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQIRM K FRTH+GHYE V+PFGLTN P+TFQ MN L+P+LR++V+VVFDD
 Sbjct 721 HQIRMKEEDIPKTAFRTHEGHYEYLVLPFGLTNAPSTFQALMNQVLRPYLRKFVLVVFDD 780
 Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP 2399
 IL+YSK+ E H DHL VL L E+ N +KKCSFGQ + LGHVIS+ GV P
 Sbjct 781 ILIYSKNEELHKDHLRIVLQVLKENNLVAN--QKKCSFGQPEI IYLGHVISQAGVAADP 837

Score = 207 bits (526), Expect(3) = 9e-170
 Identities = 110/254 (43%), Positives = 159/254 (62%), Gaps = 5/254 (1%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKIDITKINEEVQKDP 3059
 QQ W++KL+GY+F+I YK G NK DALSR+ + + W D+ E+ +D
 Sbjct 1004 QQKWSKMLMGYDFEIKYKPGIENKAADALSRKLQFSAISSVQCAEWADL---EAEILEDE 1060
 Query 3060 ALAKIREELKDNLDSPQYTLCDILYFRGRLVLLASSLWIPKLLQEFQTSMLGGHSGIY 3239
 K+ +EL +S Y L+ L ++ R+VL S I +L+EF + +GGH+GI+
 Sbjct 1061 RYRKVLQELATQGNSAVGYQLKRGRLLYKDRIVLPKGSTKILT VLKEFHDTALGGHAGIF 1120
 Query 3240 ITYRRITQSLYWIPIKGEITKFVVACHVGQRSKYQASSPAGLLQPLPIPNAIWEEISMNF 3419
 TY+RI+ YW +K +I +V C V QR+KY+A +PAG LQPLPIP+ W +ISM+F
 Sbjct 1121 RTYKRISALFYWEGMKLDIQNYVQKCEVCQRNKYEALNPAGFLQPLP IPSQGWTDISMDF 1180
 Query 3420 IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLEVPISIVSDS 3593
 I G+ K+ G D ILV VD+ +KY +FI + HPY A+ I +V KE++ L P SIVSD
 Sbjct 1181 IGGLPKTMGKDTILVVDRFTKYAHFIALSHPNYAKEIAEVFIKEVVRLHGFPTSIVSDR 1240
 Query 3594 DLIFMSHFLQELFK 3635
 D +F+S F E+FK
 Sbjct 1241 DRVFLSTFWSEMFK 1254

Score = 169 bits (427), Expect(3) = 9e-170
 Identities = 82/157 (52%), Positives = 113/157 (71%), Gaps = 0/157 (0%)
 Frame = +2

Query 2399 IL*WPMKTPKTLRGFLELTGYKKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQLQ 2578

+L WP+PK K LRGLF LTGY+R + NY K+A+PL LLK +F+W E + +A ++L+
 Sbjct 843 MLDWPIPKVEVKLRGLFGLTGYYRRFVKNYSKLAQPLNQLLKKNSQWTEGATQAFVKLK 902
 Query 2579 QAITTIPTLSMLDFSQFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMEYE 2758
 + +TT+P L +F K F +E DASGKG+G VL Q+ + +AY +K L D +KS+YE+E
 Sbjct 903 EVMTTVPVLPVPNFDKPFIFLETASGKGLGAVLMDQEGRPVAYMSKTLSDRAQAKSVYERE 962

Query 2759 SMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
 MA+VLA+Q WR YL KF I+ DQ+SLR+L DQRI
 Sbjct 963 LMAVVLAVQKWRHYLLGSKFVIHTDQSRSLRFLADQRI 999

>gi|208609055|dbj|BAG72150.1| hypothetical protein [Lotus japonicus]
 Length=1558

Score = 271 bits (694), Expect(3) = 9e-170
 Identities = 141/239 (58%), Positives = 171/239 (71%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F PKGLPP R DH I ++ GA N+RPYRYP QKNEI+ LV EML GIIR S S
 Sbjct 601 FQEPKGLPPRRRTTDHAIQLQEGASIPNIRPYRYPFYQKNEIEKLVKEMLNSGIIRHSTSP 660
 Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSP ILVK+KDG R C+DY+AL+KAT+PDKF IP++ ELLDE+ + FSK+DLK+ Y
 Sbjct 661 FSSPAILVKKKDGGRFCVDYRALNKATIPDKFPIPIIDELLDEIGA AVVFSKLDLKS GY 720
 Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQIRM K FRTH+GHYE V+PFGLTN P+TFQ MN L+P+LR++V+VVFDD
 Sbjct 721 HQIRMKEEDIPKTAFRTHEGHYEYLVLPFGLTNAPSTFQALMNQVLRPYLRKFVLVVFDD 780
 Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP 2399
 IL+YSK+ E H DHL VL L E+ N +KKCSFGQ + LGHVIS+ GV P
 Sbjct 781 ILIYSKNEELHKDHLRIVLQVLKENNLVAN--QKKCSFGQPEI IYLGHVISQAGVAADP 837

Score = 207 bits (526), Expect(3) = 9e-170
 Identities = 110/254 (43%), Positives = 159/254 (62%), Gaps = 5/254 (1%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKIDITKINEEVQKDP 3059
 QQ W++KL+GY+F+I YK G NK DALSR+ + + W D+ E+ +D
 Sbjct 1004 QQKWSKMLMGYDFEIKYKPGIENKAADALSRKLQFSAISSVQCAEWADL---EAEILEDE 1060
 Query 3060 ALAKIREELKDNLDSPQYTLCDILYFRGRLVLLASSLWIPKLLQEFQTSMLGGHSGIY 3239
 K+ +EL +S Y L+ L ++ R+VL S I +L+EF + +GGH+GI+
 Sbjct 1061 RYRKVLQELATQGNSAVGYQLKRGRLLYKDRIVLPKGSTKILT VLKEFHDTALGGHAGIF 1120
 Query 3240 ITYRRITQSLYWIPIKGEITKFVVACHVGQRSKYQASSPAGLLQPLPIPNAIWEEISMNF 3419
 TY+RI+ YW +K +I +V C V QR+KY+A +PAG LQPLPIP+ W +ISM+F
 Sbjct 1121 RTYKRISALFYWEGMKLDIQNYVQKCEVCQRNKYEALNPAGFLQPLP IPSQGWTDISMDF 1180
 Query 3420 IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLEVPISIVSDS 3593
 I G+ K+ G D ILV VD+ +KY +FI + HPY A+ I +V KE++ L P SIVSD
 Sbjct 1181 IGGLPKAMGKDTILVVDRFTKYAHFIALSHPNYAKEIAEVFIKEVVRLHGFPTSIVSDR 1240

Query 3594 DLIFMSHFLQELFK 3635
 D +F+S F E+FK
 Sbjct 1241 DRVFLSTFWSEMFK 1254

Score = 169 bits (427), Expect(3) = 9e-170

Identities = 82/157 (52%), Positives = 113/157 (71%), Gaps = 0/157 (0%)
 Frame = +2

Query	2399	IL*WMPKPTPKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQLQ	2578
Sbjct	843	+L WP+PK K LRGL LTGY+R + NY K+A+PL LLK +F+W E + +A ++L+ MLDWP+PKVKGRLRGFLGTGYRRFVKNYSKLAQPLNQLLKNNSFQWTEGATQAFVKLK	902

Query	2579	QAITTIPTLSMLDFSQKQFSIECDASGKGIGVVLTQDRKQIAYFNKALKDLTSLKSMYEKE	2758
Sbjct	903	+ +TT+P L +F K F +E DASGKG+G VL Q+ + +AY +K L D +KS+YE+E EVMTTVPVLPVPNFDKPFILETDASGKGLGAVLMQEGRPVAYMSKTLSDRAQAKSVYERE	962

Query	2759	SMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI	2869
Sbjct	963	MA+VLA+Q WR YL KF I+ DQ+SLR+L DQRI LMAVVLAVQKWRHYLLGSKFVIHTDQSRSLRFLADQRI	999

>gi|208609060|dbj|BAG72152.1| hypothetical protein [Lotus japonicus]
 Length=1369

Score = 271 bits (694), Expect (3) = 9e-170
 Identities = 141/239 (58%), Positives = 171/239 (71%), Gaps = 7/239 (2%)
 Frame = +3

Query	1698	FSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS	1877
Sbjct	412	F PKGLPP R DH I ++ GA N+RPYRYP QKNEI+ LV EML GIIR S S FQEPKGLPPRRTTDHAIQLQEGASIPNIRPYRYPFYQKNEIEKLVKEMLNSGIIRHSTSP	471

Query	1878	YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY	2057
Sbjct	472	+SSP ILVK+KDG R C+DY+AL+KAT+PDKF IP++ ELLDE+ + FSK+DLK+ Y FSSPAILVKKKDGGRFCVDYRALNKATIPDKFPIPIIDELLDEIGA AVVFSKLDLKS GY	531

Query	2058	HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLLRRYVVVFDD	2222
Sbjct	532	HQIRM K FRTH+GHYE V+PFGLTN P+TFQ MN L+P+LR++V+VFFDD HQIRMKEEDIPKTAFTHEGHYEYLVLPFGLTNAPSTFQALMNQVLRPYLRKFVLVFFDD	591

Query	2223	ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP	2399
Sbjct	592	IL+YSK+ E H DHL VL L E+ N +KKCSFGQ + LGHVIS+ GV P ILIYSKNEELHKDHLRIVLQVLKENNLVAN--QKKCSFGQPEIYILGHVISQAGVAADP	648

Score = 207 bits (526), Expect (3) = 9e-170
 Identities = 110/254 (43%), Positives = 159/254 (62%), Gaps = 5/254 (1%)
 Frame = +3

Query	2880	QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKDITKINEEVQKDP	3059
Sbjct	815	QQ W++KL+GY+F+I YK G NK DALSR+ + + + W D+ E+ +D QQKWSKLMGYDFEIKYKPGIENKAADALSRKLQFSAISSVQCAEWADL---EAEILEDE	871

Query	3060	ALAKIREELKDNLDSPQYTLCECDILYFRGLVLLASSLWIPKLLQEFQTSLMGGHSGIY	3239
Sbjct	872	K+ +EL +S Y L+ L ++ R+VL S I +L+EF + +GGH+GI+ RYRKVLQELATQGN SAVGYQLKRGRLLYKDRIVLPKGSTKILT VLKEFHDTALGGHAGIF	931

Query	3240	ITYRRITQSLYWIPIKGEITKFFVACHVGQRSKYQASSPAGLLQPLPIPNAIWEEISMNF	3419
Sbjct	932	TY+RI+ YW +K +I +V C V QR+KY+A +PAG LQPLPIP+ W +ISM+F RTYKRISALFYWEGMKLDIQNVYQKCEVCQRNKYEALNPAGFLQPLPIP SQGWTDISMDF	991

Query	3420	IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLEVPISIVSDS	3593
Sbjct	992	I G+ K+ G D ILV VD+ +KY +FI + HPY A+ I +V KE++ L P SIVSD IGGLPKAMGKDTILVVVDRTKYAHFIALSHPYNAKEIAEVFIKEVVRLHGFP TSIVSDR	1051

Query	3594	DLIFMSHFLQELFK	3635
		D +F+S F E+FK	

Sbjct 1052 DRVFLSTFWSEMFK 1065

Score = 169 bits (427), Expect (3) = 9e-170
 Identities = 82/157 (52%), Positives = 113/157 (71%), Gaps = 0/157 (0%)
 Frame = +2

Query	2399	IL*WMPKPTPKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQLQ	2578
Sbjct	654	+L WP+PK K LRGL LTGY+R + NY K+A+PL LLK +F+W E + +A ++L+ MLDWP+PKVKGRLRGFLGTGYRRFVKNYSKLAQPLNQLLKNNSFQWTEGATQAFVKLK	713

Query	2579	QAITTIPTLSMLDFSQKQFSIECDASGKGIGVVLTQDRKQIAYFNKALKDLTSLKSMYEKE	2758
Sbjct	714	+ +TT+P L +F K F +E DASGKG+G VL Q+ + +AY +K L D +KS+YE+E EVMTTVPVLPVPNFDKPFILETDASGKGLGAVLMQEGRPVAYMSKTLSDRAQAKSVYERE	773

Query	2759	SMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI	2869
Sbjct	774	MA+VLA+Q WR YL KF I+ DQ+SLR+L DQRI LMAVVLAVQKWRHYLLGSKFVIHTDQSRSLRFLADQRI	810

>gi|208609051|dbj|BAG72148.1| hypothetical protein [Lotus japonicus]
 gi|208609062|dbj|BAG72153.1| hypothetical protein [Lotus japonicus]
 Length=1558

Score = 271 bits (694), Expect (3) = 1e-169
 Identities = 141/239 (58%), Positives = 171/239 (71%), Gaps = 7/239 (2%)
 Frame = +3

Query	1698	FSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS	1877
Sbjct	601	F PKGLPP R DH I ++ GA N+RPYRYP QKNEI+ LV EML GIIR S S FQEPKGLPPRRTTDHAIQLQEGASIPNIRPYRYPFYQKNEIEKLVKEMLNSGIIRHSTSP	660

Query	1878	YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY	2057
Sbjct	661	+SSP ILVK+KDG R C+DY+AL+KAT+PDKF IP++ ELLDE+ + FSK+DLK+ Y FSSPAILVKKKDGGRFCVDYRALNKATIPDKFPIPIIDELLDEIGA AVVFSKLDLKS GY	720

Query	2058	HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLLRRYVVVFDD	2222
Sbjct	721	HQIRM K FRTH+GHYE V+PFGLTN P+TFQ MN L+P+LR++V+VFFDD HQIRMKEEDIPKTAFTHEGHYEYLVLPFGLTNAPSTFQALMNQVLRPYLRKFVLVFFDD	780

Query	2223	ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP	2399
Sbjct	781	IL+YSK+ E H DHL VL L E+ N +KKCSFGQ + LGHVIS+ GV P ILIYSKNEELHKDHLRIVLQVLKENNLVAN--QKKCSFGQPEIYILGHVISQAGVAADP	837

Score = 206 bits (525), Expect (3) = 1e-169
 Identities = 110/254 (43%), Positives = 159/254 (62%), Gaps = 5/254 (1%)
 Frame = +3

Query	2880	QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKDITKINEEVQKDP	3059
Sbjct	1004	QQ W++KL+GY+F+I YK G NK DALSR+ + + + W D+ E+ +D QQKWSKLMGYDFEIKYKPGIENKAADALSRKLQFSAISSVQCAEWADL---EAEILEDE	1060

Query	3060	ALAKIREELKDNLDSPQYTLCECDILYFRGLVLLASSLWIPKLLQEFQTSLMGGHSGIY	3239
Sbjct	1061	K+ +EL +S Y L+ L ++ R+VL S I +L+EF + +GGH+GI+ RYRKVLQELATQGN SAVGYQLKRGRLLYKDRIVLPKGSTKILT VLKEFHDTAIGGHAGIF	1120

Query	3240	ITYRRITQSLYWIPIKGEITKFFVACHVGQRSKYQASSPAGLLQPLPIPNAIWEEISMNF	3419
Sbjct	1121	TY+RI+ YW +K +I +V C V QR+KY+A +PAG LQPLPIP+ W +ISM+F RTYKRISALFYWEGMKLDIQNVYQKCEVCQRNKYEALNPAGFLQPLPIP SQGWTDISMDF	1180

Query	3420	IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLEVPISIVSDS	3593
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Sbjct 1181 I G+ K+ G D ILV VD+ +KY +FI + HPY A+ I +V KE++ L P SIVSD
IGGLPKAMGKDTILVVDRFTKYAHFIALSHYPNAKEIAEVFIKEVVRHLHGFTSIVSDR 1240

Query 3594 DLIFMSHFLQELFK 3635
D +F+S F E+FK

Sbjct 1241 DRVFLSTFWSEMFK 1254

Score = 169 bits (427), Expect(3) = 1e-169
Identities = 82/157 (52%), Positives = 113/157 (71%), Gaps = 0/157 (0%)
Frame = +2

Query 2399 IL*WPMKPTPKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQLQ 2578
+L WP+PK K LRGLF LTGY+R + NY K+A+PL LLK +F+W E + +A ++L+
Sbjct 843 MLDWPIPKKVKGLRGFLGLTGYRRFVKNYSKLAQPLNQLLKNNSFQWTEGATQAFVKLK 902

Query 2579 QAITTIPTLSMLDFSQFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMEYEKE 2758
+ +TT+P L +F K F +E DASGKG+G VL Q+ + +AY +K L D +KS+YE+E
Sbjct 903 EVMTTVPVLVPPNFDKPFIFLETASGKGLGAVLMQEGRPVAYMSKTLSDRAQAKSVYERE 962

Query 2759 SMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
MA+VLA+Q WR YL KF I+ DQ+SLR+L DQRI
Sbjct 963 LMAVVLAVQKWRHYLLGSKFVIHTDQSRSLRFLADQRI 999

>gi|208609049|dbj|BAG72147.1| hypothetical protein [Lotus japonicus]
gi|208609053|dbj|BAG72149.1| hypothetical protein [Lotus japonicus]
Length=1520

Score = 267 bits (683), Expect(3) = 6e-168
Identities = 139/239 (58%), Positives = 170/239 (71%), Gaps = 7/239 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
F PKGLPP R DH I ++ GA N+RPYRYP QKNEI+ LV EML GIIR S S
Sbjct 563 FQEPKGLPPRRTTDHAIQIQEGASIPNIRPYRYPFYQKNEIEKLVKEMLNIGIIRHSTSP 622

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
+SSP ILVK+KDG R C+DY+A++KAT+PDKF IP++ ELLDE+ + FSK+DLK+ Y
Sbjct 623 FSSPAILVKKKDGGRFCVDYRAINKATIPDKFPIIIDELEIGAAVVFSKLDLKSgy 682

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
HQIRM K FRTH+GHYE V+PFGLTN P+TFQ MN L+P+LR++V+VFF D
Sbjct 683 HQIRMKEEDIPKTAFRTHEGHYEYLVLPFGLTNAPSTFQALMNQVLRPYLRKFVLVFFYD 742

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMRP 2399
IL+YSK+ E H DHL VL L E+ N +KKCSFGQ + LGHVIS+ GV P
Sbjct 743 ILIYSKNEELHKDHLRIVLQVLKENNLVAN--QKKCSFGQPEIYYLGHVISQAGVAADP 799

Score = 205 bits (522), Expect(3) = 6e-168
Identities = 110/254 (43%), Positives = 158/254 (62%), Gaps = 5/254 (1%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKDITKINEEVQKDP 3059
QQ W++KL+GY+F+I YK G NK DALSR+ + + W D+ E+ D
Sbjct 966 QQKWSMKLMGYDYEIKYKPGIENKAADALSRKLQFSAISSVQCAEWADL---EAEILGDE 1022

Query 3060 ALAKIREELKNDLSDHPQTYLECDILYFRGLVLLASSLWIPKLLQEFQTSLMGGHSGIY 3239
K+ +EL +S Y L+ L ++ R+VL S I +L+EF + +GGH+GI+
Sbjct 1023 RYRKVLQELATQGNSAIGYQLKRGRLLYKDRIVLPKGSTKILTVLKEFHDTALGGHAGIF 1082

Query 3240 ITYRRITQSLYWIPIKGEITKFFVACHVGQRSKYQASSPAGLLQPLPIPNAIWEIISMNF 3419
TY+RI+ YW +K +I +V C V QR+KY+A +PAG LQPLPIP+ W +ISM+F
Sbjct 1083 RTYKRISALFYWEGMKLDIQNYVQKCEVCQRNKYEALNPAGFLQPLPIPSSQGWTDISDMF 1142

Query 3420 IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLEVPISIVSDS 3593
I G+ K+ G D ILV VD+ +KY +FI + HPY A+ I +V KE++ L P SIVSD
Sbjct 1143 IGGLPKAMGKDTILVVDRFTKYAHFIALSHYPNAKEIAEVFIKEVVKHLHGFTSIVSDR 1202

Query 3594 DLIFMSHFLQELFK 3635
D +F+S F E+FK

Sbjct 1203 DRVFLSTFWSEMFK 1216

Score = 168 bits (426), Expect(3) = 6e-168
Identities = 81/157 (51%), Positives = 114/157 (72%), Gaps = 0/157 (0%)
Frame = +2

Query 2399 IL*WPMKPTPKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQLQ 2578
+L WP+PK K LRGLF LTGY+R + NY K+A+PL LLK +F+W E++ +A ++L+
Sbjct 805 MLDWPIPKKVKGLRGFLGLTGYRRFVKNYSKLAQPLNQLLKNNSFQWTEEATQAFVKLK 864

Query 2579 QAITTIPTLSMLDFSQFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMEYEKE 2758
+ +TT+P L +F K F +E DASGKG+G VL Q+ + +AY +K L D +KS+YE+E
Sbjct 865 EVMTTVPVLVPPNFDKPFIFLETASGKGLGAVLMQEGRPVAYMSKTLSDRAQAKSVYERE 924

Query 2759 SMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
MA+VLA+Q WR YL +F I+ DQ+SLR+L DQRI
Sbjct 925 LMAVVLAVQKWRHYLLGSKFVIHTDQSRSLRFLADQRI 961

>gi|170660047|gb|ACB28472.1| polyprotein [Ananas comosus]
Length=953

Score = 266 bits (681), Expect(3) = 6e-159
Identities = 140/237 (59%), Positives = 169/237 (71%), Gaps = 7/237 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
F P+GLPP R DHKI +K G P NVRPYRYP QK EI+ LV EML G+I SNS
Sbjct 205 FEFPQGLPPVRLHDHDKIPLKEGTNPINVRPYRYPAYQKTEIEKLVQEMLSQGVITPSNSP 264

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
YSSPV+LVK+KDG RLC+DY++L+ +T+ DKF IP++ ELLDEL+G FS++DL++ Y
Sbjct 265 YSSPVVLVKKDGSWRCLCIDYRSLNDSTIKDKFPIPLVDELDELGSAGKLFSELDLRSGY 324

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
HQIRMH K FRTH+GHYE VMPFGLTN P+TFQ MN KP+LRR+++VFFDD
Sbjct 325 HQIRMHADDISKTAFRTHEGHYEFLVMPFGLTNAPSTFQGLMNHIFKPYLRRFVLVFFDD 384

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLM 2393
ILVYSK E HL HL L +H F V +KKC F ++ LGHVIS EGV M
Sbjct 385 ILVYSKGVEEHLCHLRTTFQVLRQHSFL---VRRKKCIFAAVQLEYLGHVISHEGVSM 439

Score = 198 bits (503), Expect(3) = 6e-159
Identities = 110/255 (43%), Positives = 159/255 (62%), Gaps = 5/255 (1%)
Frame = +3

Query 2877 NQQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKDITKINEEVQKD 3056
+QQ WVAKL+GY+++++YK G N V DALSR L +S + +I D
Sbjct 607 SQQKWVAKLMGYDYELIYKKGQENNVADALSR---SPTLLAVSAIHTDLLDQIKWSNVND 663

Query 3057 PALAKIREELKDNLDSDHPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSMLMGHSGI 3236
 L KI ++ + +++S P+YT D L +G+LV+ + +L+ F S +GGHSG+
 Sbjct 664 DKLKIIQQKQSDINSWPRTYTWQDQLRRKGLVVGSDPGLKLQLIHNHFASSIGHSGM 723

Query 3237 YITYRRITQSLYWIPIKGEITKFFVACHVGQORSKYQASSPAGLLQPLPIPNAIWEEISMN 3416
 T R++ YW ++ ++ +FV C V Q++KY+ ++PAGLLQPLPIP IW EISM+
 Sbjct 724 EATTRKLGQFYWKGLRRDVEQFVRECSVCQQNKYETAPAGLLQPLPIPEGIWTETISMD 783

Query 3417 FIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIVSD 3590
 FI G+ S+G +VI+V VD+LSKY +FI + HPY A S+ + I L +P SIVSD
 Sbjct 784 FIEGLPNSQGKEVIMVVDRLSKYAHFIALSHPYTASSVAQLFLDNIYKLHGMPRSIVSD 843

Query 3591 SDLIFMSHFLQELFK 3635
 D IF+S F QELFK
 Sbjct 844 RDTIFVSQFWQELFK 858

Score = 146 bits (369), Expect (3) = 6e-159
 Identities = 73/161 (45%), Positives = 106/161 (65%), Gaps = 0/161 (0%)
 Frame = +2

Query 2393 EAIL*WPMPTKPTKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572
 EAI WP+P T K LRGL L GYY+R + ++GKI++ L ++L FKW + A Q
 Sbjct 445 EAIQEWPLPTTAKELRGFLGLAGYRRFVKDFGKISKSLHEMLGKEGFWTNERHYAFQ 504

Query 2573 LQQAITTIPTLSMLDFSQKFSIECDASGKIGVVLTDQRKQIAYFNKALKDLTSLKSMYE 2752
 L++A++ P L++ DF+ F+IE DASG G+G VL Q + IA+ +K L S YE
 Sbjct 505 LKKAVSAAPVLALPDTFTIDFTIETDASGIGVAVLLQKGRPIAFMSKPLSPRNRQLSTYE 564

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 +E +A+V+A+Q WRPYL F I D +SL+YL++QR++T
 Sbjct 565 REMLAIVIAVQKWRPYLIGRHFKIKTDHQSLLKYLMEQVRVST 605

>gi|225465489|ref|XP_002271052.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length=1529

Score = 256 bits (653), Expect (3) = 1e-154
 Identities = 133/239 (55%), Positives = 164/239 (68%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHDKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F PKGLPP + DH I + G+ P +VRPYRYPH QK EI+ V EML GI+R SNS
 Sbjct 639 FKEPKGLPPLQVHDHCIPLVPGSGPVSVRPYRYPHFQKTEIEQQVEEMLKSGIVRPSNSP 698

Query 1878 YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 YSSPV+LVK+ DGS R+C+DYQAL++ V DKF I V+ ELLDEL+ +F K+DL++ Y
 Sbjct 699 YSSPVLLVKKSDGSRMCDIDYQALNRIIVKDKFPIISVIDELDELHAARYFFKDLRLSGY 758

Query 2058 HQIRMHKP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQIR+H P FRTH GHYE VMPF LTN P+TFQ MN K +LR++V+VVFDD
 Sbjct 759 HQIRVHPPDISKTAFTTHGHYEFLVMPFELNAPSTFQSLMNDIFKRYLRKFVLVVFDD 818

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMRP 2399
 IL+YS SWE HL H+ +L L H F K+KC FGQ + LGH+I EGV + P
 Sbjct 819 ILIYSSSWEHQLHVQFILDILRSHNMFLK--KEKCFQFGQTQIKYLGHLIDVEGVSVD 875

Score = 176 bits (446), Expect (3) = 1e-154
 Identities = 101/255 (39%), Positives = 153/255 (60%), Gaps = 10/255 (3%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDEKELQGISRPFWKDITKINEEVQKDP 3059
 QQ W++KL+GY+F + Y+ GA N V DALS ++E EL IS P + + I EEV +
 Sbjct 1042 QQKWLKSLMGYDFQVEYRKGAEENLVADALSKEEKVELVAISTPIPRWLDITKEEVLTS 1101

Query 3060 ALAKIREELKDNLDSDHPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSMLMGHSGI 3239
 L + + +++ P + + ++L+F+ ++ L + SL + ++QEF ++ H GI+
 Sbjct 1102 KLQHLVKLVQEGEVVGP--WEFKEEVLFFKSQIYLNDSLLLSVIEQFHSNT---HEGHI 1157

Query 3240 ITYRRITQSLYWIPIKGEITKFFVACHVGQORSKYQASSPAGLLQPLPIPNAIWEEISMNF 3419
 T +RI YW+ +K + ++ C V QR K + +SPAGLLQPLPIP +W +ISM+F
 Sbjct 1158 KTLQIRSVFYVWGMKKQRDRYIRHCDVCQRHKTECTSPAGLLQPLPIP TKVWSDISMDF 1217

Query 3420 IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDVKEIIV-----LLEVPISIVS 3587
 + G+ S G I V VD+LSKY +FI+I HPY A+S+ KE + L +P IV
 Sbjct 1218 VDLGPTSMGKSTIFVVVDQLSKYSHFILSHPYTAQSV--AKEFFVHVFRHLGLPELIVC 1275

Query 3588 DSDLIFMSHFLQELF 3632
 D D F S F +ELF
 Sbjct 1276 DRDPAFTSKFEWELF 1290

Score = 165 bits (417), Expect (3) = 1e-154
 Identities = 82/160 (51%), Positives = 112/160 (70%), Gaps = 0/160 (0%)
 Frame = +2

Query 2396 AIL*WPMPTKPTKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQL 2575
 A++ WP P TPK LRGL LTGY++ I NYGKIA PL ++LK +F W S +A L
 Sbjct 880 AMMEWPKPNTPKALRGFLGLTGYRKFIRNYGKIASPLTNMLKKDSFAWTFASERAFQDL 939

Query 2576 QQAITTIPTLSMLDFSQKFSIECDASGKIGVVLTDQRKQIAYFNKALKDLTSLKSMYEK 2755
 ++A+T P L++ +F+ F +ECDASG G+G VL Q ++ IA+F++AL+ L SMY+K
 Sbjct 940 KEAMTQAPVLTLPNFANAFVVECDASGSGVGVLMQCKQPIAFFSQALQGRNLLLSMYDK 999

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 E +ALVLA+Q WRPYL F + D SL++L +QRITT
 Sbjct 1000 EMLALVLAVQKWRPYLLGRFTFIVRTDHHSLKFLWEQRITT 1039

>gi|225426216|ref|XP_002263623.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length=1395

Score = 251 bits (642), Expect (3) = 1e-153
 Identities = 123/235 (52%), Positives = 165/235 (70%), Gaps = 7/235 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHDKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F+ P LPP+RE+DHKI +K G NVRPYRY + QK EI+ V +ML G+IR S S
 Sbjct 450 FAAPTSLPPTREIDHKIPLKDGTEAINVRPYRYAYFQKTEIENQVQDMLNAGLIRPSTSP 509

Query 1878 YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSPV+LVK+KDG+ R C DY+AL+ A V D+F IP + ++LDEL+G F+K+DLKA Y
 Sbjct 510 FSSPVLLVKKGDGTWRFC TDYRALNAAIVKDRFP IPTVDMLDELHGAFFTKLDLKAGY 569

Query 2058 HQIRMHKP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQIR+ P FRTH GHYE VMPFGL N P+TFQ MN+ +P+LR++++VFF D
 Sbjct 570 HQIRVSTPDIPKIAFRTHNGHYEYLVMPFGLNAPSTFQAIMNSIFRPYLRKFILVFFYD 629

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGV 2387
 IL+YS +WE HL+H+ LA L +H F+ + KC+FG+ + LGH+I+ GV
 Sbjct 630 ILIYSPTWEQHLHVQLTLAVLRQHOFYVKM--SKCAFGKQELEYLGHIIHTRGV 682

Score = 185 bits (470), Expect(3) = 1e-153
 Identities = 104/257 (40%), Positives = 150/257 (58%), Gaps = 10/257 (3%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGI---SRPFWKDITKINEEVQ 3050
 QQ WVAKLLGY+++I+++ G N DALSR E L + WK I + ++
 Sbjct 853 QQKWWAKLLGYDYEIIFRPGRENSAADALSRQESPLLAALHFSEVDIWKHIREASKSDS 912

Query 3051 KDPALAKIREELKDNLDSDHPQYTLECDILYFRGRVLASSLWIPKLLQEPQTSIMGGHS 3230
 L K K H T +L +G++++ A KLL E S +GGHS
 Sbjct 913 YVQLLGK-----KAGDPHGNLTWRDGLLLYKGVMPADHSLRAKLLYEVHNSKVGHS 967

Query 3231 GIYITYRRITQSLYWIPIKGEITKFFVACHVGQORSKYQASSPAGLLQPLPIPNAIWEEIS 3410
 GI TYRR+ Q YW + + ++V C V QR K + +PAGLLQPLPIP +WE+I+
 Sbjct 968 GILRTYRRILQQQFYWFPMHKAVQEVVQKCEVCQRIKPKAPAGLLQPLPIPAQVWEDIT 1027

Query 3411 MNFIVGMLKSGGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIV 3584
 ++FI G+ S G D ILV VDKLSK+ +FI + HP+ A+ + + ++ ++ L +P SI+
 Sbjct 1028 LDFIEGLPTSHGKDTILVVVDKLSKFAHFIPLTHPTAKVVAENFIEGVVVKLHGMPRSII 1087

Query 3585 SDSDLIFMSHFLQELFK 3635
 SD + IF+S F QE FK
 Sbjct 1088 SDRNPFIKSFQWQEFFK 1104

Score = 156 bits (395), Expect(3) = 1e-153
 Identities = 81/161 (50%), Positives = 110/161 (68%), Gaps = 0/161 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
 EA++ WP P LRGFL L GYY++ + YG IARPL +LLK G F+WN+++ +
 Sbjct 690 EAMVAWPRPSNITELRGFLGLIGYRKVFQGYGLIARPLTNLLKKGKFQWNETEATFLA 749

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYE 2752
 L+QA+T+ TL+M +FS+ F+IE DASG GIG VLTQ + IAY + AL + S+Y
 Sbjct 750 LKQAMTSTLTAMPNFSEFTTIETDASNGIGAVLTQQNRPIAYMSLALGITKQTSIYA 809

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 KE +A+V AI+ WRPYL KF I DQ+SL++ LDQR+ T
 Sbjct 810 KEMLAIVEAIRMRPYLLGRKFYIKTDQRSLSKFFLDQRVAT 850

>gi|227438239|gb|ACP30609.1| disease resistance protein [Brassica rapa subsp.
 pekinensis]
 Length=2726

Score = 255 bits (652), Expect(3) = 7e-152
 Identities = 143/264 (54%), Positives = 179/264 (67%), Gaps = 13/264 (4%)
 Frame = +3

Query 1653 PRKL--VVASTDRCVCSYFSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKT 1826
 P KL V+A D+V F+ P LPP R +H I +K G +VRPYRYPH K ++
 Sbjct 1748 PDKLLDVLAEFDQV---FALPTALPFRGKNHAINLKPGVTAISVRPYRYPHNTKVVMEQ 1804

Query 1827 LVVEML*LGIIRLSNSSSYSPVILVKRKGDS*RLCMDYQALSKATVPDKFLIPVMKELLD 2006
 +V EML GIIR S S +SSPV+LVK+KDGS R C+DY+AL+KAT+PDKF IPV+ +LLD
 Sbjct 1805 MVCEMLEAGIIRESTSPFSSPVLLVKKKGDSWRFCIDYRALNKATIPDKFPIPIDQLLD 1864

Query 2007 ELNGPIHFSKIDLKARYHQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMN 2171
 EL G FSK+DL++ YHQIRM K FRT +GHYE VMPFGLTN P TFQ MN
 Sbjct 1865 ELYGASVFSKLDLRSYGHQIRMQEEDIPKTAFTVEGHYEFVLMFGLTNAPATFQALMN 1924

Query 2172 ATLKPFLLRRYVVVFFDDILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKA 2351
 + KP+LR++V+VFFDD+L+YSK+ E H +HL VL+ L EH N +KKCSFG +
 Sbjct 1925 SIFKPYLRKFVLVFFDDVLIYSKTVEEHAHLRLVLSVLQEHKLLAN--RKKCSFGLQQI 1982

Query 2352 GCLGHVISKEGVLMRPFCSGQCLK 2423
 LGH+ISK GV QC+K
 Sbjct 1983 EYLGHIISKNGVATDAI-KTQCMK 2005

Score = 183 bits (464), Expect(3) = 7e-152
 Identities = 100/271 (36%), Positives = 159/271 (58%), Gaps = 10/271 (3%)
 Frame = +3

Query 2853 Y*ISELQNLQOY--WVAKLLGYEFDIVYKVGASNKVVDALSR-----RDDEKELQGISR 3008
 Y + + ++N +Y W+ KLLG++F IVY+ G NK D LSR R+ L ++
 Sbjct 2154 YLLEQKEVNMMEYHRWLTKLLGDFDIIVYRPGCDNKADGLSRIERNVVRMSLSLLALTI 2213

Query 3009 PFWKDITKINEEVQKDPALAKIREELKDNLDSDHPQYTLECDILYFRGRVLASSLWIPK 3188
 P + I +E++ + K + +K+ + ++ + L+++ RL+ S IP
 Sbjct 2214 PAALQVEDIYKEIEACVEIQKKIQWIKGKIVNDKFRVIDGKLWYKRLVIPKDSASIP 2273

Query 3189 LLQEFQTSIMGGHSGIYITYRRITQSLYWIPIKGEITKFFVACHVGQORSKYQASSPAGLL 3368
 LL E+ GGHS+ T +RI +W + + K+V C++ Q KY +PAGLL
 Sbjct 2274 LLSEYHDGQQGGHSGVLKTVKRIQSMFHWEGLYQRQKYVSECNICQTHKYSTLAPAGLL 2333

Query 3369 QPLPIPNAIWEEISMNFIVGMLKSGGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--V 3542
 QPLPIPNIWE++SM+F+ G+ S+G +VI+V VD+LSKY +F+ +KHP+ A + V
 Sbjct 2334 QPLPIPNIWEDVSMDFVEGLPGSQGVNVMVVDRLSKYAHFVGLKHPFTAVEVASKFV 2393

Query 3543 KEIWLLEVPISIVSDSLIFMSHFLQELFK 3635
 E++ P SIVSD D +F+S F ++LF+
 Sbjct 2394 SEVVKHHGFFRSIVSDRDRVFLSSFWKDLFR 2424

Score = 149 bits (376), Expect(3) = 7e-152
 Identities = 73/153 (47%), Positives = 104/153 (67%), Gaps = 0/153 (0%)
 Frame = +2

Query 2408 WPMKPTKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQLQQA 2587
 WP+PK+ K LRGFL LTGY+ + YG IARPL +LLK F+W+++ A L++A+
 Sbjct 2007 WPLPKSVKQLRGFLGLTGYRHYVKGYSIARPLTELLKKDGFQWSKEAELAFDSLKKAM 2066

Query 2588 TTITPSTLSMLDFSQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYKESMA 2767
 P L++ +F K F IE DASG G+G VL QD K IA+F+ L + K YE+E MA
 Sbjct 2067 VEAPVLALPNFEKPFVIESDASGFGVAVLMQDGKPIAFFSHGLTEREQLKPAYERELMA 2126

Query 2768 LVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQR 2866
 +VLA+Q W+ YL +F ++ D +SL+YLL+Q+
 Sbjct 2127 VVLAVQKWKHYLLGRQFVVHTDHRSLKYLLEQK 2159

>gi|225443027|ref|XP_002267560.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length=1463

Score = 248 bits (634), Expect(3) = 6e-151
 Identities = 124/235 (52%), Positives = 166/235 (70%), Gaps = 7/235 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRYPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F P LPP R DHKI ++ A P +V+PYRYP+ QK EI+ +V ++L G+IR SNS
 Sbjct 537 FESPTTLPPRRSHDKIPLQPSAGPVSVQPYRYPYQKTEIEKRMVKLLQSGLIRPSNSP 596

Query 1878 YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSPV+LVK+ DG+ R C+DY+AL+ T+ DK+ IPV+ ELLDEL+G +SK+DL++ Y
 Sbjct 597 FSSPVLLVKKADGAWRFCVDYRALNDITIKDKYIPVIDELDELHGAKFYSKLDLRSGY 656

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQIR+H K FRTH+GHYE VMPFGLTN P TFQ MN +P+LR+++VFF D
 Sbjct 657 HQIRVHEADIPKTAFTRTHEGHYEFIVMPFGLTNAPATFQSLMNDLFRPYLRKFI LVFFYD 716

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGV 2387
 IL+YS+SWE HL HL VL L + F + KC FG ++ LGH+IS++GV
 Sbjct 717 ILIYSRSWEDHLTHLQIVLQILSANS LFAK--ESKCRFGVLQVEYLGHIISEQGV 769

Score = 169 bits (427), Expect (3) = 6e-151
 Identities = 86/161 (53%), Positives = 112/161 (69%), Gaps = 0/161 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTKPTLRGFLGTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572
 +AI+ WP P T K +RGFL L GY++ I N+G IA PL LL F WNE + A Q
 Sbjct 777 QAIIEWPTPTTAKGVRGFLGLAGYYRKFI RNFGCIASPLTRLLSKEGFHWNEAAEMAFKQ 836

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKGIGVVLTQDRKQIAYFNKALKD LTLKSMEY 2752
 L++A+T+ P L + DFS+ F IECDASG GIG +LTQ + +AYF++ALK L+ S YE
 Sbjct 837 LKEALTSPILCLPDFSQPFVIECDASGLGIGAILTQQNQPVAYFSEALKGSALALSTYE 896

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 KE +A++ AI+ WRPYL FT+ D KSL+YLL+QRITT
 Sbjct 897 KEMLAIKAIKKWRPYLLGKPFVTRTDHKS LKYLLEQRITT 937

Score = 167 bits (423), Expect (3) = 6e-151
 Identities = 96/254 (37%), Positives = 147/254 (57%), Gaps = 5/254 (1%)
 Frame = +3

Query 2880 QQYWVAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWK DITKINEEVQKDP 3059
 Q W+ KLLGY++ I YK G N+ D+LSR E + L +S P + + +E+Q+D
 Sbjct 940 QTRWLPEKLLGYDYKIEYKRGPNQGDLSLRVVEFQFLS-LSMPHADWWSILQKEIQQDS 998

Query 3060 ALAKIREELKDNLD SHPQYTLCE DILYFRGRVLVLLASSLWIPKLLQEFQ TSLMGHSGIY 3239
 K+ E K S + + + R ++ L +S IPK+L + +S +GGH G +
 Sbjct 999 FYEKMIE--KSTSQSGHKLLQHDGVWFVKRDVYLSPTSSLIPKILADCHSSSIGHGFGEH 1056

Query 3240 ITYRRITQSLYWIPIKGEITKFV VACHVGQRSKYQASSPAGLLQPLPIPNAIWEEISMNF 3419
 T RI S W ++ + +F+ C V QR K PAGLLQPLP+P+ +W ++SM+P
 Sbjct 1057 KTL SRIKHSFVWPSMRMVKEFLQQCDCVCRKFTDCMKPAGLLQPLPVPVPHQMWT DVSMDF 1116

Query 3420 IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIIWLLVVPISIVSDS 3593
 I G+ S G+ I+V VD+L+KY +FI +KHP+ A ++ V ++ L +P SIVSD
 Sbjct 1117 IEGLPSSNGYSTIMVVVDRLTKYAHFI ALKHPFTAVTVAKAFVANVVR LHGIPTSIVSDR 1176

Query 3594 DLIFMSHFLQELFK 3635
 D +F+S F Q LF+
 Sbjct 1177 DKVFLSSFWQTLFQ 1190

>gi|89887334|gb|ABD78322.1| polyprotein [Primula vulgaris]
 Length=1359

Score = 255 bits (651), Expect (3) = 3e-150
 Identities = 134/239 (56%), Positives = 164/239 (68%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 FS PKGLPP RE HKI + G P +VRPYRYP+ QKNEI+ +V E++ G IR S S
 Sbjct 464 FSEPKGLPPEREHVHKIELIQGTNPISVRPYRYPYFQKNEIEKIVKELIESGFI RPSQSP 523

Query 1878 YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSPVILVK+ DGS R+C+DY+AL+K T+ DKF IPV+ ELLDELNG FSK+DL++ Y
 Sbjct 524 FSSPVILVKKSDGSRMCDYRALNKVTIKDKFPIPVVDELDELNGAKLFSKLDLRSGY 583

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQI+MH K FRTH+G YE VMP LTN P TFQ AMN+ KPFL + FFDD
 Sbjct 584 HQIKMHANDVSKTAFTRTHEGQYEFVMPVLVLTNAPATFQSAMNSVFKPFLENLCLFFDD 643

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP 2399
 ILVYSK+ + H+ HL VL ++ EH FF KC F Q + LGH+IS +GV P
 Sbjct 644 ILVYSKTNDHEICHLEAVLKKMSEHKFFAK--SSCKKFFQKEIDYLGHLISDQGVKADP 700

Score = 169 bits (427), Expect (3) = 3e-150
 Identities = 86/161 (53%), Positives = 118/161 (73%), Gaps = 0/161 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTKPTLRGFLGTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572
 +A+L WP+PK K LRGL LTGY+R I NYG IAR L +LLK F W+ ++ A
 Sbjct 704 KAMLEWVPVKNLKLGRGFLGLTGYRRFIRNYGGIARALT ELLKDAFLWSREAETAFNN 763

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKGIGVVLTQDRKQIAYFNKALKD LTLKSMEY 2752
 L++A+T+ P L++ DF+K F+IECDASG+G+G VL Q+++ IA+F+KALK L+ S YE
 Sbjct 764 LKKA VTSPPVLALPDFNKFTTIECDASGQGVGAVLQQEKRP IAFFSKALKGRLLTLSTYE 823

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 KE ALV AIQ WRPY+ +F + D +SL+YLL+Q+I+T
 Sbjct 824 KELYALVQAIQWRPYICCEQEFIVNTD HQSLKYLLEQKIST 864

Score = 158 bits (400), Expect (3) = 3e-150
 Identities = 93/255 (36%), Positives = 147/255 (57%), Gaps = 3/255 (1%)
 Frame = +3

Query 2877 NQQYWVAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGI-SRPFWK DITKINEEVQK 3053
 +QQ W++KLLGY F I YK GA NK DALSR +E + + + S P W+ +I + +K
 Sbjct 866 SQQKWL SKLLGYNFKIYYKQ GALNKAADALSRVNEGQLMSVVVSTPIWEIKKEIMDCYEK 925

Query 3054 DPALAKIREELKDNLD SHPQYTLCE DILYFRGRVLVLLASSLWIPKLLQEFQ TSLMGHSG 3233
 D +A+I ++ + + + + +L+++ RL + ++ K GH+G
 Sbjct 926 DQKVAEISFQIANEVLAATNFKWINGLLFYKERLYVPNNNDLIKTYAILHEDPDNGHTG 985

Query 3234 IYITYRRITQSLYWIPIKGEITKFV VACHVGQRSKYQASSPAGLLQPLPIPNAIWEEISM 3413
 + + +YW +K ++ K FV +C V Q KY ++ GLLQPLP+P W EISM
 Sbjct 986 FQKSLLLAYKEVWQGLKDLKFKFVDS CVVCQCTKYGKNAYGLLQPLPMEQ TWEISM 1045

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIIWLLVVPISIVS 3587
 +FI G+ SK ++ I V VD+L+KY +FI +KHP+ A+ + + ++ I L +P I+S
 Sbjct 1046 DFINGLPTSKNINCIWVVVDRLTKYAHFIPLKHPFGAKELANEF LNIFKLHGLPKKIIS 1105

Query 3588 DSDLIFMSHFLQELF 3632
 D D IF S F +ELF
 Sbjct 1106 DRDTIFTSDFWKELF 1120

>gi|147854459|emb|CAN78588.1| hypothetical protein [Vitis vinifera]
 Length=2232

Score = 256 bits (653), Expect(3) = 9e-149
Identities = 134/234 (57%), Positives = 164/234 (70%), Gaps = 7/234 (2%)
Frame = +3

Query 1713 GLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSSSYSPV 1892
GLPPSR++DH I + GA P NVRPYRYPH+ KNEIK LV EML GI+R S S +SSPV
Sbjct 1220 GLPPSRDIDHAIQLILGASPVNVRPYRPHILKNEIKRLVQEMLEAGIVRPSLSFSSPV 1279

Query 1893 ILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARYHQIRM 2072
+LVK+KDG R C+DY+AL+K TVPD+F IPV+ ELLD+L+G FSK+DLK+ YHQIR+
Sbjct 1280 LLVKKKDGGRFCIDYRALNKVTPDRFP IPVIDELDLKLHGATIFS KL DLKSGYHQIRV 1339

Query 2073 H-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFFDDILVYS 2237
K FRTH+GHYE VMPFGLTN P TFQ MN P L ++V+VFF DILVYS
Sbjct 1340 RQQDIPKTAFRTHEGHYEFVMPFGLTNAPATFQSLMNRIFWPHLWKFVLVFFYDILVYS 1399

Query 2238 KSWEAHLHDLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMPR 2399
K + H DHL VL+ L H N KKC F+++ LGH++S +GV P
Sbjct 1400 KDLKEHCDHLQTVLSILANHQLHVN--GKKCLFAKLQLEYLGHLSAKGVAADP 1451

Score = 174 bits (440), Expect(3) = 9e-149
Identities = 86/187 (45%), Positives = 126/187 (67%), Gaps = 0/187 (0%)
Frame = +3

Query 2883 QYVWAKLLGYEFDIVYKVGASNKVVDALSRRDEDKELQGISRPFWKDITKINEEVQKDPA 3062
Q VWAKL GY+F+I ++ G NK DALSR EL + P D I+ +V+ DP
Sbjct 1619 QKWVAKLFGYDFEIQFRPGXENKAADALSRIPISELMXALMVPSRIDTXLISQVEADPH 1678

Query 3063 LAKIREELKDNLDSPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSLMGGHSGIYI 3242
L KI++ L + D++P+Y+L+ IL ++GRLVL +S +P LLQE S++GGHSG
Sbjct 1679 LXXIKQRLXDPDAYPRYSLDHGILLYKGRVLVPKASPIVPALLQEGHASVVGHSGGLX 1738

Query 3243 TYRRITQSLYWIPIKGEITKFFVACHVGQRSKYQASSPAGLLQPLPIPNAIWEIISMNFI 3422
TY+R+T+ +W+ +K +I +FV C V Q++K SPAGLLQPLPIP+ IW+++M+FI
Sbjct 1739 TYKRLTRDFFWGMMKNDIKEFVEKCLVCQONKTLTLSPAGLLQPLPIPDKIWDVMTDFI 1798

Query 3423 VGMLKSK 3443
G+ KS+
Sbjct 1799 EGLPKSE 1805

Score = 147 bits (372), Expect(3) = 9e-149
Identities = 76/161 (47%), Positives = 106/161 (65%), Gaps = 0/161 (0%)
Frame = +2

Query 2396 AIL*WMPKPTKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQL 2575
A++ WP PK+ K LRGL LTGY+R + YG I+ PL LK F WN ++ A +L
Sbjct 1456 AMVEWPTPKSLKELRGFLGLTGYYRRFVEGYGAISWPLTQELKKDAFNWLEAEVAFQKL 1515

Query 2576 QQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTLSKSMYEK 2755
+ +TTIP L++ +FS+ F +E DASG G+G VL Q + +AYF++ L KS+YE+
Sbjct 1516 KTTMTTIPVLALENFNSQLFIVEMDASGYGLGTVMQSHRPVAYFSQVLTARERQKSIYER 1575

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTO 2878
E MA+VLA+Q WR YL F + DQ SL++LL+QRI +
Sbjct 1576 ELMAIVLAVQKWRHYLLGRHFIVRTDQSSLKFLLEQRIVNE 1616

>gi|225455084|ref|XP_002267679.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length=1499

Score = 252 bits (643), Expect(3) = 8e-148
Identities = 134/256 (52%), Positives = 174/256 (67%), Gaps = 11/256 (4%)
Frame = +3

Query 1647 KEPKRLVVASTDRVCYSFSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKT 1826
+E +K++ A D F P GLPP R+ DH+I +K A P N RPYRY +QK+ I+
Sbjct 560 EELQKMLQAFAD----VFEEPTGLPPVRDYDHQIDLKDEAGPINCPRYRPAVQKDAIEK 615

Query 1827 LVVEML*LGIIRLSNSSSYSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELL 2006
L+ EML G+IR S S Y+SPV+LVK+KDG RLC+DY+AL++ TV DKF IPV++ELL+
Sbjct 616 LIGEMLHAGVIRKSRSPYASPVVLVKKKDGSWRLCVDYRALNQVTVKDKFPIPVIEELLE 675

Query 2007 ELNGPIHFSKIDLKARYHQIRMHKP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMN 2171
EL G FSKIDL++ Y QIRMH+P F+TH+GHYE VMPFGLTN P+TFQ MN
Sbjct 676 ELGGSTIFSKIDLRSGYWQIRMHEPDVPKTAFTHEGHYEFVMPFGLTNAPSTFQSLMN 735

Query 2172 ATLKPFLRRYVVFFDDILVYSKSWEAHLHDLS*VLARLLEHYFFTNVFKKCSFGQIKA 2351
+P+LR+++VFFDDIL+YS+S+ H+ HLS L L E+ + KC FG
Sbjct 736 NIFQPYLRKFIIVFFDDILIYSRSFSDHIHHLSTALQVLRNLLYAK--SNKCFGHSSSI 793

Query 2352 GCLGHVISKEGVLMPR 2399
LGHVIS GV P
Sbjct 794 EYLGHVISSGGVYTD 809

Score = 163 bits (413), Expect(3) = 8e-148
Identities = 85/160 (53%), Positives = 111/160 (69%), Gaps = 0/160 (0%)
Frame = +2

Query 2396 AIL*WMPKPTKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQL 2575
A+ WP T K LRGL LTGY+R + +YGKIA+PL DLLK F W E S +A + L
Sbjct 814 AVRDPWTSITLQKLRGLGLTGYYRRFVKDYGKIAKPLTDLKKDAFHWTEGNSQAQFMA 873

Query 2576 QQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTLSKSMYEK 2755
+QA+ T P L++ +FSK+F IE DASG+GIG VL Q+ IAY +KAL D + S YEK
Sbjct 874 KQAMITAPVLALENFNSKEFI IETDASGQIGAVLMQEGHP IAYISKALSDRFQTLSTYEK 933

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTO 2875
E +A+++AI+ W YL D F I D +SL+YLL+QR+TT
Sbjct 934 EMLAILMAIKKWESYLVDRHFVIKTDHQLSKYLLEQVRVT 973

Score = 159 bits (401), Expect(3) = 8e-148
Identities = 96/256 (37%), Positives = 146/256 (57%), Gaps = 5/256 (1%)
Frame = +3

Query 2880 QYVWAKLLGYEFDIVYKVGASNKVVDALSRRDEDKELQGISRPFWKD--ITKINEEVQK 3053
QQ VWAKL+ Y+++I YK G N DALSR + EL +S I E
Sbjct 976 QQAWEAKLMQYDYEIYKQKQENVAADALSRI-QPAELFVLSTTILNTQLYDLIKESWGV 1034

Query 3054 DPALAKIREELKDNLDSPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSLMGGHSG 3233
DP L KI + + + ++P+Y+ + L +G+LV+ + ++L F S GGHSG
Sbjct 1035 DPQLQKIIKAKEADPAYSYPKYSWRGEELRRKGLVGVGNEQLRREILNSFHDSPFGHSG 1094

Query 3234 IYITYRRITQSLYWIPIKGEITKFFVACHVGQRSKYQASSPAGLLQPLPIPNAIWEIISM 3413
+Y+T ++I+ +YV ++ + ++V C V QR K + +GLLQPLP+P ++ +I+M
Sbjct 1095 VYVTTKQISAVVYWKLRKFVREYVRNCSVCQRFPKPNKPYSGLLQPLPVEGVFTDITM 1154

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--KEIIWLLVPEPISIVS 3587
+FI G+ KS G I V VD+L+KY +F+++ HPY A+ + V + L +P SI
Sbjct 1155 DFIEGLPKSNGKTAIFVVDRLTKYGHFMLLPHPYAKMVAQVFLDSVYKLHGLPHSITC 1214

Query 3588 DSDLIFMSHFLQELFK 3635
 D D I F S F Q E F K
 Sbjct 1215 DRDPIFTSVFWQEFFK 1230

>gi|116309032|emb|CAH66146.1| OSIGBa0114M03.4 [Oryza sativa (indica cultivar-group)]
 Length=1448

Score = 253 bits (645), Expect(3) = 1e-147
 Identities = 131/239 (54%), Positives = 163/239 (68%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIIRLSNSS 1877
 F+ P GLPP R DH+I +K+GA P VRPYRYP K+E++ M+ GI+R S+S
 Sbjct 488 FTEPTGLPPKRAHDHRITLKTGAQPVAVRPYRYPAAHKDELERQCAAMIEQGIVRRSDSP 547

Query 1878 YSSPVILVKKRDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSPV+LVK+ DGS R C+DY+AL+ TV D F IPV+ ELLDEL+G F+K+DL++ Y
 Sbjct 548 FSSPVLLVKKPDGSRFCVDYRALNALTVDKDAFPVVDDELDELHGARGFTKDLDRSGY 607

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFDD 2222
 HQ+RM HK FRTH G YE VM FGL N P TFQ MN L+PFLRR+V+VFFDD
 Sbjct 608 HQVMRPEVDVHKTAFRTHDGLYEFLVMAFGLCNAPATFQALMNDVLRPFRLRFVLVFFDD 667

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMP 2399
 IL+YSK+W HL HL VL+ L +H F V + KC+FG LGHVIS GV M P
 Sbjct 668 ILIYKSTWADHLRHLRAVLSELRQHQLF--VKRAKCAFGASSVSYLGHVISAAGVAMP 724

Score = 169 bits (428), Expect(3) = 1e-147
 Identities = 100/256 (39%), Positives = 151/256 (58%), Gaps = 9/256 (3%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDD-EDKELQGISRPFWKDITKINEEVQKD 3056
 Q +WV KLLG++F + Y+ GASN V DALSRDD +D L IS P + IT++ D
 Sbjct 891 QHHWVGKLLGDFDSVEYRSGASNTVADALSRDDVDGALLAISAPRFDITRLRHAQATD 950

Query 3057 PALAKIREELKDNLDLSDHPQYLTLECDILYFRGLVLLASSLWIPKLLQEFQTSIMG-GHSG 3233
 PAL I +E++ + P +T+ D++ + GRL + +S LLQE ++ GH G
 Sbjct 951 PALVAIHDEVRAGTRAAP-WTVVDDMVAYDGRLYIPPTS-----PLLQETMAAVHDDGHEG 1005

Query 3234 IYITYRRITQSLYWIPIKGEITKFFVACHVGQRSKYQASSPAGLLQPLPIPNAIWEIEM 3413
 ++ T R+ + ++ ++ + FV AC QR K + PAGLLQPLP+P+ +W +I +
 Sbjct 1006 VHRTLHLRLRRDFHFPNMRLVQDFVRACCTCQRYKSEHLHPAGLLQPLPVPSIVWADIGI 1065

Query 3414 NFIVGMLKSKGDFVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIWLLEVPISIVS 3587
 +F+ + + G VIL VD+ SKY +FI + HPY A S+ +I+ L VP SIVS
 Sbjct 1066 DFVEALPRVHGKTVILSVVDRFSKYCHFIPLAHPYTAESVAQFAFADIVRLHGVQPSIVS 1125

Query 3588 DSDLIFMSHFLQELFK 3635
 D D +F S F +E+ +
 Sbjct 1126 DRDPVFTSAFWREIMR 1141

Score = 151 bits (382), Expect(3) = 1e-147
 Identities = 74/163 (45%), Positives = 105/163 (64%), Gaps = 0/163 (0%)
 Frame = +2

Query 2393 EAIL*WMPKTPKTLRGFLELTGYIKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
 +AIL WP P++ + +RGFL L GYI++ + NYG +A PL LLK F W++ + A
 Sbjct 728 QAILDWPAPRSVRVAVRGFLGLAGYIRKFNHNYGTVAAPLTALLKKDGFSWDDAAATAFNA 787

Query 2573 LQQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTLSKSMYE 2752
 L+ A+TT P L M DF+K F +ECDAS G G VL QD +A+F++ + + + YE
 Sbjct 788 LKAAVTTAPILVMPDFTKIFIVECDASSHGFGAVLVQDGHVPAFFSRPVAPRHRALAAEY 847

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTTQ 2881
 +E + LV A++HWRPYL +F + D SL+YLLDQR+ T P
 Sbjct 848 RELIGLVQAVRHRPYLWGRRFIVKTDHYSKLYLLDQRLATIP 890

>gi|225443419|ref|XP_002267647.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length=1486

Score = 246 bits (628), Expect(3) = 2e-147
 Identities = 132/256 (51%), Positives = 172/256 (67%), Gaps = 11/256 (4%)
 Frame = +3

Query 1647 KEPRKLVVASTDRVCYSFSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKT 1826
 +E +K++ A D F P GLPP R+ DH+I +K A P N RPYRY +QK+ I+
 Sbjct 547 EELQKMLQAFAD----VFEEPTGLPPVRDYDHQIDLKDEARPINCRPYRYAAVQKDAIEK 602

Query 1827 LVVEML*LGIIIRLSNSSYSSPVILVKKRDGS*RLCMDYQALSKATVPDKFLIPVMKELL 2006
 L+ EML G+IR S S Y+S +LVK+KDGS RLC+DY+AL++ TV DKF IPV++ELL+
 Sbjct 603 LIGEMLHAGVIRQSRSPYASSGVLVKKKDGSRWLCVDYRALNQVTVDKFPPIPVIEELLE 662

Query 2007 ELNGPIHFSKIDLKARYHQIRMHQP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMN 2171
 EL G FSKIDL++ Y QIRMH+P F+TH+GHYE VMPFGLTN P+TFQ MN
 Sbjct 663 ELGGSTIFS KIDLRSYGWQIRMHEPNVPKTAFTKEGHYEFLVMPFGLTNAPSTFQSLMN 722

Query 2172 ATLKPFLRRYVVFDDILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKA 2351
 +P+LR+++VFFDDIL+YS+S+ H+ HLS L L E+ + KC FG
 Sbjct 723 NIFQPYLRKFLVFFDDILIYSRSFSDHIHLSIALQVLRENLLYAK--STKCFFGHSSI 780

Query 2352 GCLGHVISKEGVLMP 2399
 LGHVIS GV P
 Sbjct 781 EYLGHVISSGGVYTD 796

Score = 166 bits (421), Expect(3) = 2e-147
 Identities = 86/160 (53%), Positives = 112/160 (70%), Gaps = 0/160 (0%)
 Frame = +2

Query 2396 AIL*WMPKTPKTLRGFLELTGYIKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQL 2575
 A+ WP P T K LRGLF LTGYI+R + +YGKIA+PL DLLK F W E S +A + L
 Sbjct 801 AVRWDWPTITLQKLRGLGLTGYIRRFVVDYGKIAKPLDLLKKDAFWHTEGSNQAFMAL 860

Query 2576 QQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTLSKSMYEK 2755
 +QA+ T P L++ +FSK+F IE DASG+GIG VL Q+ IAY +KAL D + S YEK
 Sbjct 861 KQAMITTPVLALPNFSKEFIETDASGQIGAVLMQEGHP IAYISKALSDRFQTLSTYEK 920

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 E +A+++AI+ W YL D F I D +SL+YLL+QR+TT
 Sbjct 921 EMLAILMAIKKWSYLVDRHFVKTQDQSLKYLLEQRTVT 960

Score = 160 bits (405), Expect(3) = 2e-147
 Identities = 97/256 (37%), Positives = 146/256 (57%), Gaps = 5/256 (1%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDDKELQGISRPFWKD--ITKINEEVQK 3053
 QQ WVAKL+ Y++++I YK G N DALSR + EL +S I E
 Sbjct 963 QQAWVAKLMQYDYEIRYKQGENVAADALSRI-QPAELFVLSTTILNTQLYDLIKESWGV 1021

Query 3054 DPALAKIREELKDNLDSPQYITLECDILYFRGRVLVLLASSLWIPKLLQEFQTSMLMGHSG 3233
 DP L KI + + + ++P+Y+ + L +G+LV+ + ++L F S GGHSG
 Sbjct 1022 DPQLQKIIKAKEADPSAYPKYSWRGEELRRKGKLVVGVNEQLRREILNSFHDSPGTGGHSG 1081

Query 3234 IYITYRRITQSLYWIPIKGEITKFVVACHVGQRSKYQASSPAGLLQPLPIPNAIWEEISM 3413
 +Y+T +RI+ +YW ++ + ++V C V QR K + +GLLQPLP+P ++ +I+M
 Sbjct 1082 VVVTTKRISAVVYWKGLRKFVREYVRNCSVCQRFPENKPYSGLLQPLPVPEGVFTDITM 1141

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLLEVPISIVS 3587
 +FI G+ KS G I V VD+L+KY +F+++ HPY A+ + V + L +P SI
 Sbjct 1142 DFIEGLPKSNGKTAIFVVVDRLTKYGHFMLLPHPHYTAKMVAQVFLDSVYKLHGLPHSITC 1201

Query 3588 DSDLIFMSHFLQELFK 3635
 D D IF S F QE FK
 Sbjct 1202 DRDPIFTSVFWQEFFK 1217

>gi|225463073|ref|XP_002269644.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length=1168

Score = 250 bits (638), Expect(3) = 5e-147
 Identities = 134/257 (52%), Positives = 175/257 (68%), Gaps = 11/257 (4%)
 Frame = +3

Query 1644 NKEPRKLVVASTDRVCYSFSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRYPHLQKNEIK 1823
 N+E +K++ A D F P GLPP R+ DH+I +K A P N RPY+Y +QK+ I+
 Sbjct 228 NEELQKMLQAFAD----VFEEPTGLPPVRDYDHQIDLKDEAGPINCPRKYAAVQKDAIE 283

Query 1824 TLVVEML*LGIIRLSNSSSYSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELL 2003
 L+ EML G+IR S S Y+S V+LVK+KDGS RLC+DY+AL++ TV DKF IPV++ELL
 Sbjct 284 KLIGEMLHAGVIRQSRSPYASLVVLVKKKDGSWRLCVDYRALNQVTVKDKFPPIVIEELL 343

Query 2004 DELNGPIHFHFKIDLKARYHQIRMHKPF-----TFRTHQGHYESPVMFGLTNTPTTFQ*AM 2168
 +EL G FSKIDL++ Y QIRMH+P F+TH+GHYE VMPFGLTN P+TFQ M
 Sbjct 344 EELGGSTIFSKIDLSRGYVQIRMHEDVPKTAFTKTHEGMYEFLVMPFGLTNAPSTFQSLM 403

Query 2169 NATLKPFLLRRYVVVFDDILVYSKSWEAHLHLS*VLARLLEHYFFTNVFKKKCSFGQIK 2348
 N +P+LR++++VVFDDIL+YS+S+ H+ HLS L L E+ + KKC FG
 Sbjct 404 NNIFQPYLRKFLVVFDDILYRSFFDHIHLSIALQVLRENLLYAK--SKKCFGHSS 461

Query 2349 AGCLGHVISKEGVLMRP 2399
 LGHVIS GV P
 Sbjct 462 IEYLGHVISSGGVYTDP 478

Score = 165 bits (417), Expect(3) = 5e-147
 Identities = 85/160 (53%), Positives = 111/160 (69%), Gaps = 0/160 (0%)
 Frame = +2

Query 2396 AIL*WPMKPTPKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQL 2575
 A+ WP P T K LRGFL LTGY+R + +YGKIA+PL DLLK F W E S +A + L
 Sbjct 483 AVRDPWPTITLKLRLGFLGLTGYRRFVKDYGKIAKPLTDLKDAFWHTEGNSQAFMAL 542

Query 2576 QQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTDQRQIAYFNKALKDLTSLKSMYEK 2755
 +Q + T P L++ +FSK+F IE DASG+GIG VL Q+ IAY +KAL D + S YEK
 Sbjct 543 KQVMITAPVLALPNFSKEFIETDASGGIGAVLMQEGHPIAYISKALSDRFQTLSTYEK 602

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 E +A+++AI+ W YL D F I D +SL+YLL+QR+TT
 Sbjct 603 EMLAILMAIKKWEYIVDRHFVIKTDHQSLKYLLQQRVTT 642

Score = 156 bits (395), Expect(3) = 5e-147
 Identities = 96/256 (37%), Positives = 145/256 (56%), Gaps = 5/256 (1%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKD--ITKINEEVQK 3053
 QQ WVAKL+ Y++++I YK G N DALSR + EL +S I E
 Sbjct 645 QQAWWAKLMQYDYEIYKQKQKENVAAADALSRI-QPAELFVLSTTILNTQLYDLIKESWGV 703

Query 3054 DPALAKIREELKDNLDSPQYITLECDILYFRGRVLVLLASSLWIPKLLQEFQTSMLMGHSG 3233
 D L KI + + + ++P+Y+ + L +G+LV+ + ++L F S GGHSG
 Sbjct 704 DLELQKIIKAKEADPSAYPKYSWRGEELQKKGKLVVGVNEQLRREILNSFHDSPGTGGHSG 763

Query 3234 IYITYRRITQSLYWIPIKGEITKFVVACHVGQRSKYQASSPAGLLQPLPIPNAIWEEISM 3413
 +Y+T +RI+ +YW ++ + ++V C V QR K + +GLLQPLP+P ++ +I+M
 Sbjct 764 LYVTTKRISAVVYWKGLRKFVREYVRNCSVCQRFPENKPYSGLLQPLPVPEGVFTDITM 823

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLLEVPISIVS 3587
 +FI G+ KS G I V VD+L+KY +F+++ HPY A+ + V + L +P SI
 Sbjct 824 DFIEGLPKSNGKTTIFVVVDRLTKYGHFMLLPHPHYTAKMVAQVFLDSVYKLHGLPHSITC 883

Query 3588 DSDLIFMSHFLQELFK 3635
 D D IF S F QE FK
 Sbjct 884 DRDPIFTSVFWQEFFK 899

>gi|15451607|gb|AAK98731.1|AC090485_10 Putative retroelement [Oryza sativa Japonica Group]
 gi|108706172|gb|ABF93967.1| retrotransposon protein, putative, unclassified [Oryza sativa japonica cultivar-group]
 Length=1461

Score = 244 bits (624), Expect(3) = 3e-145
 Identities = 129/239 (53%), Positives = 158/239 (66%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRYPHLQKNEIKTLVEML*LGIIRLSNSS 1877
 F+ P GLPP R DH I +K G P VRPYRYP K+E++ M+ GI+R S+S+
 Sbjct 493 FTEPTGLPPQGRDHAIVLKQGTSPAVRFPYRYPAAHKDELERQCAAMISQGIIVRRSDSA 552

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFHFKIDLKARY 2057
 +SSPV+LVK+ D S R C+DY+AL+ TV D F IPV+ ELLDEL+G FSK+DL++ Y
 Sbjct 553 FSSPVLLVKKADSSWRFCVDYRALNALTVDKDAFPIPVVDELDELHARFFSKDLRLSGY 612

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMFGLTNTPTTFQ*AMNATLKPFLLRRYVVVFDD 2222
 HQ+RM HK FRTH G YE VMPFGL N P TFQ MN L+ FLRR+V+VFDD
 Sbjct 613 HQVRMRPEDIHKTAFRTHDGLYEFLVMPFGLCNAPATFQALMNDVLRSLRRFVLVFDD 672

Query 2223 ILVYSKSWEAHLHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP 2399
 IL+YS +W HL HL VL L EH F + + KC+FG LGHVIS GV M P
 Sbjct 673 ILIYSDTADHRLHRLRAVLTVLREHKLF--IKRSKCAFVDSVAYLGHVISAAGVAMDP 729

Score = 167 bits (424), Expect(3) = 3e-145
 Identities = 95/256 (37%), Positives = 148/256 (57%), Gaps = 8/256 (3%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRD--EDKELQGISRPFWKDITKINEEVQK 3053
 Q +WV KLLG++F + YK GA+N V DALSRD ED + +S P + I ++ +
 Sbjct 896 QHHWVGKLLGFDFTVEYKPGAANTVADALSRDTTEDASVVLVSAPRFDIERLRAQDV 955

Query 3054 DPALAKIREELKDNLDSDHPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSMLGGHSG 3233
 Sbjct 956 DPAL ++ E++ + P +++ ++ F GRL L +S + ++L+ GH G
 DPALVALQAEIRSGTRAGP-WSMADGMVLFAGRLYLPPASPLLEQVLRVHVEE---GHEG 1011

Query 3234 IYITRRITQSLYWIPIKGEITKFFVACHVQGRSKYQASSPAGLLQPLPIPNAIWEEISM 3413
 Sbjct 1012 + T R+ + ++ +K + FV C V QR K + PAGLL PLP+P +W ++++
 VQRTLHLRLRRDFHFPNMKSVVQDFVRTCEVCQRYKAHLQAPAGLLPLPVPQGVWTDVAL 1071

Query 3414 NFIVGMLKSKGDFVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIWLLEVPISIVS 3587
 Sbjct 1072 +F+ + + +G VIL VD+ SKY +FI + HPY A S+ V EI+ L VP S+VS
 DFVEALPRVRGKSVILTVVDRFSKYCHFIPLAHPYSAESVAQVFFAEIIVRLHGVQPSMVS 1131

Query 3588 DSDLIFMSHFLQELFK 3635
 Sbjct 1132 D D +F S F EL +
 DRDPVFTSAFWSELMR 1147

Score = 153 bits (387), Expect (3) = 3e-145
 Identities = 75/163 (46%), Positives = 107/163 (65%), Gaps = 0/163 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTKTLRGFLELTGYIKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
 Sbjct 733 +AI WP P++ + +RGFL L GYY++ + NYG IA PL LLK F W E + A
 QAIREWQPQRSARAVRGFLGLAGYRKFFVHNYGTIAAPLTALLKKEGFATEAATAAFDA 792

Query 2573 LQQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMYE 2752
 Sbjct 793 L+ A+++ P L+M DF+K F++ECDAS G G VL QD +A+F++ + + + YE
 LKAAVSSAPILAMPDFTKAFTECDASSHGFGAVLIQDGHPLAFFSRPVAPRRHALAAYE 852

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTP 2881
 Sbjct 853 +E + LVLA++HWRPYL FT+ D SL+YLLDQR++T P
 RELIGLVLAVRHWRPYLWGRHFTVKTDHYSKLYLLDQRLSTIP 895

>gi|27764548|gb|AAO23078.1| polyprotein [Glycine max]
 Length=1552

Score = 246 bits (628), Expect (3) = 6e-145
 Identities = 127/237 (53%), Positives = 160/237 (67%), Gaps = 7/237 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 Sbjct 573 F+ P LPP RE DH I +K G+ P VRPYRYPH QK++I+ ++ EML GII+ SNS
 FAVPASLPPQREQDHAIPKQSGSPVKVRPYRYPHTQKQDQIEKMIQEMLVQGIIQPSNSP 632

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 Sbjct 633 +S P++LVK+KDGS R C DY+AL+ TV D F +P + ELLDEL+G +FSK+DL++ Y
 FSLPILLVKKKGDSWRFC TDYRALNAITVKDSFPMP TVDELDELHGAQYFSKDLRLSGY 692

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 Sbjct 693 HQI + K FRTH GHYE VMPFGLTN P TFQ MN + LR++V+VVFDD
 HQILVQPEDREKTAFTFRTHGHYEWLVMPFGLTNAPATFQCLMKNKIFQFALRKFLVVFDD 752

Query 2223 ILVYSKSWEAHLHL*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVL 2393
 Sbjct 753 IL+YS SW+ HL HL VL L +H F + KCSFG + LGH +S GV M
 ILIYSASWKDHLKHLESVLQTLKQHLFARL--SKCSFGDTEVDVYLGHKVSGLGVSM 807

Score = 176 bits (447), Expect (3) = 6e-145
 Identities = 96/254 (37%), Positives = 150/254 (59%), Gaps = 7/254 (2%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDEDKELQGISRPFWKDITKINEEVQKDP 3059
 Sbjct 976 QQ W+ K LGY+F I YK G N+ DALSR + S P + ++ + DP
 QQAWLHKFLGYDFKIEYKPGKDNQAADALSRMF----MLAWSEPHSIFLEELRARLISDP 1031

Query 3060 ALAKIREELKDNLDSDHPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSMLGGHSGIY 3239
 Sbjct 1032 L ++ E K D+ YT+ +LY++ R+V+ A + K+LQE+ +S +GGH+GI
 HLKQLMETYKQGADAS-HYTVREGLLYWKDRVVPAAEEIIVNKILQEYHSSPIGGHAGIT 1090

Query 3240 IYITRRITQSLYWIPIKGEITKFFVACHVQGRSKYQASSPAGLLQPLPIPNAIWEEISMNF 3419
 Sbjct 1091 T R+ YW ++ ++ ++ C + Q++K + PAGLLQPLPIP +WE+++M+F
 RTLARLKAQFYWPWKQEDVKAYIQKCLICQQAASNNTLPAGLLQPLPIPQVWEDVAMDF 1150

Query 3420 IVGMLKSKGDFVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIVSDS 3593
 Sbjct 1151 I G+ S G VI+V +D+L+KY +FI +K Y ++ + + + I+ L +P SIVSD
 ITGLPNSFGLSVIMVMDRLTKYAHFIPLKADYNSKVVAAEFMSHIVKLHGIPRSIVSDR 1210

Query 3594 DLIFMSHFLQELFK 3635
 Sbjct 1211 D +F S F Q LFK
 DRVFTSTFWQHLEK 1224

Score = 142 bits (357), Expect (3) = 6e-145
 Identities = 75/161 (46%), Positives = 104/161 (64%), Gaps = 0/161 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTKTLRGFLELTGYIKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
 Sbjct 813 +A+L WP P K LRGFL LTGYI+R I +Y IA PL DLL+ +F WN ++ A ++
 QAVLDWPTPNNVKQLRGFLGLTGYIYRRFIKSYANIAGPLTDLLQKDSFLWNNEAAAFVK 872

Query 2573 LQQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMYE 2752
 Sbjct 873 L++A+T P LS+ DFS+ F +E DASG G+G VL Q+ IAYF+K L +S Y
 LKKAMTEAPVLSLPDFSQPFLETDASGIGVAVLGQNGHPIAYFSKKLAPRMQKQASAYT 932

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 Sbjct 933 +E +A+ A+ +R YL KF I DQ+SL+ L+DQ + T
 RELLATEALS KFRHYLLGNKFIIRTDQRLSLKSLMDQSLQT 973

>gi|242070717|ref|XP_002450635.1| hypothetical protein SORBIDRAFT_05g008466
 [Sorghum bicolor]
 gi|241936478|gb|EES09623.1| hypothetical protein SORBIDRAFT_05g008466 [Sorghum
 bicolor]
 Length=1507

Score = 251 bits (641), Expect (3) = 5e-144
 Identities = 131/239 (54%), Positives = 161/239 (67%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 Sbjct 566 F+ P GLPP R DH+I +K+GA P VRPYRYP K+E++ M+ GI+R S+S
 FADPTGLPPKRAHDHRTITLKAGAQPVAVRPYRYPAAHKDELERQCAAMIEQGIVRRSDSP 625

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 Sbjct 626 +SSPV+LVK+ DGS R C+DY+AL+ TV D F IPV+ ELLDEL+G F+K+DL++ Y
 FSSPVLLVKKPDGSRWFCVDYRALNALTVDKAFPIPVVDELDELHGAKEFTKDLRLSGY 685

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 Sbjct 686 HQ+RM HK FRTH G YE VM FGL N P TFQ MN L+PFLRR+V+VVFDD
 HQVRMRPEDVHKTAFTFRTHDGLYEFLVMAFGLCNAPATFQALMNDVLRPFLRRFVLVVFDD 745

Query 2223 ILVYSKSWEAHLHL*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMP 2399
 Sbjct 753 IL+YS++W HL HL VL L H F V + KCSFG LGHVIS GV M P

Sbjct 746 ILIYSRTWADHLRHLRAVLDELQHHQLF--VKRSKCSFGAPSVAYLGHVISAAGVAMDP 802

Score = 164 bits (414), Expect(3) = 5e-144
Identities = 99/256 (38%), Positives = 147/256 (57%), Gaps = 9/256 (3%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDD-EDKELQGISRPFWKDITKINEEVQKD 3056

Sbjct 969 QHHWVGKLLGDFDSVEYRSGATNVVADALSRDDTEGAAMASAPRFDLIDRLRHAQATD 1028

Query 3057 PALAKIREELKDNLDSDHPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSIMG-GHSG 3233

Sbjct 1029 PALVALYAEVRSRGARAAP-WALVDGMLTYDGRLYIPPTS----PLLQEVVAIHNHDGHEG 1083

Query 3234 IYITYRRITQSLYWIPIKGEITKFFVACHVQGRSKYQASSPAGLLQPLPIPNAIWEIEISM 3413

Sbjct 1084 VHTLHRLRRDFHFFSMRRVQAFVQACGTCQQYKSDHLRPAAGLLQPLPVPASVWADIGI 1143

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLVEVPISIVS 3587

Sbjct 1144 DFIEALPKVQKGTVILSVDRFSKYCHFIPLAHPYTAESVAQAFFADVRLHGVQPSIVS 1203

Query 3588 DSDLIFMSHFLQELFK 3635

Sbjct 1204 DRDPVFTSAFWQELMR 1219

Score = 146 bits (369), Expect(3) = 5e-144
Identities = 71/163 (43%), Positives = 105/163 (64%), Gaps = 0/163 (0%)
Frame = +2

Query 2393 EAIL*WPMKPTKPTLGRFLELTGYIKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572

Sbjct 806 QAIHDWPAPRSVRAVRGFLGLAGYYRKFFVHGYGALAAPLSALLKKEGFSWDDAAASAFAA 865

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKIGVVLTDQRKQIAYFNKALKDLTLKSKSMYE 2752

Sbjct 866 LKAAVTSAPVLAMPDFTKLFTVECDASTVGFGAVLTQEGHPVAFFSRPVAPRHRALAAEY 925

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTOP 2881

Sbjct 926 RELIGLVQAVRHRWPYLVGRSFIVKTDHYSKLYLLDQRLATIP 968

>gi|242095940|ref|XP_002438460.1| hypothetical protein SORBIDRAFT_10g020018
[Sorghum bicolor]
gi|241916683|gb|EER89827.1| hypothetical protein SORBIDRAFT_10g020018 [Sorghum
bicolor]
Length=1437

Score = 243 bits (620), Expect(3) = 1e-143
Identities = 124/239 (51%), Positives = 157/239 (65%), Gaps = 7/239 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVPRYPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877

Sbjct 486 FAEVGLPPPRTRDHSIVLKTGALPVAVRPYRYPAAHKKDELERQCATMMEQGIVRRSDSA 545

Query 1878 YSSPVILVKKRDKGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057

Sbjct 546 FSSPVLLVKKPDGSRWFCVDYRALNALTIKDAFPIPVVDELDELHGACYFTKLDLRSYG 605

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFVFFDD 2222

Sbjct 606 HQVRMRPADIHKTAFHHTDGLYEFVMAFGLCNAPATFQALMNDVLRPFLRRFVLFVFFDD 665

Query 2223 ILVYSKSWEAHLHDLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMP 2399

Sbjct 666 ILIYSSTWADHLRHLRAVDELQRHKLFLK--RSKCAFAAASVAYLGHVISAAGVAMDP 722

Score = 163 bits (412), Expect(3) = 1e-143
Identities = 92/256 (35%), Positives = 146/256 (57%), Gaps = 8/256 (3%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDD-EDKELQGISRPFWKDITKINEEVQK 3053

Sbjct 889 QHHWVGKLLGDFDTVEYKPGHNSAVADALSRDDTVEEGTVLVLSAPRFEFVQRLRQAHAT 948

Query 3054 DPALAKIREELKDNLDSDHPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSIMGGHSG 3233

Sbjct 949 DPALVALQQEISAGTRALP-WALSDGLVTYSGRLYLPPAS---PLLQEALRAVHEEGHEG 1004

Query 3234 IYITYRRITQSLYWIPIKGEITKFFVACHVQGRSKYQASSPAGLLQPLPIPNAIWEIEISM 3413

Sbjct 1005 VQRTLHRLRRDFHFFHMKTVVQDFVRGCSICQRHKEHLHPAGLLPLPVPQGVSDIAM 1064

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLVEVPISIVS 3587

Sbjct 1065 DFVEALPRVKGKSVILTVDVDRFSKYCHFIPLAHPYSAEGVAQAFFADVRLHGIPQSIIVS 1124

Query 3588 DSDLIFMSHFLQELFK 3635

Sbjct 1125 DRDTVFTSNFWRELMR 1140

Score = 154 bits (389), Expect(3) = 1e-143
Identities = 74/163 (45%), Positives = 107/163 (65%), Gaps = 0/163 (0%)
Frame = +2

Query 2393 EAIL*WPMKPTKPTLGRFLELTGYIKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572

Sbjct 726 QAVRDWPQPRSAVARVGRFLGLAGYYRKFFVHNYGTIAAPLTALLKKGDFSWSAEAAAFDA 785

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKIGVVLTDQRKQIAYFNKALKDLTLKSKSMYE 2752

Sbjct 786 LKDAVTSAPVLAMPDFSQFVVECDASSHGFGAVLVHEGHPIAFFSRPVAPRHRQALAAEY 845

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTOP 2881

Sbjct 846 RELIGLVHAVRHRWPYLVGRSFIVKTDHYSKLYLLDQRLSTIP 888

>gi|242065034|ref|XP_002453806.1| hypothetical protein SORBIDRAFT_04g018075
[Sorghum bicolor]
gi|241933637|gb|EES06782.1| hypothetical protein SORBIDRAFT_04g018075 [Sorghum
bicolor]
Length=1414

Score = 243 bits (620), Expect(3) = 2e-142
Identities = 128/239 (53%), Positives = 159/239 (66%), Gaps = 7/239 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNS 1877
 Sbjct 446 F+ P G+PP R DH I +K G+ P VRPYRYP K+E++ M+ GI+R S+S+ 505
 FTEPSGMPPPRRARDHAITLPGSAPVVVRPYRPAHKDELERQCTAMIQQGIVRRSDSA

Query 1878 YSSPVILVKRDKGS*RLCMDYQALSKATVPDKFLIPVMKELDELNGPIHFSKIDLKARY 2057
 Sbjct 506 +SSPV+LVK+ DGS R C+DY+AL+ TV D F IPV+ ELLDEL+G F+K+DL++ Y 565
 FSSPVLLVKKADGSGWRFCVDYRALNALTVDKDAFPIPVDELDELHGARFFTKLDRSGY

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 Sbjct 566 HQ+RM HK FRTH G YE VMPFGL N P TFQ MN L+ +LRR+V+VVFDD 625
 HQVRMPEDVHKTAFRTHDGLYEFLVMPFGLCNAPATFQALMNDVLRAYLRRFVLVVFDD

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMP 2399
 Sbjct 626 IL+YS +W HL HL VL L H F V + KCSFG LGHVIS GV M P 682
 ILIYSTTWADHLRHLRVLDILRRHRLF--VKRSKCSFGVSSVAYLGHVISAAGVAMP

Score = 163 bits (412), Expect(3) = 2e-142
 Identities = 96/259 (37%), Positives = 149/259 (57%), Gaps = 12/259 (4%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRREDKE----LQGISRPFWKDITKINEEV 3047
 Sbjct 849 Q +WV KLLG++F + YK GASN V DALSRD +++ LQ IS P + I ++ 908
 QHHWVGKLLGDFTFVEYKSGASNTVADALSRDTEDESVGGIQAISAPRFDIARLRHAQ

Query 3048 QKDPALAKIREELKDNLDSPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSI-MGG 3224
 Sbjct 909 DPAL I ++++ + P +T+ ++ + GRL + SS L+QE ++ G 963
 ATDPAVLTIHDDIRAGSRAAP-WTVADGMVLYDGRLYIIPSS----PLVQEIVA AVHYDG

Query 3225 HSGIYITYRRITQSLYWIPIKGEITKFVAVCHVGQSKYQASSPAGLLQPLPIPNAIWEE 3404
 Sbjct 964 H G+ T R+ + ++ ++ + FV AC QR K + PAGLL PLP+P +W + 1023
 HEGVQRTLHRLRRDFHFPQMRIVQDFVRACVTCQRYKSEHLLPAGLLPLPVPTVVWAD

Query 3405 ISMNFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIWLLEVPIS 3578
 Sbjct 1024 I ++F+ + + +G VIL VD+ SKY +FI + HPY A ++ +I+ L VP S 1083
 IGLDFVEALPRVQGSVILTVDRFSKYCHFIALAHPTYAETVAQAFFTDIVRLHGVP

Query 3579 IVSDSDLIFMSHFLQELFK 3635
 Sbjct 1084 +VSD D +F S F +EL + 1102
 MVSDRDPVFTSAFWRELMR

Score = 150 bits (378), Expect(3) = 2e-142
 Identities = 75/163 (46%), Positives = 105/163 (64%), Gaps = 0/163 (0%)
 Frame = +2

Query 2393 EAIL*WMPKTPKTLRGFLLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASI 2572
 Sbjct 686 +AI WP P++ + +RGFL L GYY++ + NYG IA PL LLK F W ++ A 745
 QAIHDWPQPSRAVRGFLGLAGYRKFFVHNYGAIAPLTALLKKKEGFTWGAEAEAFSA

Query 2573 LQQAITTIPTLSMLDFSQKQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYE 2752
 Sbjct 746 L+ A+T+ P L++ DFSK F +ECDAS G G VL Q+ IA+F++ + S + YE 805
 LKGAVTSAPVLTLPDFSKPFIVECDASTYGFAGVLIQEGHPIAFFSRPVAPRHRSLAAYE

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRIITQP 2881
 Sbjct 806 +E + LVLA++HWRPYL +F + D SL+YLLDQR+ T P 848
 RELIGLVLA VRHWRPYLWGRRFIVKTDHYSKLYLLDQRLATIP

>gi|225432842|ref|XP_002279912.1| PREDICTED: similar to polyprotein [Vitis
 vinifera]
 Length=1528

Score = 259 bits (661), Expect(3) = 7e-140
 Identities = 131/240 (54%), Positives = 166/240 (69%), Gaps = 7/240 (2%)
 Frame = +3

Query 1695 SFGPKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNS 1874
 Sbjct 547 +F+ P LPP R+DH+I + P NVRPYRYPH QK EI+ LV EML GIIR S + 606
 NFAPSSSLPPQRQLDHRIPLLPNTTPVNVRPYRYPHFQKEEIEKLVGEMLRDGIIRPSTN

Query 1875 SYSSPVILVKRDKGS*RLCMDYQALSKATVPDKFLIPVMKELDELNGPIHFSKIDLKAR 2054
 Sbjct 607 +SSPV+LVK+KDG+ R C+DY+AL+ TV D+F IP + ELLDEL G FSK+DL+A 666
 PFSSPVLLVKKKGDTWRFCVDYRALNAVTVKDRFP IPTVDELDELGYASVFSKLDLRAG

Query 2055 YHQIRMHKP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2219
 Sbjct 667 YHQ+R+H P FRTH+GHYE VMPFGL+N P+TFQ MN+ + LR++V+VVFDD 726
 YHQVRIHPPDIETKTAFRTHGHEHYEFVMPFGLSNAPSTFQALMNSVFRDLRKFVLVVFDD

Query 2220 DILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMP 2399
 Sbjct 727 DILVYSKSWE H HL V + L H F + KC FG ++ LGH IS +GV + P 784
 DILVYSKSWEDHQHLEMFVSVLASHSLFAKL--SKCEFGCVSELSYLGHRISDQGVAVEP

Score = 162 bits (411), Expect(3) = 7e-140
 Identities = 97/256 (37%), Positives = 141/256 (55%), Gaps = 6/256 (2%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRREDKE--ELQGISRPFWKDITKINEEVQK 3053
 Sbjct 951 QQ W+ KLLG++FDI Y+ G N+ DALSR E LQ +S+P + E Q+ 1010
 QQKWLTKLLGDFDICRYRGRENQPADALSRLVEHTYMAIQIVSKPVMAIWALKEFYQQ

Query 3054 DPALAKIREELKDNLDSPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSIMGGHSG 3233
 Sbjct 1011 P A + + + D Y + +L+F G++V+ S +L EF + +GGH+G 1068
 HPESAHLMQSAQQ--DDSTGYAVREGLLWFNGKVVPDPSALQRLILIEFHNTPVGGHAG

Query 3234 IYITYRRITQSLYWIPIKGEITKFVAVCHVGQSKYQASSPAGLLQPLPIPNAIWEEISM 3413
 Sbjct 1069 + T RI YW ++ + FV C V Q K +P GLLQPLPIP IW+ ISM 1128
 MQRTLRSIASMFYWPQMRQLVRDFVARCQVCQAIFKPFNKAPQGLLQPLPIPQGIWDSISM

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSI--VDVKEIWLLEVPISIVS 3587
 Sbjct 1129 +F+ + + G VI+V VD+LSK +F V+ + A + + +KEI+ L P +I+ 1188
 DFTVTHLPPASGKSVIMVVDRLSKQAHFAVLPSAFNAPMVAALFIKEIVRLHGFPPTTIIP

Query 3588 DSDLIFMSHFLQELFK 3635
 Sbjct 1189 D D +FMS F QELFK 1204
 DQDPVFMSFQELFK

Score = 126 bits (316), Expect(3) = 7e-140
 Identities = 71/160 (44%), Positives = 90/160 (56%), Gaps = 0/160 (0%)
 Frame = +2

Query 2396 AIL*WMPKTPKTLRGFLLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQL 2575
 Sbjct 789 AI WP+P T K LRGL L GYY+R + Y PL LL F W +++ A L 848
 AIQKWPLPATIKELRGFLGLCGYRRFVYRYASTTAPLTKLLCKNAFVWTKATGAFEAL

Query 2576 QQAITTIPTLSMLDFSQKQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYEK 2755
 Sbjct 849 + A+ T P L+M DFS F ++ DASG GIG VL Q IAYF+K L +S Y + 908
 KHALATTPVLAMPDFSNFVLQTDASGSGIGAVLVQKGHP IAYFSKELPSKLRRSAYCR

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRIIT 2875
 Sbjct 909 E A+ AIQ WR YL +F + D +SLR L +Q I T 948
 EMFAITEAIQKWRQYLLGRRFIVETDQSLRALHNTIQT

>gi|115457692|ref|NP_001052446.1| Os04g0316700 [Oryza sativa (japonica cultivar-group)]
Length=1605

Score = 250 bits (639), Expect(3) = 2e-139
Identities = 125/236 (52%), Positives = 164/236 (69%), Gaps = 7/236 (2%)
Frame = +3

Query 1707 PKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSSSYSS 1886
Sbjct 666 PKGLPP R DH I +KSGA P N+RPYR PH QK ++ ++ E++ I++S+ YSS
PKGLPPRRNCDHVITLKS GAEPNLRPYRVPHYQKEAMEKIIAELIESKEIQVSDIPYSS 725

Query 1887 PVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELDELNGPIHFSKIDLKARYHQI 2066
Sbjct 726 PAVMVRKKDGSWRLCVDYRQLNAQT VKNKFPMP IIEDLLDELNGAKVFSKDLRSGYHQI 785

Query 2067 RM-----HKPTFRTHQGHYESPVMFGLTNTPTTFQ*AMNATLKPFLRRYVVFDDILV 2231
Sbjct 786 RM K FRTH GHYE VMPFGLTN PTTFQ MN L PFLR+YV+VFFDDIL+
RMA TQDIPKTA FRTHLGHYEYQVMPFGLT NAPTTFQSLMNQVLAPFLRKYVLVFFDDILI 845

Query 2232 YSKSWEAHL D H L S *V L A R L L E H Y F F T N V F K K C S F G Q I K A G C L G H V I S K E G V L M R P 2399
Sbjct 846 YSK W H +H+ V+ L E+ + K K C + F G L G H + I S + + G V P
Y S K D W A E H K E H I R Q V M K V L E E N K L V V K L -- K K C A F G L P S V T Y L G H I I S Q D G V A T D P 899

Score = 157 bits (397), Expect(3) = 2e-139
Identities = 88/254 (34%), Positives = 139/254 (54%), Gaps = 2/254 (0%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKDITKINEEVQKDP 3059
Sbjct 1066 Q + KL+ Y++ I YK G N V DALSR ++ Q I+ + + I + D
Q H K L L L K L M E Y D Y S I E Y K A G K E N L V A D A L S R I P P A E Q C Q A I T T V I P E W R D I Q R S Y E G D V 1125

Query 3060 ALAKIREELKDNLD SHPQY T L E C D I L Y F R G R L V L L A S S L W I P K L L Q E F Q T S L M G G H S G I Y 3239
Sbjct 1126 K I + D+ Y+ E +L ++GR+ + ++ +L++ + +S GGHSG+
Q A H K I L S L I G T E G D T D G S Y S Q E A G L L R Y K G R I Y V G E N T E I R E E L I R S Y H S S A F G G H S G M R 1185

Query 3240 I T Y R R I T Q S L Y W I P I K G E I T K F V V A C H V G Q R S K Y Q A S S P A G L L Q P L P I P N A I W E E I S M N F 3419
Sbjct 1186 T Y R I Y W +K + F+ C + Q +K + G L L P L +P+ W I +M+ F
A T Y H R I K S L F Y W P G L K K A V E G F I R E C P I C Q V T K A E H I H I P G L L D P L E V P D M A W A H I T M D F 1245

Query 3420 I V G M L K S K G F D V I L V E V D K L S K Y R Y F I V I K H P Y F A R S I V D -- V K E I I W L L E V P I S I V S D S 3593
Sbjct 1246 + G+ K S G D V I L V V D +L+K Y +F I + H P Y +V+ + I L +P++I++D
V E G L P K S N G K D V I L V V D R L T K Y A H F I A M A H P Y T V E Q V V E L F M N N I H R L H G M P M A I T D R 1305

Query 3594 D L I F M S H F L Q E L F K 3635
Sbjct 1306 D I F S Q E + F K
D R I F T S Q L F Q E I F K 1319

Score = 139 bits (349), Expect(3) = 2e-139
Identities = 70/159 (44%), Positives = 104/159 (65%), Gaps = 0/159 (0%)
Frame = +2

Query 2393 E A I L * W P M P K T P K T L R G F L E L T G Y Y K R S I C N Y G K I A R P L I D L L K * G N F K W N E D S I K A S I Q 2572
Sbjct 903 E I +P PK+ L R F L +T G Y Y +R I N Y G + R P L D +L K F +W + +A
E K I A T Y P T P K S V T D L R K F L G M T G Y Y R R F I K N Y G I V C R P L H D M L K K E G F Q W E R E Q T E A F E T 962

Query 2573 L Q Q A I T T I P T L S M L D F S K Q F S I E C D A S G K G I G V V L T Q D R K Q I A Y F N K A L K D L T L S K S M Y E 2752
Sbjct 2573 L + + T P L S + D F +K +F I E D A G G I G V L Q + +A Y F +K L ++S +Y E

Sbjct 963 L K T H M C T S P V L S L P D F T K E F V I E A D A C G N G I G A V L M Q S G R P L A Y F S K T L G P K A A A Q S I Y E 1022

Query 2753 KESMALVLA IQHW RPYLPD*KFTIYIDQKSLRYLLDQRI 2869
Sbjct 1023 KE+MA++ A++ WR Y+ + I DQ+SL+++++QR+
KEAMAILEALKWRHYVLGSRLLIKTDQQSLKFMMNQRL 1061

>gi|32492359|emb|CAE05990.1| OSJNBa0004L19.22 [Oryza sativa (japonica cultivar-group)]
Length=1586

Score = 250 bits (639), Expect(3) = 2e-139
Identities = 125/236 (52%), Positives = 164/236 (69%), Gaps = 7/236 (2%)
Frame = +3

Query 1707 PKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSSSYSS 1886
Sbjct 666 PKGLPP R DH I +KSGA P N+RPYR PH QK ++ ++ E++ I++S+ YSS
PKGLPPRRNCDHVITLKS GAEPNLRPYRVPHYQKEAMEKIIAELIESKEIQVSDIPYSS 725

Query 1887 PVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELDELNGPIHFSKIDLKARYHQI 2066
Sbjct 726 PAVMVRKKDGSWRLCVDYRQLNAQT VKNKFPMP IIEDLLDELNGAKVFSKDLRSGYHQI 785

Query 2067 RM-----HKPTFRTHQGHYESPVMFGLTNTPTTFQ*AMNATLKPFLRRYVVFDDILV 2231
Sbjct 786 RM K FRTH GHYE VMPFGLTN PTTFQ MN L PFLR+YV+VFFDDIL+
RMA TQDIPKTA FRTHLGHYEYQVMPFGLT NAPTTFQSLMNQVLAPFLRKYVLVFFDDILI 845

Query 2232 YSKSWEAHL D H L S *V L A R L L E H Y F F T N V F K K C S F G Q I K A G C L G H V I S K E G V L M R P 2399
Sbjct 846 YSK W H +H+ V+ L E+ + K K C + F G L G H + I S + + G V P
Y S K D W A E H K E H I R Q V M K V L E E N K L V V K L -- K K C A F G L P S V T Y L G H I I S Q D G V A T D P 899

Score = 157 bits (397), Expect(3) = 2e-139
Identities = 88/254 (34%), Positives = 139/254 (54%), Gaps = 2/254 (0%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKDITKINEEVQKDP 3059
Sbjct 1066 Q + KL+ Y++ I YK G N V DALSR ++ Q I+ + + I + D
Q H K L L L K L M E Y D Y S I E Y K A G K E N L V A D A L S R I P P A E Q C Q A I T T V I P E W R D I Q R S Y E G D V 1125

Query 3060 ALAKIREELKDNLD SHPQY T L E C D I L Y F R G R L V L L A S S L W I P K L L Q E F Q T S L M G G H S G I Y 3239
Sbjct 1126 K I + D+ Y+ E +L ++GR+ + ++ +L++ + +S GGHSG+
Q A H K I L S L I G T E G D T D G S Y S Q E A G L L R Y K G R I Y V G E N T E I R E E L I R S Y H S S A F G G H S G M R 1185

Query 3240 I T Y R R I T Q S L Y W I P I K G E I T K F V V A C H V G Q R S K Y Q A S S P A G L L Q P L P I P N A I W E E I S M N F 3419
Sbjct 1186 T Y R I Y W +K + F+ C + Q +K + G L L P L +P+ W I +M+ F
A T Y H R I K S L F Y W P G L K K A V E G F I R E C P I C Q V T K A E H I H I P G L L D P L E V P D M A W A H I T M D F 1245

Query 3420 I V G M L K S K G F D V I L V E V D K L S K Y R Y F I V I K H P Y F A R S I V D -- V K E I I W L L E V P I S I V S D S 3593
Sbjct 1246 + G+ K S G D V I L V V D +L+K Y +F I + H P Y +V+ + I L +P++I++D
V E G L P K S N G K D V I L V V D R L T K Y A H F I A M A H P Y T V E Q V V E L F M N N I H R L H G M P M A I T D R 1305

Query 3594 D L I F M S H F L Q E L F K 3635
Sbjct 1306 D I F S Q E + F K
D R I F T S Q L F Q E I F K 1319

Score = 139 bits (349), Expect(3) = 2e-139
Identities = 70/159 (44%), Positives = 104/159 (65%), Gaps = 0/159 (0%)
Frame = +2

Query 2393 E A I L * W P M P K T P K T L R G F L E L T G Y Y K R S I C N Y G K I A R P L I D L L K * G N F K W N E D S I K A S I Q 2572

Sbjct 903 E I +P PK+ LR FL +TGY+R I NYG + RPL D+LK F+W + +A
EKIATYPTPKSVTDLRKFLGMYRRFKNYGI VCRPLHDLKKKEGFQWEREQTEAFET 962

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDILTSLKSMYE 2752
L+ + T P LS+ DF+K+F IE DA G GIG VL Q + +AYF+K L ++S+YE

Sbjct 963 LKTHMCTSPVLSLPDFTKEFVIEADACGNGIGAVLMQSGRPLAYFSKTLGPKAAQSIYE 1022

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
KE+MA++ A++ WR Y+ + I DQ+SL++++QR+

Sbjct 1023 KEAMAILEALKKWRHYVLGSRLIKTDQQLKFMNQL 1061

>gi|115438795|ref|NP_001043677.1| Os01g0640000 [Oryza sativa (japonica cultivar-group)]
Length=1660

Score = 241 bits (614), Expect (3) = 2e-139
Identities = 125/253 (49%), Positives = 167/253 (66%), Gaps = 7/253 (2%)
Frame = +3

Query 1650 EPRKLVVASTDRVCYSFSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRYPHLQKNEIKTL 1829
+P L+ D + F+ P GLPP R + H+I +++G VRPYRY H+QK+E++

Sbjct 648 QPGDLMTDLLDLVKDLFTPEPHGLPPERHLCHRIRLEAGVSAVAVRPYRYAHQKDELERQ 707

Query 1830 VVEML*LGIIRLSNSSYSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDE 2009
+ML G+IR S+S++SSP +L+K+ DGS R C+DY+AL+ T+ DKF IPV +EL DE

Sbjct 708 CDDMLRHGVIRPSSSAFSSPALLIKKCDGSRFCVDYRALNDKTIKDKFPIPVAEELFDE 767

Query 2010 LNGPIHFSKIDLKARYHQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNA 2174
L G F+K+D+++ YHQ+ M HK FRTHQG +E VMPFGLTN P TFQ MN

Sbjct 768 LRGAKEFTTKLDMRSGYHQVLMHPDDVHKTAFRTHQGLFEFLVMPFGLTNPATFQALMND 827

Query 2175 TLKPLRRYVVVFFDDILVYSKSWEAHLDLHS*VLARLLEHYFFTNVFKKCSFGQIKAG 2354
L PFLRR+V+VFFDDIL+YS SW HL H+ VL L +H ++ + KC FG

Sbjct 828 VLLPFLRRFVLVFFDDILYSSSWSEHLRHVRTVLQTLQDHCLE--HLKRSKCEFGLTSA 885

Query 2355 CLGHVISKEGVLM 2393
LGHVIS +GV M

Sbjct 886 YLGHVISGDGVAM 898

Score = 153 bits (386), Expect (3) = 2e-139
Identities = 74/163 (45%), Positives = 108/163 (66%), Gaps = 0/163 (0%)
Frame = +2

Query 2393 EAIL*WPMPTKPTKTLRGFLELTGYIKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572
+A+L WP+PKT + +RGFL L GYY+R I ++G IA PL LL+ F+W++++ A +

Sbjct 904 QAVLDWPVKTAVRAVRGFLGLAGYRRFIRDFGAIAAPLTALLRKEGFRWSDEAAAFRK 963

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDILTSLKSMYE 2752
LQ A+T P L + DF++ F +ECDASG G+G VL Q +A+F+ + + YE

Sbjct 964 LQHALTAAPVLQLPDFNRDFIVECDASGTGLGAVLHQGGGPVAFFSMPAPRAHAKLAAYE 1023

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRIITQ 2881
+E + LV A++HWRPYL +F I D SLR+LLDQR++T P

Sbjct 1024 RELIGLVKAVRHWRPYLWGRRFIIRTDHYSRLRFLDLQRLSTIP 1066

Score = 152 bits (384), Expect (3) = 2e-139
Identities = 92/255 (36%), Positives = 142/255 (55%), Gaps = 7/255 (2%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDED-KELQGISRPFWKDITKINEEVQKD 3056
Q +W +KLLG++F + YK G +N V DALSRDE E +S P + + + EV

Sbjct 1067 QHHWASKLLGFDFAVEYKPGTANVVADALSRRDEHLAEAFVLSAPHFSLDDVVRREVAST 1126

Query 3057 PALAKIREELKNDLSHPQYITLEDILYFRGLVLLASSLWIPKLLQEFQTSMLGGHSGI 3236
P+LA +R+++ P + + ++ + R+ + SS +P +L+ GH G

Sbjct 1127 PSLASLRDDIIRGAKP-PPWAFKDLGLVLKDRVFIPESSPLLPAVLELAHG---GHEGT 1182

Query 3237 YITYRRITQSLYWIPIKGEITKFFVACHVQQRSKYQASSPAGLLQPLIPINAIWEEISMN 3416
T R+ + + + FV AC QR+K + PAGLLQ LP+P+A+W +I+M+

Sbjct 1183 QKTMFRLRADHFVPRDRVLVQDFVRACLTQCRNKTEHLQPAQLLQSLPVP SAVWADIAM 1242

Query 3417 FIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIILWLEVPISIVSD 3590
F+ G+ + G VIL VD+ SK+ +FI + HPY A ++ +I+ L VP SIVSD

Sbjct 1243 FVEGLPRVHGKTIVILTVDRFSKFAHFIPLSHPYTATTVAFAFFGDIVRLHGVPSIVSD 1302

Query 3591 SDLIFMSHFLQELFK 3635
D +F S F ELF+

Sbjct 1303 RDPVFTSKFWTELFR 1317

>gi|115481476|ref|NP_001064331.1| Os10g0317000 [Oryza sativa (japonica cultivar-group)]
gi|15217201|gb|AAK92545.1|AC051624_3 Putative retroelement [Oryza sativa Japonica Group]
gi|31431040|gb|AAP52878.1| retrotransposon protein, putative, unclassified, expressed [Oryza sativa (japonica cultivar-group)]
gi|113638940|dbj|BAF26245.1| Os10g0317000 [Oryza sativa Japonica Group]
Length=1476

Score = 232 bits (591), Expect (3) = 1e-138
Identities = 122/239 (51%), Positives = 157/239 (65%), Gaps = 7/239 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRYPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
F+ P+GLPP R DH I + GA P VRPYRYP K+E++ M+ G+IR S S+

Sbjct 508 FAEPRLGPPPRGRDHAIHLLPGAPPVAVRPYRYPVAHKDELERQCAVMMEQGLIRRSTSA 567

Query 1878 YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
+SSPV+LVK+ DGS R C+DY+AL+ T+ D + IPV+ ELLDEL+G F+K+DL++ Y

Sbjct 568 FSSPVLLVKKADGSRFCVDYRALNAITIKDAYPIPVVDELDELHGAKFTTKDLRSGY 627

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFFDD 2222
HQ+RM K FRTH G YE VMPFGL N P TFQ MN L+ +LRR+V+VFFDD

Sbjct 628 HQVRMAEDVAKTAFRTHDGLYEFLVMPFGLCNAPATFQALMNDILRIYLRRFVLVFFDD 687

Query 2223 ILVYSKSWEAHLDLHS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMRP 2399
IL+YS +W HL H+ VL L +H F V + KC+FG LGH+I GV M P

Sbjct 688 ILIYNTWADHLRHIRAVLLLRQHRLF--VKRSKCAFGVSSISYLGHIIATGVSMDP 744

Score = 159 bits (402), Expect (3) = 1e-138
Identities = 93/255 (36%), Positives = 143/255 (56%), Gaps = 7/255 (2%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDEDK-ELQGISRPFWKDITKINEEVQKD 3056
Q +WV KLLG++F + YK GASN V DALSRD D+ + +S P + I ++ +

Sbjct 911 QHHWVGKLLGFDFTEYKSGASNVVADALSRRDTEGAVALSAPRFDYIERLRAAQTTTE 970

Query 3057 PALAKIREELKNDLSHPQYITLEDILYFRGLVLLASSLWIPKLLQEFQTSMLGGHSGI 3236
PAL IR+ ++ S P + L ++ F RL + SS + ++L T GH G+

Sbjct 971 PALVAIRDAIQAGTRSAP-WALRDGMVMFDSRLYIPSSPLLHEILAAIHTD---GHEGV 1026

Query 3237 YITYRRITQSLYWIPIKGEITKFVVACHVGQRSKYQASSPAGLLQPLPIPNAIWEISMN 3416
T R+ + + ++ + +FV AC QR+K + P GLL PLP+P +W +I ++

Sbjct 1027 QRTLHRLRRDFHSPAMRRVQEFVRACDTCQRNKSEHLHPGGLLLPLPVPPTTVWADIGLD 1086

Query 3417 FIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLVEPISIVSD 3590
F+ + + G VIL VD+ SKY +FI + HPY A S+ +I+ L +P S+VSD

Sbjct 1087 FVEALPRVGGKTVILTVDRFSKYCHFIPLAHPYTAESVAQAFYADIVRLHGIPQSMVSD 1146

Query 3591 SDLIFMSHFLQELFK 3635
D +F S F +EL +

Sbjct 1147 RDPVFTSSFWRELMR 1161

Score = 152 bits (384), Expect (3) = 1e-138
Identities = 73/163 (44%), Positives = 107/163 (65%), Gaps = 0/163 (0%)
Frame = +2

Query 2393 EAIL*WPMKPTKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
+A++ WP P++ +T+RGFL L GYY++ +YG IA PL L K F+W+++ A

Sbjct 748 QAVVDWPQPSARTVRGFLGLAGYRKVFVHDYGTIAAPLTALTKKEGFRWSDEVATAFHA 807

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYE 2752
L+ A+TT P L++ DF K F +ECDAS G G VL QD+ +A+F++ + + + YE

Sbjct 808 LKHAVTTAPVLAALPDFVKPFVVECDASTHGFGAVLLQDKHPLAFFSRPVAPRHRALAAE 867

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTP 2881
+E + LVLAH+HWRPYL F + D SL+YLLDQR+ T P

Sbjct 868 RELIGLVLAIRHWRPYLWGRAFVVRTDHSYSLYLLDQRLATIP 910

>gi|115462807|ref|NP_001055003.1| Os05g0241900 [Oryza sativa (japonica cultivar-group)]
gi|53981172|gb|AAV24812.1| putative polyprotein [Oryza sativa Japonica Group]
Length=1475

Score = 253 bits (645), Expect (3) = 2e-138
Identities = 125/236 (52%), Positives = 167/236 (70%), Gaps = 7/236 (2%)
Frame = +3

Query 1707 PKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSSYSS 1886
PKGLPP RE DH I ++SAG P N+RPYR PH QK ++ ++ E++ I+ S+S YSS

Sbjct 551 PKGLPPKRECDHVINLQSGAVPPNIRPYRVPHYQKEAMENIINELIESKEIQTSDSPYSS 610

Query 1887 PVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARYHQI 2066
P ++V++KDGS R+C+DY+ L+ TV +KF +P++++LLDELNG FSK+DL++ YHQI

Sbjct 611 PAVMVRKKDGSWRMCVDYRQLNAQTVKNKFPMPPIEDLLDELNGARISFKDLRLSGYHQI 670

Query 2067 RM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDDILV 2231
RM HK FRTH GHYE VMPFGLTN P TFQ MN L PFLRR+V+VFFDDIL+

Sbjct 671 RMAEKDVHKTAFRTHLGHYEYQVMPFGLTNDPATFQSLMNHVLAPFLRRFVLVFFDDILI 730

Query 2232 YSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP 2399
YSK+ HL+H+ V+ L +++ + KKC+FG LGHVIS++GV P

Sbjct 731 YSKTRAHEHLEHVLMQALQDNHLVIKL--KKCAFGLASVSYLGHVISQDGVATDP 784

Score = 154 bits (388), Expect (3) = 2e-138
Identities = 92/260 (35%), Positives = 139/260 (53%), Gaps = 10/260 (3%)
Frame = +3

Query 2880 QQYWVAKLLGYEFDIVYKVGASNKVVDALSRRDEDKELQGISRPF-----WKDITKINE 3041
Q + KL+ Y++ I YK G N V DALSR + + + P W I I

Sbjct 951 QHKLLLLKMEYDYTIEYKSGKENLVADALSRLPQKEAVADRCHPMTVVPIEW--IVDIQR 1008

Query 3042 EVQKDPALAKIREELKDNLDSDHPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSIMG 3221
+ D KI + D +Y LE +L ++GR+ + ++ +L+ ++S G

Sbjct 1009 SYENDVQAHKILSLIGTAADPDREYKLEAGLLKYKGRIVGEATDIRRQLITTYHSSSFG 1068

Query 3222 GHSGIYITYRRITQSLYWIPIKGEITKFVVACHVGQRSKYQASSPAGLLQPLPIPNAIWE 3401
GHSG+ T+ RI YW ++GE+ +F+ C Q +K + GLL PL IP+ W

Sbjct 1069 GHSGMRATHHRIKMLFYWHGMRGEVERFIRECPTCQITKSEHVHIPGLLNPLEIPDMAWT 1128

Query 3402 EISMNFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIIWLLVEPI 3575
I+M+FI G+ KS+G DVILV VD+L+KY +FI + HPY +V+ + I L +P+

Sbjct 1129 HITMDFIEGLPKSQGKDVLVVVDRLTKYAHFTALAHYPDVEQVVEAFMNNIHKHMGPM 1188

Query 3576 SIVSDSDLIFMSHFLQELFK 3635
I++D D IF S QE+FK

Sbjct 1189 VIITDRDRIFTSSSLFQEIFK 1208

Score = 136 bits (342), Expect (3) = 2e-138
Identities = 68/154 (44%), Positives = 97/154 (62%), Gaps = 0/154 (0%)
Frame = +2

Query 2408 WPMKPTKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQLQQA 2587
WP PK +R FL +TGY+R I YG I RP+ D+LK F+W D A L+ +

Sbjct 793 WPTPKLDVTVDRKFLGMTGYRRFIQGYGTICRPIHMDLKKNGFQWGADQTTAFETLKHKL 852

Query 2588 TTITPTLSMLDFSQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYEKESMA 2767
T P L++ DF + F+IE DA G GIG VL Q + IA+F+KAL +S+YEKE+MA

Sbjct 853 RTSFVLALPDFDQAFTEADACGVGIGAVLMQGGRIAPFFSKALGPKAAGSQSIYEKEAMA 912

Query 2768 LVLAHQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
++ A++ WR Y+ K I DQ+SL++++ QR+

Sbjct 913 ILEALKKWRHYVLGSKLIKTQDQSLKFMMGQRL 946

>gi|115457202|ref|NP_001052201.1| Os04g0191000 [Oryza sativa (japonica cultivar-group)]
gi|38346036|emb|CAE01900.2| OSJNBa0059D20.8 [Oryza sativa (japonica cultivar-group)]
gi|113563772|dbj|BAF14115.1| Os04g0191000 [Oryza sativa Japonica Group]
Length=1463

Score = 236 bits (602), Expect (3) = 4e-138
Identities = 125/239 (52%), Positives = 158/239 (66%), Gaps = 11/239 (4%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
F P GLPP R DH I +K + P VRPYRYP K+E++ M+ G++R S+S

Sbjct 491 FGEPTGLPPRGRDHAIVLKPSAPVAVRYPYRPAHKDELERQCAAMIEQGQVVRSDSP 550

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
+SSPV+LVK+ DGS R C+DY+AL+ TV D F IPV +DEL+G F+K+DL++ Y

Sbjct 551 FSSPVLLVKKADGSRWFCVDYRALNALTVDKDAFPIPV----VDELHGARFFTKDLRLSGY 606

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
HQ+RM HK FRTH G YE VMPFGL N P TFQ MN L+PFLRR+V+VFFDD

Sbjct 607 HQVRMPEDVHKTAFRTHDGLYEFLVMPFGLCNAPATFQALMNDVLRPFLRRFVLVFFDD 666

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP 2399

Sbjct 667 IL+YS++W HL HL VL+ L +H F V + KC+FG LGHVIS+ GV M P
ILIIYSETWTDHLRHLRTLVSRLRQHRLF--VKRSKCTFGSPSVSYLGHVISEAGVAMPD 723

Score = 164 bits (416), Expect (3) = 4e-138
Identities = 97/255 (38%), Positives = 150/255 (58%), Gaps = 7/255 (2%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDD-EDKELQGISRPFWKDITKINEEVQKD 3056
Q +WV KLLG++F + YK GA+N V DALSRDD E+ + +S P + I+K+++ ++D
Sbjct 890 QHHWVGKLLGDFDAVEYKPGAANTVADALSRDDTEEGAILALSAPRDFDISKLHDAQRD 949

Query 3057 PALAKIREELKDNLDLSDHPQYTTLECDILYFRGRLVLLASSLWIPKLLQEFQTSMLMGHSGI 3236
PAL +R+E+ + P + L D+L + L + +S P + + + GH G+
Sbjct 950 PALTALRDEVSAGRTGP-WALVDDLLQYNSWLYIPAS---PLAREITEATHEDGHEGV 1005

Query 3237 YITYRRITQSLYWIPIKGEITKFFVACHVGQSRKYQASSPAGLLQPLIPNAIWEEISMN 3416
T R+ + + +K + +V +C V QR K + SPAGLL PLP+P +W +I+++
Sbjct 1006 KRTMHLRLREFHIPNMKQLVQDQWVRSCAVCQRYKSEHLSAGLLPLPVPQGVWTDIALD 1065

Query 3417 FIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--KEIIWLLEVPISIVSD 3590
FI + + +G VIL VD+ SKY +FI + HPY A S+ EI+ L VP S+VSD
Sbjct 1066 FIEALPRVRGKSVILTVDVDRFSKYCHFIPLAHPYSAESVAQAFFAEIVHLHGVPQSMVSD 1125

Query 3591 SDLIFMSHFLQELFK 3635
D IF S F +EL +
Sbjct 1126 RDPIFTSTFWRELMR 1140

Score = 141 bits (355), Expect (3) = 4e-138
Identities = 71/163 (43%), Positives = 103/163 (63%), Gaps = 0/163 (0%)
Frame = +2

Query 2393 EAIL*WMPKPTKTLRGFLELTGYKYRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
+AI W +P++ + +R FL L GYY++ + NYG IA PL L K F W ED+ A
Sbjct 727 QAIHEWLVR SARAVRSFGLGAGYRK FVHNYGTIAAPLTALTKKDGFSWTEDTAAAFDA 786

Query 2573 LQQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTQDRKQIAYFNKALKDLTLSKSMYE 2752
L+ A+T+ P L+M DF+K F++E DAS G G VL QD +A+F++ + + + YE
Sbjct 787 LKAAVTSAPVLAMPDFAKPFTVEGDASTHGFGAVLVQDGHVPFAFFSRPVVLRHRAAAYE 846

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTOP 2881
+E + LV A++HWRPYL +F + D SL+YLLDQR+ T P
Sbjct 847 RELIGLVHAVRHWRPYLWGRRFVVKTDHYSKLYLLDQRLATIP 889

>gi|147772855|emb|CAN73669.1| hypothetical protein [Vitis vinifera]
Length=1308

Score = 247 bits (630), Expect (3) = 4e-138
Identities = 122/235 (51%), Positives = 164/235 (69%), Gaps = 7/235 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
F+ P LPP+RE+DHKI K G VRPYRY + QK EI+ V +ML G+IR S +
Sbjct 400 FAAPTSLLPAREIDHKIPPKDGTAEIKVRPYRYAYFQKTEIENQVQDMLNAGLIRPSTNP 459

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
+SSPV+LVK+KDG+ R C DY+AL+ ATV D+F IP + ++LDEL+G F+K+DLKA Y
Sbjct 460 FSSPVLLVKKKDGTWRFC TDYRALNAATVKDRFPIPTVDDMLDELHGAAFFTKLDLKAGY 519

Query 2058 HQIRMHQP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFFDD 2222

Sbjct 520 HQIR+ P FRTH GHYE VMPFGL N P+TFQ MN+ +P+LR++++VFFD+
HQIRVSTPDIPKTAFRTHNGHYEYLVMPFGLCNAPSTFQAIMNSIFRPYLRKFILVFFDB 579

Query 2223 ILVYSKSWEAHLHLDS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGV 2387
IL+YS +WE HL+H+ LA L +H F+ V K +FG+ + LGH+I+ GV
Sbjct 580 ILIYSPTEWQHLEHVQXTLAVLRQHGFY--VKXSKXAFGKQELEYLGHIIITHRGV 632

Score = 149 bits (375), Expect (3) = 4e-138
Identities = 93/259 (35%), Positives = 136/259 (52%), Gaps = 34/259 (13%)
Frame = +3

Query 2874 LNQQYVWAKLLGYEFDIVYKVGASNKVVDALSRDDKELQGI---SRPFWKDITKINEE 3044
L QQ VVAKLLGY+++I+++ G N DALSR E L + WK +I E
Sbjct 801 LEQQKWVAKLLGYDYETIIFRTGRENSAADALSRQESPLLATLHFSEVDIWK---QIREA 857

Query 3045 VQKDPALAKIREELKDNLDLSDHPQYTTLECDILYFRGRLVLLASSLWIPKLLQEFQTSMLMG 3224
+ D + + + + D H T +L ++G++V+ A KLL E S +GG
Sbjct 858 FKSDSYVQLLGKAGD---PPHGNLTWHDGLLLYKGVVVPADHSLRAKLLYEVHDSKVG 915

Query 3225 HSGIYITYRRITQSLYWIPIKGEITKFFVACHVGQSRKYQASSPAGLLQPLIPNAIWEE 3404
HSGI TYRR+ Q YW + + FV C V WE+
Sbjct 916 HSGILRTYRRLQQQFYWPKMHKAVQXVQKCEV-----WED 951

Query 3405 ISMNFIIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIIWLLEVPIS 3578
I+++FI G+ S G D ILV VD+LSK+ +FI + HP+ A+ +V+ ++ ++ L +P
Sbjct 952 ITLDFIEGLPTSHGKDTILVVVDRLSKFAHFIPLTHTPFTAKVVVENFIEGVVVLHGMPRF 1011

Query 3579 IVSDSDLIFMSHFLQELFK 3635
I+SD D IF+S F QE FK
Sbjct 1012 IISDRDPIFISKFWQEFFK 1030

Score = 146 bits (368), Expect (3) = 4e-138
Identities = 79/161 (49%), Positives = 106/161 (65%), Gaps = 0/161 (0%)
Frame = +2

Query 2393 EAIL*WMPKPTKTLRGFLELTGYKYRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
EA++ P P LRGFL LTGY++ + YG IARPL +LLK F+WN+ + A +
Sbjct 640 EAMVAVPRPSNITELRGFLGLTGYRKFVQGYGLIARPLTNLLKKEKFQWNDKAEAAFLA 699

Query 2573 LQQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTQDRKQIAYFNKALKDLTLSKSMYE 2752
L+QA+T+ TL+M F++ F+IE DASG GIG VLTQ IAY + AL + S+Y
Sbjct 700 LKQAMTSTXTLAMPNFTPEPTIETDASGNGIGAVLTQQNXPIAYMSXALGITQTWSIYA 759

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
KE +A+V AI+ WRPYL KF I DQ+SL+ LDQ+ T
Sbjct 760 KEMLAIVEAIRLWRPYLLGRKFYIKTDQQSLKIFLDQHVAT 800

>gi|115468162|ref|NP_001057680.1| Os06g0493000 [Oryza sativa (japonica cultivar-
group)]
Length=1573

Score = 235 bits (599), Expect (3) = 1e-137
Identities = 125/236 (52%), Positives = 157/236 (66%), Gaps = 7/236 (2%)
Frame = +3

Query 1707 PKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSSYSS 1886
P LPP R+ DH I + GA P NVRPYR P+ +KN ++ LV ++L I+ S S YSS
Sbjct 654 PVALPPQRDCDHTIPLIPGAKPVNVRPYRLPYQKKNALVELVQQLTSQTIQPSMSPYSS 713

Query 1887 PVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARYHQI 2066
 P ILVK+KDG+ RLC+DY+ L+ +T+ +K+ IPV+++LLDEL G FSKIDL++ YHQI
 Sbjct 714 PAILVKKKDGTTWRLCVDYRQLNASTIKNKYPFVIEDLLDELQGAQIFSKIDLRSGYHQI 773

Query 2067 RM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFDDILV 2231
 RM HK F TH GH+E VMPFGLTN P TFQ MN L P+LR++V+VFFDDIL+
 Sbjct 774 RMHAADVHKTAFTSLHGHFEYLVMPFGLTNAPATFQALMNKILAPYLRKFVLVFFDDILI 833

Query 2232 YSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVMRMP 2399
 YSKS H HLS VL L H F KC FGQ + LG++IS GV P
 Sbjct 834 YSKSATEHAQHLSLVLQLLRHHQLFAK--PSKCVFGQDQVEYLYGISSSGVATDP 887

Score = 173 bits (439), Expect(3) = 1e-137
 Identities = 102/255 (40%), Positives = 146/255 (57%), Gaps = 5/255 (1%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQG-ISRPFWKDITKINEEVQKD 3056
 Q + KLL Y++ I YK G NK DALSR + L + P W IT++ D
 Sbjct 1054 QHKLKLLKSLSYDQKIEYKKGQENKAADALSRMQQLNALTTTVIVPQW--ITEVAASYSTD 1111

Query 3057 PALAKIREELKDNLDSDHPQYTTLECDILYFRGRLVLLASSLWIPKLLQEFQTSMLGGHSGI 3236
 P ++ L SHP YTL+ IL ++ +V+ A + +LL F S +GGHSG
 Sbjct 1112 PKCHELESHLHIAPQSHPPYTLKGGILRYKGVVGVAGNTLREQLLVSFHDSALGGHSGE 1171

Query 3237 YITYRRITQSLYWIPIKGEITKFVAVCHVGQRSKYQASSPAGLLQPLPIPNAIWEEISMN 3416
 TY+R+ Q YW +K +T+V AC V Q++K + + PAGLLQPLP+P W I+M+
 Sbjct 1172 RATYQRMKQLFYWPGMKLAVTQFVKACPVCKQNKTEHNPAGLLQPLPEMAWHSITMD 1231

Query 3417 FIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIVSD 3590
 F+ G+ KS+G DVI V VD+ +KY +FI + HP+ A I+ ++ L +P IVSD
 Sbjct 1232 FVEGLPKSEKGDVIVVDRFTKYAHFIPLSHPFTADQILTQFLEHFYKHLGLPTVIVSD 1291

Query 3591 SDLIFMSHFLQELFK 3635
 D IF S +E+F+
 Sbjct 1292 RDRIFTSSTWKEVFE 1306

Score = 131 bits (330), Expect(3) = 1e-137
 Identities = 68/160 (42%), Positives = 97/160 (60%), Gaps = 0/160 (0%)
 Frame = +2

Query 2393 EAIL*WPMPKTPKTLRGFLELTGYIKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572
 +A+ WP P + LRGL L GYY+R I N+G I RP+ D LK NF WE +A
 Sbjct 891 QAVQNWPTPTSITELRGFLGLGYYRRFIKNGFIICRPMFDALKNNFHWQEVQQAFA 950

Query 2573 LQQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYE 2752
 ++ + P L+M DFS F +E DASG GIG VL Q+ + +AY +KA+ + S Y+
 Sbjct 951 IKLQLAQAPVLAMPDFSLPFILEADASGHGIGAVLMQNGRPLAYLSKAIGPKAAALSTYD 1010

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRIT 2872
 KE++A++ A++ W+ Y I DQ SL+Y+ +QRIT
 Sbjct 1011 KEALAILEALKKWKHYFLGTSLIIRTDQASLKYINEQRIT 1050

>gi|147852240|emb|CAN80132.1| hypothetical protein [Vitis vinifera]
 Length=1371

Score = 252 bits (643), Expect(3) = 2e-136
 Identities = 134/256 (52%), Positives = 174/256 (67%), Gaps = 11/256 (4%)
 Frame = +3

Query 1647 KEPRKLVVASTDRVCYSFSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKT 1826
 +E +K++ A D F P GLPP R+ DH+I +K A P N RPYRY +QK+ I+
 Sbjct 560 EELQKMLQAFAD----VFEEPTGLPPVRDYDHQIDLKDEAGPINCRCPYRYAAVQKDAIEK 615

Query 1827 LVVEML*LGIIRLSNSSYSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELL 2006
 L+ EML G+IR S S Y+SPV+LVK+KDG RLC+DY+AL++ TV DKF IPV++ELL+
 Sbjct 616 LIGEMLHAGVIRQSRSPYASPVVLVKKKDGSRWRLCVDYRALNQVTVKDKFPIPVIEELLE 675

Query 2007 ELNGPIHFSKIDLKARYHQIRMHKKP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMN 2171
 EL G FSKIDL++ Y QIRMH+P F+TH+GHYE VMPFGLTN P+TFQ MN
 Sbjct 676 ELGGSTIFSKIDLRSGYQWIRMHEPDVPKTAFKTHEGHYEFLVMPFGLTNAPSTFQSLMN 735

Query 2172 ATLKPFLRRYVVFDDILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKA 2351
 +P+LR+++VFFDDIL+YS+S+ H+ HLS L L E+ + KC FG
 Sbjct 736 NIFQPYLRKIFLVFFDDILYRSFSDHIHLSIAQVQLRENLLYAK--SNKCFFGHSSI 793

Query 2352 GCLGHVISKEGVLMP 2399
 LGHVIS GV P
 Sbjct 794 EYLGHVISSGGVYTD 809

Score = 151 bits (382), Expect(3) = 2e-136
 Identities = 92/254 (36%), Positives = 141/254 (55%), Gaps = 16/254 (6%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISRPFWKDITKINEEVQKDP 3059
 QQ WVAKL+ Y+++I YK G N DALSR + EL +S + + DP
 Sbjct 958 QQAWWAKLMQYDYEIRYKQKENVAADALSRI-QPAELFVLSTTILNTQLRSRLRKEADP 1016

Query 3060 ALAKIREELKDNLDSDHPQYTTLECDILYFRGRLVLLASSLWIPKLLQEFQTSMLGGHSGIY 3239
 + ++P+Y+ + L +G+LV+ + ++L F S GGHS+Y
 Sbjct 1017 S-----AYPKYSWRGEELRRKGLVVGNEQLRREILNSFHDSPSTGGHSGVY 1063

Query 3240 IITYRRITQSLYWIPIKGEITKFVAVCHVGQRSKYQASSPAGLLQPLPIPNAIWEEISMNF 3419
 +T +RI+ +YW ++ + ++V C V QR K + +GLLQPLP+P ++ +I+M+F
 Sbjct 1064 VTTKRISVSVVYWKGLRKFVREYVRNCSVCQRFPENKPYSGLLQPLPVPEGVFTDITMDF 1123

Query 3420 IVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIWLLEVPISIVSDS 3593
 I G+ KS G I V VD+L+KY +F+++ HPY A+ + V + L +P SI D
 Sbjct 1124 IEGLPKSNKGTEIFVVDRLTKYGHFMLLPHPYTAKMVAQVFLDSVYKHLGLPYSITCDR 1183

Query 3594 DLIFMSHFLQELFK 3635
 D IF S F QE FK
 Sbjct 1184 DPIFTSVFVQEFFK 1197

Score = 132 bits (333), Expect(3) = 2e-136
 Identities = 74/160 (46%), Positives = 99/160 (61%), Gaps = 18/160 (11%)
 Frame = +2

Query 2396 AIL*WPMPKTPKTLRGFLELTGYIKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQL 2575
 A+ WP P T K LRGL LTGY+R++ F E S +A + L
 Sbjct 814 AVRDPWPTPITLKLQRLGLTGYRRTL-----FTGTGEGSNQAFMAL 855

Query 2576 QQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYEK 2755
 +QA+ T P L++ +FSK+F IE DASG+GIG VL Q+ IAY +KAL D + S YEK
 Sbjct 856 KQAMITAPVLALPNFSKEFIETDASGQIGAVLMQEGHP IAYISKALSDRFQTLSTYEK 915

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 E +A++AI+ W YL D F I D +SL+YLL+QR+TT
 Sbjct 916 EMLAILMAIKKWEYSYLVDRHFVKTDRHQLSKYLLQQRVTT 955

>gi|147837833|emb|CAN62821.1| hypothetical protein [Vitis vinifera]
Length=1357

Score = 249 bits (635), Expect(3) = 3e-136
Identities = 134/256 (52%), Positives = 173/256 (67%), Gaps = 11/256 (4%)
Frame = +3

Query 1647 KEPRKLVVASTDRVCYSFSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKT 1826
+E +K++ A TD F P GLP R+ DH+I +K A P N RPYRY +QK+ I+
Sbjct 475 EELQKMLQAFTD----VFEEPTGLPLVRDYDHQIDLKDEAGPINCPRPYRAAVQKDAIEK 530

Query 1827 LVVEML+LGIIRLSNSSYSSPVILVKKRDGS*RLCMDYQALS KATVPDKFLIPVMKELLD 2006
L+ EML G+IR S S Y+SPV+LVK+KDGS RLC+DY+AL++ TV DKF IPV++ELL+
Sbjct 531 LIGEMLHAGVIRQSRSPYTSPPVLVKKKDGSRWLCVDYRALNQVTVDKDFPIPVIEELLE 590

Query 2007 ELNGPIHFSKIDLKARYHQIRMHPK-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMN 2171
EL G FSKIDL++ Y QIRMH+P F+TH+GHYE VMPFGLTN P+TFQ MN
Sbjct 591 ELGGSTIFSKIDLRSGYWQIRMHEPDVPKTAFTKTHEGHYEFVMPFGLTNAPSTFQSLMN 650

Query 2172 ATLKPFLRRYVVVFFDDILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKA 2351
+P+LR+++ VFFDDIL+YS+S+ H+ HLS L L E+ + KC FG
Sbjct 651 NIFQPYLRKFIPIVFFDDILIYSRSFSDHIHLSIALQVLRENLLYAK--SNKCFGHSSI 708

Query 2352 GCLGHVISKEGVLMRP 2399
LGHVIS GV P
Sbjct 709 EYLGHVISSGGVYTD 724

Score = 166 bits (421), Expect(3) = 3e-136
Identities = 86/160 (53%), Positives = 112/160 (70%), Gaps = 0/160 (0%)
Frame = +2

Query 2396 AIL*WMPKPTPKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQL 2575
A+ WP P T K LRGL L TGYY+R + +YGKIA+PL DLLK F W E S +A + L
Sbjct 729 AVRDPWPTPTTLKQLRGFLGTGYRRFVKDYGKIAKPLDLLKDAFWHTEGNSQAFMAL 788

Query 2576 QQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMYEK 2755
+QA+ T P L++ +FSK+F IE DASG+GIG VL Q+ IAY +KAL D + S YEK
Sbjct 789 KQAMITAPVLAIPNFSEKFIETDASGGIGAVLMQEGHP IAYISKALSDRQTLSTYEK 848

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
E +A+++AI+ W YL D F I D +SL+YLL+QR+TT
Sbjct 849 EMLAILMAIKKWEYSYLVDHRHFIKTDHQLSLKYLLEQRVTT 888

Score = 120 bits (301), Expect(3) = 3e-136
Identities = 76/223 (34%), Positives = 116/223 (52%), Gaps = 29/223 (13%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDEDKELQGISRPFWKD--ITKINEEVQK 3053
QQ VAKL+ Y+++I YK G N DALSR + EL +S I E
Sbjct 891 QQALVAKLMQYDYEIRYKQKENVAADALSRI-QPAELFVLSTTILNTQLYDLIKESWGV 949

Query 3054 DPALAKIREELKDNLDSPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSLMGGHSG 3233
DP L KI + + + ++P+Y+ F S GGHSG
Sbjct 950 DPLOKRIIAKEADPSAYPKYSC-----FHDSPTGGHSG 983

Query 3234 IYITYRRITQSLYWIPIKGEITKFVACHVGQRSKYQASSPAGLLQPLPINAIWEEISM 3413
+Y+T +RI+ +YW ++ + ++V C V QR K + +GLLQPLP+P ++ +I+M
Sbjct 984 VVVTTKRISVVVYWKGLRKFVREYVRNCSVCQRKFENPKPYSGLLQPLVPEGVFTDITM 1043

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV 3542
+FI G+ KS G I V VD+L+KY +F+++ HPY + + V
Sbjct 1044 DFIEGLPKSNGKMTIFVVVDRLTKYGHFMLLPHPYTTKMQAV 1086

>gi|18568267|gb|AAL75999.1|AF466646_7 putative polypeptide [Zea mays]
Length=2749

Score = 254 bits (650), Expect(3) = 1e-135
Identities = 130/237 (54%), Positives = 166/237 (70%), Gaps = 7/237 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
F+ P+GLPP+R DH+I + GA P VRPYRYP LQK+E++ ML GIIR S S
Sbjct 912 FAEPQGLPPARPVDHRIHLLPGAAPVAVRPYRYPQLQKDELERQCSAMLAQGIIRPSTSP 971

Query 1878 YSSPVILVKKRDGS*RLCMDYQALS KATVPDKFLIPVMKELLDDELNGPIHFSKIDLKARY 2057
+S+PV+LV++ D S R C+DY+AL+ T DKF IPV+ ELDEL+G F+K+DL++ Y
Sbjct 972 FSAPVLLVRKPDNSWRFCIDYRALNAKTSKDKFPIPVVDELDELHGAHFFTKDLRSGY 1031

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFFDD 2222
HQ+RMH K FRTH+GHYE VMPFGL+N P TFQ MN L+P+LR+YV+VFFDD
Sbjct 1032 HQVRMHPADVEKTAFTRTHGHYEFVMPFGLSNAPATFQALMNDVLRPYLRKYVLFVFFDD 1091

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLM 2393
IL+YSK+W HL H+S VL L +H ++ + KCSFG LGHVIS GV M
Sbjct 1092 ILIYKTAWEHLQHISIVLHALRDHQL--HLKRSKCSFGARSVAYLGHVISAAGVAM 1146

Score = 145 bits (367), Expect(3) = 1e-135
Identities = 74/163 (45%), Positives = 103/163 (63%), Gaps = 0/163 (0%)
Frame = +2

Query 2393 EAIL*WMPKPTPKTLRGFLELTGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQL 2572
EA+ WP P + + LRGL L GYY++ I ++G IA PL LL+ F W++D+ A Q
Sbjct 1152 EAVSSWPAPHSARGFLRGFLGAGYYRKFRDVGIVIAAPLTRLRLRRDAFTWDDDTQAAFOQ 1211

Query 2573 LQQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMYE 2752
L+ A+TT P L M +F K F ++CDASG G G VL Q +A+F++ L + YE
Sbjct 1212 LKTAITLTPGVLPMPNFKEFTFVVDASGTGFGAVLHQGAGPVAFVSRFPVTRHLKLAAYE 1271

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTQP 2881
+E + LV A++HWRPYL F + D SL+YLLDQR++T P
Sbjct 1272 RELIGLVQAVRHWRYLWGRHFAVRTHYSLKYLDDQLRLSTVP 1314

Score = 133 bits (335), Expect(3) = 1e-135
Identities = 89/269 (33%), Positives = 133/269 (49%), Gaps = 25/269 (9%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDED-----KELQGISRPFWKDI 3026
Q W++KL G++F++ Y+ G N DALSRD + +S P + +
Sbjct 1315 QHQWLSKLFGEFDEVEYRPGRLNVAADALSRRDAELLQPSAGELGAAALALSGPSFAFL 1374

Query 3027 TKINEEVQKDPALAKIREELKDNLDSPQYTLECDILYFRGRVLVLLASSLWIPK----LL 3194
I P +++ ++L+D + P + LE +L L S +++P
Sbjct 1375 DDIRATATSPDSSRLCQQLQDGTLTAP-WRLEDGLL-----LHGSRIYVPHNGDLRH 1426

Query 3195 QEFQTSMLGGHSGIYITYRRITQSLYWIPIKGEITKFVACHVGQRSKYQASSPAGLLQ 3374
Q + GH GI T R+ Y + + +V C QR+K + PAGLLQ
Sbjct 1427 QAILLASAGHEGIQKTLHRLRAEFVPGDRTLVADWVRTCTTCQRNKTTETLQAPAGLLQ 1486

Query 3375 LPIPNAIWEIEISMNFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KE 3548
 L +P+ +W +ISM+FI G+ K G VIL VD+ SKY +FI + HPY A S+
 Sbjct 1487 LQVPSQVWADISMDFIIEGLPKVGGKSVILTVVDRFSKYAHFIPLGHPYTAASVARAFFDG 1546

Query 3549 IIWLLEVPISIVSDSDLIFMSHFLQELFK 3635
 I+ L P SIVSD D +F H ++LKF
 Sbjct 1547 IIVRLHGFPPSSIVSDRDPVFTGHVWRDLFK 1575

>gi|242093834|ref|XP_002437407.1| hypothetical protein SORBIDRAFT_10g026363 [Sorghum bicolor]
 gi|241915630|gb|EER88774.1| hypothetical protein SORBIDRAFT_10g026363 [Sorghum bicolor]
 Length=1609

Score = 246 bits (628), Expect(3) = 1e-135
 Identities = 130/237 (54%), Positives = 162/237 (68%), Gaps = 7/237 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIIRLSNSS 1877
 F+ P GLPP+R+ DH+I +K P VRPYRYP LQK+E++ ML G IR S S
 Sbjct 671 FAEPDGLPPARDCDHRIHLKPATEPVAVRPYRYPQLQKDELERQCDAMLQQTIRASTSP 730

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELDELNGPIHFSKIDLKARY 2057
 +S+PV+LVK++DGS R C+DY+AL+ ATV DKF IPV++ELLDEL G F+K+DL++ Y
 Sbjct 731 FSAPVLLVKKQDGSWRFCVDYRALNSATVKDKFPIPVVEELLDELRGARFFTKDLDRSGY 790

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFDD 2222
 HQIR+H K FRTH GH+E VMPFGL+N P+TFQ MN LKPFLRR V+VFFDD
 Sbjct 791 HQIRVHPDDVAKTAFRTHHGHFEFLVMPFGLSNAPSTFQALMNTVLKPFLLRRCVLFVFFDD 850

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLM 2393
 IL+YS +W HL L VL L H ++ + KCSF LGHVIS GV M
 Sbjct 851 ILIYSATWTEHLLQLRAVLDVLRTHSL--HLKRSKCSFAATSVHYLGHVISHAGVSM 905

Score = 147 bits (370), Expect(3) = 1e-135
 Identities = 91/265 (34%), Positives = 142/265 (53%), Gaps = 17/265 (6%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRREDKEL-----QGISRPFWKDI 3026
 Q +W++KL+GY+F I ++ G N V DALSRRD D L +S P ++
 Sbjct 1074 QNHWSIKLMGYDFRIEFRPGRFNVVADALSRRDGDAPLLSTLPSAEPVLAALSTPTFQOLF 1133

Query 3027 TKINEEVQKDPALAKIREELKNDLSDHPQYTLECDILYFRGLVLLASSLWIPKLLQEFQ 3206
 ++ +E L + EE+ + L+ +L +GR+ + ASS +LQ
 Sbjct 1134 DELRQEFAASDELRAVCEEVAAG-GRGADWALQDGLLLHKG RVYVPASSSVFDDVLQLAH 1192

Query 3207 TSLMGHSGHSIYITYRRITQSLYWIPIKGEITKFVACHVQGRSKYQASSPAGLLQPLP 3386
 T+ H GI T +R+ + + + ++ AC QR+K +A PAGLLQPLP+P
 Sbjct 1193 TN---AHEGIQKTQLRLRTEFFIEHRRTVHDYIRACATCQRNKSEAMHPAGLLQPLPVP 1249

Query 3387 NAIWEIEISMNFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWL 3560
 + +W +I+M+F+ + K G VIL VD+ SKY +FI + HPY A S+ ++I+ L
 Sbjct 1250 SKVWADIAMDFAELPKVHGKSVILTVVDRFSKYAHFIPLGHPYTAASVARAFFRDIVRL 1309

Query 3561 LEVPISIVSDSDLIFMSHFLQELFK 3635
 P SIVSD D +F + ++LKF
 Sbjct 1310 HGFPPDSIVSDRDPVFTGNVWRDLFK 1334

Score = 140 bits (353), Expect(3) = 1e-135

Identities = 69/162 (42%), Positives = 101/162 (62%), Gaps = 0/162 (0%)
 Frame = +2

Query 2396 AIL*WMPKPTPKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQL 2575
 A+ WP P++ + LRGLF L GYY+R I +YG IA PL LL+ F W ++ A L
 Sbjct 912 AVQSWQPPRSARGLRGFLGLAGYRRFIKDYGAIAAPLTSLLRKNAFLWTAEEADAFSAL 971

Query 2576 QQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLSKSMYEK 2755
 +QA++ P L + DF+ +F ++CDASG G G VL Q +A+F++ L + YE+
 Sbjct 972 KQALSAAPVHLHLPDFNLEFFVDCDASGSGFGLVHQQEGPLAFFSRPFAVRHLKVAAYER 1031

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRIITQP 2881
 E + LV A++HWRPYL F + D +L++LLDQR++T P
 Sbjct 1032 ELIGLVQAVRHRWPYLGWSFIVRTDHYALKFLLDQRLSTIP 1073

>gi|38346992|emb|CAD40278.2| OSJNBb0062H02.17 [Oryza sativa (japonica cultivar-group)]
 gi|38347666|emb|CAE05600.2| OSJNBa0054D14.1 [Oryza sativa (japonica cultivar-group)]
 Length=1629

Score = 248 bits (632), Expect(3) = 2e-135
 Identities = 167/432 (38%), Positives = 235/432 (54%), Gaps = 38/432 (8%)
 Frame = +3

Query 1164 MKLR*EL*GQEVIIIDNRASHNFISNKLVLHKL-GLSIDPTKPYMRLGDSNRKSTQGCC 1340
 M++ ++ G+E++IL+D+ +S +FIS ++ L G+ P M G + CC
 Sbjct 478 MRMLGQIQGKEILILVDSGSSASFISKRVASSLMGVLEQPVHVQVMVAGGAKLH----CC 533

Query 1341 KNLKN-SWEL---IPW*DISIYIsweewt*llellswKH-----WEKLR*IGGP*VCLL 1490
 + N W+ + + ++ + L +H W I +
 Sbjct 534 SEILNCEITQGHVFFTNLKVLELNNYDMILGMDWLMQHSPTVDWTTKSLI----IAYA 589

Query 1491 STKIRIW*SRRSWFIEDNDHFENIAKNS*QGS*DDVHVVG*QQLCGTN*FNKEPRKLTV 1670
 T+I+++ R D + +I+ + +D V N Q C F E ++ +
 Sbjct 590 GTQIQLYGVR-----SDTEQCAHISSKQLREL-NDRTAVSNLVQFCV--FALEYQEQIP 641

Query 1671 ASTDRVCYSFSG-----PKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVE 1838
 V FS PKGLPP R+ DH I + GA P NVRPYR +QKNEI++ V E
 Sbjct 642 EVVQTVLTFESSVFDEPKGLPPIRQFDHTIPLLPAGAGPVNVRPYRPTPIQKNEIESQVQE 701

Query 1839 ML*LGIIIRLSNSSYSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELDELNG 2018
 ML GII+ S+S +SSPV+LVK+KDGS R C+DY+ L+ TV +K+ +PV+ ELLDEL G
 Sbjct 702 MLSKGIIPQSSSPSSPVLLVKKKDGSRFCVDYRHLNATVKNKYLPVIDELLDELDEL 761

Query 2019 PIHFSKIDLKARYHQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLK 2183
 FSK+DL++ YHQIRM HK F+TH GH+E V+PFGLT+ P TFQ MN+ L
 Sbjct 762 AQWFSKLDLRSGYHQIRMPDDEHKTAFTQTHHGHFEFRVLPFGLTSAFATFQGVMSVLA 821

Query 2184 PFLRRYVVFVFFDDILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLG 2363
 LRR V+VF DDIL+YSKS E H+ HL V LL+H V + KCSF Q + LG
 Sbjct 822 TLLRRCVLFVFDIILYYSKSLEEHVQHLKTVFQILLKHQL--KVKRKCSFAQQLAYL 879

Query 2364 HVISKEGVLMRP 2399
 H+I GV P
 Sbjct 880 HIIQPNGVSTDP 891

Score = 150 bits (378), Expect(3) = 2e-135
 Identities = 87/252 (34%), Positives = 139/252 (55%), Gaps = 4/252 (1%)
 Frame = +3

Query 2892 VAKLLGYEFDIVYKVGASNKVVDALSRR--DEDKELQGISRPFWKDITKINEEVQKDPAL 3065
 + KLLG + I++K G N DALSR + EL +S + I I DP
 Sbjct 1063 LTKLLGLRYKIIFKKGIDNSAADALSRYPGSDRVELSALSVAVPEWINDIVAGYSSDPDA 1122

Query 3066 AKIREELKDNLDSDHPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSIMGGHSGIYIT 3245
 + L N + P ++L +LYF+ RL + + ++L T+ +GGHSGI +T
 Sbjct 1123 CSKVQTLCLNSGAVPNFSLRNGVLVFQNLRLVWGHNVQQRILANLHTAAVGGHSGIQVT 1182

Query 3246 YRRITQSLYWIPIKEITKFFVACHVQQRSKYQASSPAGLLQPLPIPNAIWEIEISMNFI 3425
 Y+R+ Q W ++ + ++V AC V Q++K + G+LQPLP+P+ W+ +S++F+
 Sbjct 1183 YQRVKQLFAWPRLRATVVQYVQACSVQQAQSEHVKYPGMLQPLPVPDHAQIVSLDFVE 1242

Query 3426 GMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIVSDSDL 3599
 G+ KS F+ ILV VDK SKY +F+ + HP+ A + + ++ I L +P S++SD D
 Sbjct 1243 GLPKSASFNCILVVVDKFSKYSHFVPLTHPFSALDVAEAYMQHIHRLHGLPQSLISDRDR 1302

Query 3600 IFMSHFLQELFK 3635
 IF S LF+
 Sbjct 1303 IFTSTLWTTLFR 1314

Score = 135 bits (339), Expect (3) = 2e-135
 Identities = 70/157 (44%), Positives = 101/157 (64%), Gaps = 1/157 (0%)
 Frame = +2

Query 2408 WPMPTKPTKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GN-FKWNEDSIKASIQLQQA 2584
 WP P + K LR FL L+GYY++ + NYG +++PL +LL+ G + W ++ A L+QA
 Sbjct 900 WPAPTSVKELRSFLGLSGYYRKFVRNYGILSKPLTNLLRKGQLYIWTAEATEDAFQALKQA 959

Query 2585 ITTIPTLSMLDFSKQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTLSKSMYEKESM 2764
 + T L+M DF F +E DAS KGIG VL Q+ +A+ ++AL S YEKES+
 Sbjct 960 LITATLAMPDQPTFPVVEDDASDKGIGAVLQNNHPLAFLSRALGLRHPGLSTYEKESL 1019

Query 2765 ALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 A++LA+ HWRPYL +F I D +SL +L +QR+TT
 Sbjct 1020 AIMLAVDHWRYLPQHDEFFIRTDHRSALFLTEQRLTT 1056

>gi|242085372|ref|XP_002443111.1| hypothetical protein SORBIDRAFT_08g008675
 [Sorghum bicolor]
 gi|241943804|gb|EES16949.1| hypothetical protein SORBIDRAFT_08g008675 [Sorghum
 bicolor]
 Length=1456

Score = 249 bits (636), Expect (3) = 3e-135
 Identities = 128/239 (53%), Positives = 161/239 (67%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F+ P G+PP R DH I +K+GA P VRPYRYP K+E++ ML GIIR S+S+
 Sbjct 500 FAEPHGMPQRARDHAINLKAGAPVAVRPYRYPAAHKDELEKQCATMLQGGIIRSDSA 559

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSPV+LVK+ D R C+DY+AL+ TV D F IPV+ ELLDEL+G F+K+DL++ Y
 Sbjct 560 FSSPVLLVKKADSGWRFCIDYRALNALTVDKTFPIPVVDELDELHGACFFTKLDRSGY 619

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFVDD 2222
 HQ+RM HK FRTH G YE VMPFGL N P TFQ MN L+PFLRR+V+VFFDD
 Sbjct 620 HQVRMLPADVHKTAFTRDGLYEFLVMPFGLCNAPATFQALMNDVLRPFLRRFVLVFFDD 679

Query 2223 ILVYSKSWEAHLHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMP 2399

Sbjct 680 IL+YS++W HL HL V + L H F + + KC+FG+ LGHV S EGV M P
 ILIYSETWADHLRLRAVFSSELRRHRLF--IKRSKCAFGEATVAYLGHVTSAEGVAMDP 736

Score = 158 bits (399), Expect (3) = 3e-135
 Identities = 92/259 (35%), Positives = 146/259 (56%), Gaps = 12/259 (4%)
 Frame = +3

Query 2880 QQYVWVAKLLGYEFDIVYKVGASNKVVDALSRRDEDKELQG----ISRPFWKDITKINEEV 3047
 Q +WV KLLG++F + YK G +N V DALSRD ++E G +S P + IT++ +
 Sbjct 887 QHHWVGKLLGDFDSVEYKPGVNTTVADALSRRDTEETAGAVLALSAPRFDFITRLRQAN 946

Query 3048 QKDPALAKIREELKDNLDSDHPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSIM-GG 3224
 DPA+ +RE++ P ++ D++ + GRL + S LLQE ++ G
 Sbjct 947 AGDPAMVALREDISSGARGMPWSVVD--DMVQYSGRLYIPPGS----PLLQELVLAVHEDG 1001

Query 3225 HSGIYITYRRITQSLYWIPIKEITKFFVACHVQQRSKYQASSPAGLLQPLPIPNAIWEIE 3404
 H G+ T R+ + ++ +K + + + C V QR K + P GLL PL +P IW +
 Sbjct 1002 HEGVQRTLRLRRDFHFPNMKQVQELIRVCVVCQRYKSEHLQPTGLLLPLSVPQGIWTD 1061

Query 3405 ISMNFIIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--KEIWLLEVPIS 3578
 I+++F+ + + +G VIL VD+ SKY +F+ + HPY A S+ + +I+ L VP S
 Sbjct 1062 IALDFVEALPRVRGKTIVLTVDVDRFSKYCHFVPLAHPHYTAESVAEFAFFADIVRLHGVPOS 1121

Query 3579 IVSDSDLIFMSHFLQELFK 3635
 +VSD D +F S F EL +
 Sbjct 1122 MVSDRDPVFTSAFWCELMR 1140

Score = 125 bits (313), Expect (3) = 3e-135
 Identities = 64/163 (39%), Positives = 98/163 (60%), Gaps = 16/163 (9%)
 Frame = +2

Query 2393 EAIL*WPMPTKPTKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572
 +AI WP+P++ + LRGFL L GYY++ + NYG + + A
 Sbjct 740 QAIRDWPVPRSVRALRGFLGLAGYYRKFVLNYGA-----TDAASAFAFGA 783

Query 2573 LQQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTLSKSMYE 2752
 L+ A+T+ P L+M DF+K F++ECDAS G G VL Q+ IA+F++ + + + YE
 Sbjct 784 LKAAVTSAPVLTMPDFAKPTVECDASTHGFGAVLIQEGHPIAFFSRPVAPRHRALAAEY 843

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTQP 2881
 +E + LV A++HWRPYL +F + D +L+YLLDQR++T P
 Sbjct 844 RELIGLVHAVRHWRYPLWGRRFVVKTDHYNLKYLLDQRLSTIP 886

>gi|62733109|gb|AA95226.1| retrotransposon protein, putative, unclassified [Oryza
 sativa
 Japonica Group]
 Length=1513

Score = 243 bits (619), Expect (3) = 6e-135
 Identities = 122/236 (51%), Positives = 160/236 (67%), Gaps = 7/236 (2%)
 Frame = +3

Query 1707 PKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSSYSS 1886
 PKGLPP R DH I +K GA P N+RPYR PH QK ++ ++ E++ I++SNS YSS
 Sbjct 621 PKGLPPQRGCDHVITLKDGAIPPNLRPYRVPHHQKEAMEKIIAELIESKEIQVSNSPYSS 680

Query 1887 PVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARYHQI 2066
 P ++V++KDGSLC+DY+ L+ TV +KF +P++++LLDELNG F+K+DL + YHQI
 Sbjct 681 PAVMVRKDKGSRWLKVDYRQLNAQTVKNKFPMP IIEDLLDELNGAKIFTKLDMLSGYHQI 740

Query 2067 RMHKP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFDDILV 2231
 RM +P FRTH GHYE VMPFGLTN P TFQ MN L PF R++V+VFFDDIL+
 Sbjct 741 RMSRPDIPKTAFRTHLGHYEYQVMPFGLTNAPATFQSLMNQVLAPFFRKFLVVFDDILI 800

Query 2232 YSKSWEAHLHDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMP 2399
 YSK E H +H+ VL L + + KKC+FG LGH+IS+ GV P
 Sbjct 801 YSKDREEHKEHIRLVQLKANNLV--IKPKKCAFLSSVSYLGHIIISQNGVATDP 854

Score = 149 bits (376), Expect (3) = 6e-135
 Identities = 91/260 (35%), Positives = 134/260 (51%), Gaps = 10/260 (3%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISR-----PFWKDITKINE 3041
 Q + KL+ Y++ I YK G N V DALSR +D+ I P W I +
 Sbjct 1021 QHKLKLLKMEYDYIIIEYKAGKDNVADALSRPQDQLQTEICNAITVVIPKW--IIDVQN 1078

Query 3042 EVQKDPALAKIREELKDNLDSPQYTLCEIDILYFRGRLVLLASSLWIPKLLQEFQTSLMG 3221
 + D KI + N D Y+ E IL F+GR+ + + L++++ S G
 Sbjct 1079 SYEGDVQAHKILSMIGTNSDPDQHYSFENGILRFKGRIVYGEETSIRTNLIRDYHCSAFG 1138

Query 3222 GHSGIYITYRRITQSLYWIPIKGEITKFVACHVGRSKYQASSPAGLLQPLPIPNAIWE 3401
 GHSG+ T+ RI YW +K + F+ C V Q +K + GLL PL + + W
 Sbjct 1139 GHSGMRATHHRIKALFYWPGGLKKTVMFIRECPVCQITKVEHIIHIPGLLNPLEVLDMAWT 1198

Query 3402 EISMNFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIWLLEVPI 3575
 I+M+FI G+ KSK D ILV VD+L+KY +F+ + HPY +V++ I L +P+
 Sbjct 1199 HITMDFIEGLPKSKWKDAILVVVDRLTKYAHFLALSHPSVEQVVEIFMNNIHLHGMPM 1258

Query 3576 SIVSDSDLIFMSHFLQELFK 3635
 +I+ D D IF S QE+FK
 Sbjct 1259 AIIIDRDRIFTSQLFQEIFK 1278

Score = 139 bits (350), Expect (3) = 6e-135
 Identities = 71/159 (44%), Positives = 105/159 (66%), Gaps = 0/159 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTKTLRGFLELTGYIKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
 E I+ WP+PK LR FL +TGY+R I Y I RPL D+LK F+W E +A
 Sbjct 858 EKIVSWPIPKNVTDLRKFLGMTGYRRFIQGYVLICRPLHMDLKKEGFQWGEKQTEAFKF 917

Query 2573 LQQAITTIPTLSMLDFSKQFSIECDASGKIGVVLTDQRKQIAYFNKALKDLTSLKSMYE 2752
 L+Q + + P L++ DFSK+F+IE DA G GIG VL Q + IA+++K+L ++S+YE
 Sbjct 918 LKQKMCSSPVLTLPDFSKEFTIEADACGTGIGAVLMQGDRIAFYKSLGPKAAAQSIYE 977

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
 KE+MA++ A++ WR Y K I DQ+SL++++QR+
 Sbjct 978 KEAMAILEALKWRHYFLGSKLVIKTDQQSLKHHMNQRL 1016

>gi|108864085|gb|ABA91843.2| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]
 Length=1411

Score = 243 bits (619), Expect (3) = 6e-135
 Identities = 122/236 (51%), Positives = 160/236 (67%), Gaps = 7/236 (2%)
 Frame = +3

Query 1707 PKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIIRLSNSSYS 1886

Sbjct 519 PKGLPP R DH I +K GA P N+RPYR PH QK ++ ++ E++ I++SNS YSS 578
 PKGLPPQRGCDHVITLKDGAIPPNLRPYRVPHHQKEAMEKIIAELIESKEIQVSNSSPYSS

Query 1887 PVILVKKRKGDS*RLCMDYQALSKATVPDKFLIPVMKELDELNGPIHFSKIDLKARYHQI 2066
 P ++V++KDG RLC+DY+ L+ TV +KF +P++++LLDELNG F+K+DL + YHQI
 Sbjct 579 PAVMVRKKDGSRWRLCVDYRQLNAQTVMKNKFPMPIIEDLLDELNGAKIFTKLDLMSGYHQI 638

Query 2067 RMHKP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFDDILV 2231
 RM +P FRTH GHYE VMPFGLTN P TFQ MN L PF R++V+VFFDDIL+
 Sbjct 639 RMSRPDIPKTAFRTHLGHYEYQVMPFGLTNAPATFQSLMNQVLAPFFRKFLVVFDDILI 698

Score = 149 bits (376), Expect (3) = 6e-135
 Identities = 91/260 (35%), Positives = 134/260 (51%), Gaps = 10/260 (3%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRDEDKELQGISR-----PFWKDITKINE 3041
 Q + KL+ Y++ I YK G N V DALSR +D+ I P W I +
 Sbjct 919 QHKLKLLKMEYDYIIIEYKAGKDNVADALSRPQDQLQTEICNAITVVIPKW--IIDVQN 976

Query 3042 EVQKDPALAKIREELKDNLDSPQYTLCEIDILYFRGRLVLLASSLWIPKLLQEFQTSLMG 3221
 + D KI + N D Y+ E IL F+GR+ + + L++++ S G
 Sbjct 977 SYEGDVQAHKILSMIGTNSDPDQHYSFENGILRFKGRIVYGEETSIRTNLIRDYHCSAFG 1036

Query 3222 GHSGIYITYRRITQSLYWIPIKGEITKFVACHVGRSKYQASSPAGLLQPLPIPNAIWE 3401
 GHSG+ T+ RI YW +K + F+ C V Q +K + GLL PL + + W
 Sbjct 1037 GHSGMRATHHRIKALFYWPGGLKKTVMFIRECPVCQITKVEHIIHIPGLLNPLEVLDMAWT 1096

Query 3402 EISMNFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIWLLEVPI 3575
 I+M+FI G+ KSK D ILV VD+L+KY +F+ + HPY +V++ I L +P+
 Sbjct 1097 HITMDFIEGLPKSKWKDAILVVVDRLTKYAHFLALSHPSVEQVVEIFMNNIHLHGMPM 1156

Query 3576 SIVSDSDLIFMSHFLQELFK 3635
 +I+ D D IF S QE+FK
 Sbjct 1157 AIIIDRDRIFTSQLFQEIFK 1176

Score = 139 bits (350), Expect (3) = 6e-135
 Identities = 71/159 (44%), Positives = 105/159 (66%), Gaps = 0/159 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTKTLRGFLELTGYIKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
 E I+ WP+PK LR FL +TGY+R I Y I RPL D+LK F+W E +A
 Sbjct 756 EKIVSWPIPKNVTDLRKFLGMTGYRRFIQGYVLICRPLHMDLKKEGFQWGEKQTEAFKF 815

Query 2573 LQQAITTIPTLSMLDFSKQFSIECDASGKIGVVLTDQRKQIAYFNKALKDLTSLKSMYE 2752
 L+Q + + P L++ DFSK+F+IE DA G GIG VL Q + IA+++K+L ++S+YE
 Sbjct 816 LKQKMCSSPVLTLPDFSKEFTIEADACGTGIGAVLMQGDRIAFYKSLGPKAAAQSIYE 875

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
 KE+MA++ A++ WR Y K I DQ+SL++++QR+
 Sbjct 876 KEAMAILEALKWRHYFLGSKLVIKTDQQSLKHHMNQRL 914

>gi|10140673|gb|AAG13508.1|AC068924_13 putative gag-pol polyprotein [Oryza sativa Japonica Group]
 Length=1608

Score = 231 bits (588), Expect(3) = 8e-135
 Identities = 125/239 (52%), Positives = 154/239 (64%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 FS P LPP R DH I + GA P N+RPYRY K+EI+ V EML G+I+ S+S
 Sbjct 615 FSEPTLPPKRNCDHHIPLVEGAKPVNLRPYRYKPAKLDIERQVAEMLRSGVIQPS SSP 674

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELDELNGPIHFSKIDLKARY 2057
 +SSP +LVK+KDG+ RLC+DY+ L+ TV K+ +PV+ ELLDEL G FSK+DL+A Y
 Sbjct 675 FSSPALLVKKKDGTWRLCIDYRQLNDVTVKSKYPVPVIDELDELAGSKWFSKLDLRAGY 734

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQIRM +K F+TH GHYE VM FGLT P TF AMN TL P LR++ +VFFDD
 Sbjct 735 HQIRMAEGDEYKTAFTQTHSGHYEYKVMFGLTGAPATFLSAMNETLSPVLRKFALVFFDD 794

Query 2223 ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGVLMPR 2399
 IL+YS + E HL H+ VL L H+ V KCSF Q+ LGHVI GV P
 Sbjct 795 ILIYSPTLELHLQHVRTVLQLLSAHQW--KVLSKCSFAQQEISYLGHVIGAGVATDP 851

Score = 152 bits (383), Expect(3) = 8e-135
 Identities = 78/157 (49%), Positives = 104/157 (66%), Gaps = 1/157 (0%)
 Frame = +2

Query 2408 WPMPTKPTKLRGFLELTGYKRSICNYGKIARPLIDLLK*G-NFKWNEDSIKASIQLQQA 2584
 WP P T K LRGLF L GYY++ + +G I++PL LLK G FKW + A QL+QA
 Sbjct 860 WPQPTTIKKLRGLGLAGYRKFVRHFGILSKPLTQLLKKGIPFKWTEPEISAFQQLKQA 919

Query 2585 ITTIPTLSMLDFSQFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTLSKSMYEKESM 2764
 + P L++ DFSK F+IE DAS GIG VL+Q++ IAY ++AL T S YEKE M
 Sbjct 920 LVAAPVLALPDFSKHFTIETDASDVGIGAVLSQEKHPIAYLSRALGPKTRGLSTYEKEYM 979

Query 2765 ALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 A++LA++HWRPYL +F I D SL +L +QR+ T
 Sbjct 980 AIIlaveHWRPYLQQGEFIILTDHHSMLHLTEQRLHT 1016

Score = 148 bits (373), Expect(3) = 8e-135
 Identities = 92/256 (35%), Positives = 142/256 (55%), Gaps = 7/256 (2%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDED--KELQGISR--PFWKDITKINEEVQ 3050
 QQ KLLG ++ I Y+ G SN DALSR+ E+ IS P W + ++ + Q
 Sbjct 1019 QQKAFTKLLGLQYKICYRKGVSNAADALSRRSEPISEVAIASECIPSW--MQELMQGYQ 1076

Query 3051 KDPALAKIREELKDNLDSPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSIMGGHS 3230
 D ++ EL + +S Y L IL ++G++ + ++ KL+ E + +GGHS
 Sbjct 1077 LDGQSQQLLAEALAI SPNSRKDYQLCQGLIKYKGIWVGNTALQHLVNLHATPLGGHS 1136

Query 3231 GIYITYRRITQSLYWIPIKGEITKFVVACHVGQRSKYQASSPAGLLQPLIPNAIWEEIS 3410
 G +TYR++ W +K I + + +C V ++K + GLLQPLP+P W+ IS
 Sbjct 1137 GFPVTRYKVSLSFAWPGMKKLIKEQLQSCQVCLQAKPDRARYPGLLQPLPVPAGAWQTIS 1196

Query 3411 MNFIVGMLKSGFVDILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIV 3584
 ++FI G+ +S ++ ILV VDK SKY +FI + HP+ A + +K I L +P +I+
 Sbjct 1197 LDFIEGLPRSSHYNILVVDKFSKYSHFIPLSHPFNAGGVAQEFMKNIYKLHGLPRAII 1256

Query 3585 SDSDLIFMSHFLQELF 3632
 SD D IF S F +LF
 Sbjct 1257 SDRDKIFTSQFWDQLF 1272

>gi|115486613|ref|NP_001068450.1| Os11g0677100 [Oryza sativa (japonica cultivar-group)]
 Length=1445

Score = 229 bits (583), Expect(3) = 2e-134
 Identities = 124/259 (47%), Positives = 165/259 (63%), Gaps = 11/259 (4%)
 Frame = +3

Query 1650 EPRKLVVASTDRVCYSFSG----PKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNE 1817
 E + V A ++ F+G P+GLPP+R DH+I + GA P N+RPYRY K+E
 Sbjct 465 EEHQNVPAVPQKILQEFAGVFAEPRGLPPTRYCDHRIPLIEGAQPVNLRPYRYNPELKDE 524

Query 1818 IKTLVVEML*LGIIRLSNSSYSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKE 1997
 I+ V EML G+I+ S S++SSP +LV++K G+ RLC+DY+ L+ T+ K+ +P++KE
 Sbjct 525 IERQVAEMLSSGVIQPSQSTWSSPALLVRKKYGTWRLCVDYRHLNALTIKSKYPVPIIKE 584

Query 1998 LLELNGPIHFSKIDLKARYHQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ* 2162
 LLEL+G FSK+DL+A YHQIRM HK F+TH HYE VM FGLT P TFQ
 Sbjct 585 LLELSGAKWFSKLDLRAGYHQIRMVPGEEHKTAFQTHSSHYEYRVMFGLTGAPATFQG 644

Query 2163 AMNATLKPFLRRYVVVFDDILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQ 2342
 MN TL LR+ +VFFDDILVYS ++HL HL VL L + ++ V KCSF Q
 Sbjct 645 VMNKTLASVLKRCALVFFDDILVYSPDLQSHLTHLQVQLLRQDHW--QVKMSKCSFAQ 702

Query 2343 IKAGCLGHVISKEGVLMPR 2399
 + LGH+I +GV P
 Sbjct 703 PQVSYLGHIIAGQGVSTEP 721

Score = 153 bits (387), Expect(3) = 2e-134
 Identities = 93/255 (36%), Positives = 146/255 (57%), Gaps = 12/255 (4%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRD--EDKELQGISRPFWKDITKINEEVQK 3053
 QQ KLLG ++ I Y+ G+SN V DALSR+ E +L IS ++ + ++
 Sbjct 889 QQRAFTKLLGLQYKIGYRKGSSNAVDALSRRREVGEQQLSAIS-----EVTKGYEQ 940

Query 3054 DPALAKIREELKDNLDSPQYTLECDILYFRGRLVLLASSLWIPKLLQEFQTSIMGGHSG 3233
 DP +++ EL N + YTL ++ ++GR+ + ++ KL+ E + +GGHSG
 Sbjct 941 DPHTSQLLAEALAINSIKHEHYTL SHGLIRYKGRIWIGNNTDLQNKLIAELHNNPIGGHSG 1000

Query 3234 IYITYRRITQSLYWIPIKGEITKFVVACHVGQRSKYQASSPAGLLQPLIPNAIWEEISM 3413
 +TYRRI + W +K ++ + C V ++K + GLLQPLP+P W+ I+M
 Sbjct 1001 FFPVTRYRRIKRLFAWPGMKKQVKCQLQHCQVCIAKPERVKYPGLLQPLPVPAGAWQTITM 1060

Query 3414 NFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIVS 3587
 +F+ G+ KS+ ++ ILV VDK SKY +F+ + HP+ A ++ +K I L +P IVS
 Sbjct 1061 DFLEGLPKSERYNCILVVVDKFSKYAHFVPLTHPFTAETVATAFMKNIYKLHGMPRVIVS 1120

Query 3588 DSDLIFMSHFLQELF 3632
 D D IF S F + LF
 Sbjct 1121 DRDKIFTSQFWEYLF 1135

Score = 147 bits (370), Expect(3) = 2e-134
 Identities = 77/160 (48%), Positives = 107/160 (66%), Gaps = 1/160 (0%)
 Frame = +2

Query 2399 IL*WPMPTKPTKLRGFLELTGYKRSICNYGKIARPLIDLLK*G-NFKWNEDSIKASIQL 2575
 +L WP P + K LRGLF L GYY++ + N+G I++PL LL+ G +F+W ++ A QL
 Sbjct 727 VLTWPTPISVKKLRGLGLAGYRKFVNKFGIISKPLTQLLRKGVSVFRWGEAEAAQQL 786

Query 2576 QQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTQDRKQIAYFNKALKDLTSLKSMYEK 2755
 +QA+T+ P L + DFSKQF++E +AS GIG VL+Q+ IAY +KAL + S YEK
 Sbjct 787 KQALTSAPVLGLPDFSKQFTVETNASDAGIGAVLSQEGHPIAYLSKALGPRSKGLSTYEK 846

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 E MA++LA+ HWR YL +F I D SL +L DQR+ T
 Sbjct 847 ECMAILLAVDHWRSYLQHQEFLLITDYHSLVHLDDQRLHT 886

>gi|242085414|ref|XP_002443132.1| hypothetical protein SORBIDRAFT_08g010830
 [Sorghum bicolor]
 gi|241943825|gb|EES16970.1| hypothetical protein SORBIDRAFT_08g010830 [Sorghum
 bicolor]
 Length=1462

Score = 223 bits (568), Expect (3) = 2e-133
 Identities = 122/237 (51%), Positives = 154/237 (64%), Gaps = 11/237 (4%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F+ P+GLPP R DH I ++ GA P P + K+E++ M+ G+IR S+S+
 Sbjct 476 FAEPQGLPPRSRDHGITLQPGAPPVAYGPPAH---KDELERQCAVMQOGLIRRSSA 531

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSPV+LVK+ DGS R C+DY+AL+ TV D F IPV+ ELLDEL G F+K+DL++ Y
 Sbjct 532 FSSPVLLVKKADGSRFCVDYRALNAITVKDAFFIPVVDDELDELRGAKFFTKLDLRSGY 591

Query 2058 HQIRMH-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQ+RM K FRTH G YE VMPFGL N P TFQ MN L+PFLRR+V+VFFDD
 Sbjct 592 HQVRMRASIDKTAFRTHDGLYEFVMPFGLCNAPATFQALMNDVLRFLRRFVLVFFDD 651

Query 2223 ILVYSKSWEAHLHDLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLM 2393
 IL+YS SW HL HL VL L H F V + KC+FG LGH+IS+ GV M
 Sbjct 652 ILIYSTSWADHLRLRAVLTVLQHHQLF--VKRSKCAFGVSSISYLGHIISEAGVAM 706

Score = 154 bits (389), Expect (3) = 2e-133
 Identities = 97/257 (37%), Positives = 140/257 (54%), Gaps = 15/257 (5%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRRDEKELQ-GISRPFWKDITKINEEVQKD 3056
 Q +WV KLLGY+F + YK GA N V DALSRD + + IS P + I ++ + +D
 Sbjct 875 QHHWVGKLLGYDFSVEYKPGAQNTVADALSRRDTPGEGVLAISAPRFDIERLQAQVQD 934

Query 3057 PALAKIREELKDNLDSPQYTLCECDILYFRGRLVLLASSLWIPK---LLQEFQTSLMG-G 3224
 PAL IR+EL S P ++ LV S L++P LL+E ++ G
 Sbjct 935 PALVAIRDELTAAGRSAPWSIID-----GLVTYDSRLYVPSVSALLREIVAACHDDG 986

Query 3225 HSGIYITYRRITQSLYWIPIKGEITKFVACHVGQSKYQASSPAGLLQPLPIPNAIWEE 3404
 H G+ T R+ + ++ + + FV AC QR K + PAGLL PLP+P +W +
 Sbjct 987 HEGVQRTLHRLRRDFHFPDMGRVVQDFVRACPTCQRFKTEHLHPAGLLPLPVPTGVWTD 1046

Query 3405 ISMNFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIIWLLEVPIS 3578
 I ++FI + + KG VIL VD+ SKY +FI + HPYFA S+ I+ L +P S
 Sbjct 1047 IGLDFIETLPRVKGKSVILTAVDRFSKYCHFIPLAHPYFAESVAQAFYSGIVRLHGLPQS 1106

Query 3579 IVSDSDLIFMSHFLQEL 3629
 +VSD D I+ + + L
 Sbjct 1107 MVSDRDPIYNTAYQSSL 1123

Score = 149 bits (376), Expect (3) = 2e-133
 Identities = 73/163 (44%), Positives = 106/163 (65%), Gaps = 0/163 (0%)
 Frame = +2

Query 2393 EAIL*WPMPTKPTKLRGFLLELTGGYKRSICNYGKIARPLIDLK*GNFKWNEDSIKASIQ 2572
 +A+ WP P++ + +RGFL L GYY++ + +YG IA PL LLK F W +D+ A
 Sbjct 712 QAVADWPQPRSAVRGFLGLAGYYRKQVQDYGTIAAPLTALLKKDGFATWDDAAAAFQA 771

Query 2573 LQQAITTIPTLSMLDFSKQFSIECDASGKGIGVVLTQDRKQIAYFNKALKDLTSLKSMYE 2752
 L+ AIT+ P L++ +F +F +ECDAS G G VL QD+ IA+F++ + S + YE
 Sbjct 772 LKAAITSAPVLALPNFQLEFIVECDASTHGFAGVLLQDKHPIAFFSRPVAPRHRSLAAYE 831

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTQP 2881
 +E + IV AI+HWRPYL +FT+ D SL +LLDQR++T P
 Sbjct 832 RELIGLVHAIRHWRPYLWGRRTVTRTDHYSNLFLLQRLSTIP 874

>gi|116309424|emb|CAH66499.1| H0321H01.8 [Oryza sativa (indica cultivar-group)]
 Length=1602

Score = 225 bits (574), Expect (3) = 6e-133
 Identities = 121/239 (50%), Positives = 156/239 (65%), Gaps = 7/239 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
 F P+GLPP R DH I + GA P N+RPYR+ K+EI+ + EML G+I+ S S
 Sbjct 598 FQEPGLPPRRACDHTINLIPGAKPINLRPYRHNPAKDEIEKQITEMLSSGVIQHSQSP 657

Query 1878 YSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 +SSP ILVK+KDG+ RL +DY+ L+ TV K+ +PV++ELDEL G F+K+DL++ Y
 Sbjct 658 FSSPAILVKKKDGTRWLRVIDYRQLNNITVTKYPVPIEELDELTAQWFTKLDLRSGY 717

Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFDD 2222
 HQIRM K F+TH GHYE VM FGLT P TF AMN TLK LR++ +VFFDD
 Sbjct 718 HQIRMAEGEEPKTAFTQTHSGHYEYKVMFGLTGAPATFLKAMNDTLKSVLRKALVFFDD 777

Query 2223 ILVYSKSWEAHLHDLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP 2399
 IL+YS + +HL+HL VL L H++ V KCSFGQ + LGH+I GV P
 Sbjct 778 ILIYSPTLSSHLEHLKQVLQLLRNHHW--KVLSKCSFGQQQLSYLGHIIIGVNGVATDP 834

Score = 157 bits (396), Expect (3) = 6e-133
 Identities = 91/249 (36%), Positives = 142/249 (57%), Gaps = 4/249 (1%)
 Frame = +3

Query 2898 KLLGYEFDIVYKVGASNKVVDALSRR--DEDKELQGISRPFWKDITKINEEVQKDPALAK 3071
 KLLG ++ I Y+ G+SN DALSR+ D + E+ IS + + ++ + +KD AK
 Sbjct 1008 KLLGLQYKICYRKGSNAADALSRRKFQDSNSEIFAISSSVPQWLMVETQGYEKDAQAAK 1067

Query 3072 IREELKDNLDSPQYTLCECDILYFRGRLVLLASSLWIPKLLQEFQTSLMGHSGIYITYR 3251
 + L + + H Y L+ I+ ++ R+ + + KL++E S +GGHSG +TYR
 Sbjct 1068 LLSTLAIHPEKHIIHYFLDNGIIRYKNRIWGNPNELQKLIRELHASPVGHSFGFPVITYR 1127

Query 3252 RITQSLYWIPIKGEITKFVACHVGQSKYQASSPAGLLQPLPIPNAIWEEISMNFIVGM 3431
 +I Q W +K I + V C V ++K GLLQPLP+P W+ +S++FI G+
 Sbjct 1128 KIKQLFAWPNMKMIKESVQRQVCLQAKPDRKYPGLLQPLVPPEGSWQAVSLDFIEGL 1187

Query 3432 LKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIIWLLEVPISIVSDSLIF 3605
 KS G++ ILV VD+ SKY +F+ +KHP+ A + + I L +P +IVSD D IF
 Sbjct 1188 PKSAGYNCILVVDRFSKYAHFALKHPFTAIDVAQAMFYHKLHGLPQTIVSDRDKIF 1247

Query 3606 MSHFLQELF 3632

S ++LF
 Sbjct 1248 TSQLWEQLF 1256

Score = 142 bits (358), Expect (3) = 6e-133
 Identities = 75/160 (46%), Positives = 103/160 (64%), Gaps = 1/160 (0%)
 Frame = +2

Query 2399 IL*WPMKPTKTLRGFLELTGYKRSICNYGKIARPLIDLLK*G-NFKWNEDSIKASIQL 2575
 +L W +P + K LRGL L GYY++ + N+G I++PL LL+ G + W ++ A L
 Sbjct 840 VLDWAVPVSTKKLRGLGLAGYYRKFVNFGIISKPLTQLLRKGVYVWTTETDNAFHTL 899

Query 2576 QQAITTIPTLSMLDFSQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYEK 2755
 +QA+ + P LS+ DF K F++E DAS GIG VL+QD+ IAY +KAL T S YEK
 Sbjct 900 KQALASAPVLSLPDFQKTFVETDASDCGIGAVLSQDKHPIAYVSKALGPRTRGLSTYEK 959

Query 2756 ESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 E MA++LA+ HWR YL +F I D SL +L DQR+ T
 Sbjct 960 ECMAILLAVDHWSYQLHGEFIILTDHSLMHLSDQRLHT 999

>gi|78183243|emb|CAJ00274.1| hypothetical protein [Lotus japonicus]
 Length=1508

Score = 232 bits (591), Expect (3) = 2e-132
 Identities = 125/236 (52%), Positives = 162/236 (68%), Gaps = 8/236 (3%)
 Frame = +3

Query 1698 FSGPKGLPPSREV-DHKIAIKSGAYPDNVRPYRYPHLQKNEIKTLVVEML*LGIIRLSNS 1874
 F P LPP R + DHKI +K G+ P ++RPYRYP QK+ I +V E+L G+I+ S+S
 Sbjct 572 FEEPAQLPPFRGIHDHKIILKDGSNFVSLRPYRYPQAQKDVIDKMKVLESGVIQPSSS 631

Query 1875 SYSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKAR 2054
 ++SP++LVK+KDGS R+C+DY+ L+ TV KF IP++++LLDEL G FSK+DL+A
 Sbjct 632 PFASPIVLVKKKDGSWRMCDVYRKLNDMTVKAFFIPLVEDLDELGGAKIFSKDLRAG 691

Query 2055 YHQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFDD 2219
 YH+RM K F+TH G YE VMPFGLTN P+TFQ AMNA PFLR+ V++FFD
 Sbjct 692 YHQLRMRPEDVEKTAFTQTHSGQYEVVMPFGLTNAPSTFQAMNAIFAPFLRKSVLIFDD 751

Query 2220 DILVYSKWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGV 2387
 DILVYS + EABL HL V A L +H F+ V + KC+F LGH IS GV
 Sbjct 752 DILVYSATVEAHLQHLREVFAVLRKHSFY--VKRSKCAFFTPVIEYLGHFISASGV 805

Score = 149 bits (377), Expect (3) = 2e-132
 Identities = 91/252 (36%), Positives = 133/252 (52%), Gaps = 9/252 (3%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRREDKELQ----GISRPFWKDITKINEEV 3047
 Q WV KL+G + I YK G N V DALSR + Q IS W +T +
 Sbjct 976 QYRWVTKLMGLSYVVIQYKRGKENNVADALSRASHGELFQLSVSSISSELWGLLT---QAY 1032

Query 3048 QKDPALAKIREELKDNLDLSDHPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSIMGGH 3227
 D AL ++ ++ H Y++ L+ + RL++ +S +L+ +S GGH
 Sbjct 1033 AADALQQLISQVLAQPQLHAHYSVVDGFLFRKHRLMIPNNSQVRTLILEWLHSSHQGGH 1092

Query 3228 SGIYITYRRITQSLYWIPIKGEITKFVNVACHVGQRSKYQASSPAGLLQPLIPINAIWEEI 3407
 SGI T RI +W + ++ F+ C R KY+ + GLLQPLPIP +W+ I
 Sbjct 1093 SGIRATVVRKISLFFWKGLSKDVADFIQKCECLCKYERVASPGLLQPLIPAGVWQSI 1152

Query 3408 SMNFIVGMLKSGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISI 3581

+M+FI + KS G D I V +D+LSKY +FI + HPY A ++ + +KE+ L P +I
 Sbjct 1153 AMDFIDKLPKSHGKDAIWVIDRLSKYAHFIPLTHPYTASTLAEIFIKEVYRLHGAPSNI 1212

Query 3582 VSDSDLIFMSHF 3617
 VSD D +F S F
 Sbjct 1213 VSDRDPLFTSTF 1224

Score = 141 bits (355), Expect (3) = 2e-132
 Identities = 73/161 (45%), Positives = 102/161 (63%), Gaps = 0/161 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTKTLRGFLELTGYKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572
 +AI WP P T K LRGL LTGY+R I Y +A PL DLL+ F W+ + A +Q
 Sbjct 813 KAIQDWPEPVTIKQLRGFLGLTGYRRFICKGYSILASPLTDLRLKDFHWSAASAAFLQ 872

Query 2573 LQQAITTIPTLSMLDFSQFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYE 2752
 L+ A+ P L++ D K F++E DAS GIG VL QD+ A+ +K L S+Y+
 Sbjct 873 LKNALVQAPVLAIPDLQKPFVETDASSTGIGAVLLQDKHPVAFISKVLSPRNRLLSVYD 932

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 +E +ALV A+ W YL +FTI DQ+SL++LL+QR++T
 Sbjct 933 RELLALVHAVTKWHQYLAIQQTILTDDQSLKFLLEQRLST 973

>gi|77555174|gb|ABA97970.1| retrotransposon protein, putative, unclassified,
 expressed [Oryza
 sativa (japonica cultivar-group)]
 Length=1548

Score = 222 bits (565), Expect (3) = 3e-132
 Identities = 117/235 (49%), Positives = 151/235 (64%), Gaps = 7/235 (2%)
 Frame = +3

Query 1698 FSGPKGLPPSREV-DHKIAIKSGAYPDNVRPYRYPHLQKNEIKTLVVEML*LGIIRLSNS 1877
 F LPP R +DH I++ + P N RPYRYP QK+EI+ V ML G+I S S
 Sbjct 598 FQDSNTLPPHRVLDHVISLPLNSVPVNARPYRYPQAQKDEIERQVSTMLSAGLISPSCSP 657

Query 1878 YSSPVILVKRKDGS*RLCMDYQALS KATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
 ++SPV+LVK+KD S R C+DY+ L+ T+ +KF +P++ ELLDEL G FSK+DL++ Y
 Sbjct 658 FASPVLLVKKKDNWRFCVDYRRLNDLTIKNKFLPIVDELDELACTQFFSKDLRSGY 717

Query 2058 HQIRM-----KPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVFDD 2222
 HQIRM K F+TH GH++ VMPFGLTN P TFQ MN+ P+LR++V+V DD
 Sbjct 718 HQIRMQESDEFKTAFTKTHGHGFQFRVMPFGLTNAPATFQCLMNSIFAPYLRKFVLVFMDD 777

Query 2223 ILVYSKWEAHLDHLS*VLARLLEHYFFTNVFKKCSFGQIKAGCLGHVISKEGV 2387
 ILVYSKSW HL HL VL L +H + KCSF + LGH+IS GV
 Sbjct 778 ILVYSKSWTHLKLRLCVLQLLQHQQLCAKL--SKCSFAAPQLEYLGHIIISAAGV 830

Score = 172 bits (437), Expect (3) = 3e-132
 Identities = 100/256 (39%), Positives = 147/256 (57%), Gaps = 6/256 (2%)
 Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRREDKELQGIS--RPFWKDITKINEEVQK 3053
 Q+ + KL+G ++ YK GA NK DALSR LQ IS +P W + ++
 Sbjct 1002 QRKAMTKLIGLQYKQYKRGAEKNSADALSRVGHFFSLQAISIAQPVW--VQEVVNSYVV 1059

Query 3054 DPALAKIREELKDNLDLSDHPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSIMGGHSG 3233
 D + EL + ++L ++ +GR+ L A+S K++ F S +GGHSG
 Sbjct 1060 DNQAQSLLTALMSPNASGFSLVHGLIKKGRWLWANSALHTKIISFHDASIGGHSG 1119

Query 3234 IYITYRRITQSLYWIPIKGEITKFFVACHVGQSKYQASSPAGLLQPLPIPNAIWEEISM 3413
 + TY R+ + W +K + +F+ C V Q++K++ S GLLQPLPIP W++ISM
 Sbjct 1120 VMATYHRVKKLFVWKGKLSVVEEFIQCCVVCQKAKHEHCSSPGLLQPLPIPITGAWQDISM 1179

Query 3414 NFIVGMLKSKGDFVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIVS 3587
 +FI G+ SKG DVILV VD+ +KY +F+ +KHP+ A + D + ++ L +P SIVS
 Sbjct 1180 DFIEGLPLSKGSDVILVVDRFTKYAHFLPLKHPFTAVQVADNYLSKVASLYGMPKSIVS 1239

Query 3588 DSDLIFMSHFLQELFK 3635
 D D IF SHF Q LFK
 Sbjct 1240 DRDKIFTSHFWQHLFK 1255

Score = 127 bits (320), Expect(3) = 3e-132
 Identities = 70/163 (42%), Positives = 103/163 (63%), Gaps = 1/163 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTPKTLRGFLELTGYIKRSICNYGKIARPLIDLLK*G-NFKWNEDSIKASI 2569
 + +L WP+P LRGFL LTGYI++ + NYG +A+PL LLK F W E + KA
 Sbjct 838 KVMLQWPVPTNLTELRGFLGTGYIKRVKFNKGILAKPLTVLLKKNVFWTEHTQKAFD 897

Query 2570 QLQQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMY 2749
 L+ A+++ P L + +F+K F+IE DA GIG VL+Q+ +A+++KAL S+Y
 Sbjct 898 SLKLAMSSPTVLVLPNFAKPFITETDACSTGIGAVLSQEGHPVAFYSKALGINNQKLSIY 957

Query 2750 EKESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITTQ 2878
 EKE +A+++AI WRPYL F I D +SL +L DQ + ++
 Sbjct 958 EKEFLAIMMAIDKWRPYLLRGPFVIRTDHQSLCHLDDQLLGSE 1000

>gi|78183241|emb|CAJ00278.1| hypothetical protein [Lotus japonicus]
 Length=1508

Score = 232 bits (591), Expect(3) = 3e-132
 Identities = 125/236 (52%), Positives = 162/236 (68%), Gaps = 8/236 (3%)
 Frame = +3

Query 1698 FSGPKGLPPSREV-DHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNS 1874
 F P LPP R + DHKI +K G+ P ++RPYRYP QK+ I +V E+L G+I+ S+S
 Sbjct 572 FEEPAQLPPFGRIGHDKIILKDGSNPVSRLRPYRPPAQKDVIDKMVKELLESVGIQPSSS 631

Query 1875 SYSSPVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKAR 2054
 ++SP++LVK+KDGS R+C+DY+ L+ TV KF IP++++LLDEL G FSK+DL+A
 Sbjct 632 PFASPIVLVKKKDGSRWCMVDYRKLNDMTVAKFPIPLVEDLDELGGAKIFSKDLRLAG 691

Query 2055 YHQIRM-----HKPTFRTHQGHYESPVMFGLTNTPTTFQ*AMNATLKPFLLRYYVVFDD 2219
 YHQ+RM K F+TH G YE VMPFGLTN P+TFQ AMNA PFLR+ V++FFD
 Sbjct 692 YHQLRMRPEDVEKTAFTQTHSGQYEVVMPFGLTNAPSTEQGAMNAIFAFPLRKSVLIFD 751

Query 2220 DILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGV 2387
 DILVYS + EAHL HL V A L +H F+ V + KC+F LGH IS GV
 Sbjct 752 DILVYSATVEAHLQHLREVFVAVLRKHSFY--VKRSKCAFFTPVIEYLGHFISASGV 805

Score = 149 bits (376), Expect(3) = 3e-132
 Identities = 90/252 (35%), Positives = 133/252 (52%), Gaps = 9/252 (3%)
 Frame = +3

Query 2880 QQYWVAKLLGYEFDIVYKVGASNKVVDALSRDEDEKELQ----GISRPFWKDITKINEEV 3047
 Q WV KL+G + I YK G N V DALSR + Q +S S W +T +
 Sbjct 976 QYRWVTKLMGLSYVIQYKRGKENVADALSRASHGELFQLSVSSVSSELWGLLT---QAY 1032

Query 3048 QKDPALAKIREELKDNLDSPQYTLCECDILYFRGRLVLLASSLWIPKLLQEFQTSMLMGGH 3227
 D AL ++ ++ H Y++ L+ + RL++ +S +L+ +S GGH
 Sbjct 1033 AADEALQQLISQVLAQFQLHAHYSVVDGFLFRKRLMIPNNSQVRTLILEWLHSSHQGGH 1092

Query 3228 SGIYITYRRITQSLYWIPIKGEITKFFVACHVGQSKYQASSPAGLLQPLPIPNAIWEEI 3407
 SGI T RI +W + ++ F+ C R KY+ + GLLQPLPIP +W+ I
 Sbjct 1093 SGIRATVVRIKSLFFFWKGLSKDVADEFIQKCTCLRCKYERVASPGLLQPLPIPAGVWQSI 1152

Query 3408 SMNFIVGMLKSKGDFVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISI 3581
 +M+FI + KS G D I V +D+LSKY +FI + HPY A ++ + +KE+ L P +I
 Sbjct 1153 AMDFIDKLPKSHGKDAIWVVIDRLSKYAHEFIPLTHPYTASTLAEIFIKEVYRLHGAPSN 1212

Query 3582 VSDSDLIFMSHF 3617
 VSD D +F S F
 Sbjct 1213 VSDRDPLFTSTF 1224

Score = 141 bits (355), Expect(3) = 3e-132
 Identities = 73/161 (45%), Positives = 102/161 (63%), Gaps = 0/161 (0%)
 Frame = +2

Query 2393 EAIL*WPMKPTPKTLRGFLELTGYIKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQ 2572
 +AI WP P T K LRGFL LTGYI+R I Y +A PL DLL+ F W+ + A +Q
 Sbjct 813 KAIQDWPEPVTIKQLRGFLGLTGYIYRRFIKGYSLASPLTDLRLKDGFWHSAASAAFLQ 872

Query 2573 LQQAITTIPTLSMLDFSQKFSIECDASGKGIGVLTQDRKQIAYFNKALKDLTSLKSMYE 2752
 L+ A+ P L++ D K F++E DAS GIG VL QD+ +A+ +K L S+Y+
 Sbjct 873 LKNALVQAPVLAIPDLQKPFVETDASSTGIGAVLLQDKHPVAFISKVLSPRNRLSVYD 932

Query 2753 KESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRITT 2875
 +E +ALV A+ W YL +FTI DQ+SL++LL+QR++T
 Sbjct 933 RELLALVHAVTKWHQYLAIQQFTILTQQSLKFLLEQRLST 973

>gi|115482042|ref|NP_001064614.1| Os10g0419000 [Oryza sativa (japonica cultivar-group)]
 gi|31432119|gb|AAP53789.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]
 Length=1611

Score = 238 bits (607), Expect(3) = 1e-131
 Identities = 119/236 (50%), Positives = 159/236 (67%), Gaps = 7/236 (2%)
 Frame = +3

Query 1707 PKGLPPSREVDHKIAIKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSSYSS 1886
 PKGLPP R DH I +K G+ P N+RPYR PH QK ++ ++ E+ IR+S+S Y S
 Sbjct 689 PKGLPPRRSCDHVINLKVSGSEPNLRPYRPHQKGAEMDIITELFRTQEIIRISDSPIYVS 748

Query 1887 PVILVKRKDGS*RLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARYHQI 2066
 P ++V++KDGS RLC+DY+ L+ T+ +KF +P++++LLDEL+G FSK+DL++ YHQI
 Sbjct 749 PAVMVRKKGDSWRCLVDYRQLNAQTIKNKFPMP IIEDLDELHGAKVFSKDLRSGYHQI 808

Query 2067 RM-----HKPTFRTHQGHYESPVMFGLTNTPTTFQ*AMNATLKPFLLRYYVVFDDILV 2231
 RM K FRTH GHYE VMPFGLTN P TFQ MN L PFLR++V+VFF DIL+
 Sbjct 809 RMAEGDIPKTAFTRLHGHYEYNVMPFGLTNAPATFQALMNQVLAPFLRKFVLVFFADILI 868

Query 2232 YKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGVLMRP 2399
 YSK+ HL+H+ V+ L + + KKC FG + LGH+IS EGV P
 Sbjct 869 YSKTQSEHLEHIKLVMQALSANQLVRL--KKCEFLDRVSYLGHIISSEGVSTDP 922

Score = 157 bits (397), Expect (3) = 1e-131
Identities = 94/258 (36%), Positives = 141/258 (54%), Gaps = 8/258 (3%)
Frame = +3

Query 2880 QQYVWAKLLGYEFDIVYKVGASNKVVDALSRREDKELQ----GISRPFWKDITKINEEV 3047
Q + KL+ +++ I YK G N V DALSR KE Q + P W + I
Sbjct 1089 QHKKLLKLMEFDYVIEYKSGKENLVADALSRPNLKEEQCLPITVVVPEW--VQDIKRSY 1146
Query 3048 QKDPALAKIREELKDNLDLSDHPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSMLGGH 3227
++D KI ++ + D Y LE +L ++GR+ + ++ LL+ + S GGH
Sbjct 1147 EEDIFAHKILSLIETDGDPERHYKLESGLLKYGRIYVGETTEIRMLLLEAYHASYFGGH 1206
Query 3228 SGIYITRRITQSLYWIPIKGEITKFFVACHVQGRSKYQASSPAGLLQPLPIPNAIWEEI 3407
SGI TY RI Q YW +K ++ ++ C Q +K + GLL PL +P+ W I
Sbjct 1207 SGIRATYHRIKQLFYWPGGLKKQVEHYIRECPCTQITKAEHIHIPGLLNPLEVPMAWTHI 1266
Query 3408 SMNFIVGMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVDV--KEIWLLEVPISI 3581
+M+FI G+ KS+G DVILV VD+L+KY +F+ + HPY +V + I L +P+ I
Sbjct 1267 TMDFIEGLPKSQGKDVILVVVDRLTKYAHFALSHPHYTVQVQIFMDNIHKLHGMPMVI 1326
Query 3582 VSDSDLIFMSHFLQELFK 3635
V+D D +F S+F QE+FK
Sbjct 1327 VTDRDRVFTSNFFQEIFK 1344

Score = 125 bits (313), Expect (3) = 1e-131
Identities = 65/151 (43%), Positives = 95/151 (62%), Gaps = 0/151 (0%)
Frame = +2

Query 2417 PKTPKTLRGFLELTGYIKRSICNYGKIARPLIDLLK*GNFKWNEDSIKASIQLQQAITTI 2596
PK +R FL + GYY+R I YG I RPL DLLK FKW + +A L++ +
Sbjct 934 PKNVTEVREFLGMAGYRRFIKGYGVICRPLDHLKDKGFKWGDTOQAEFELLKEKMCNS 993
Query 2597 PTLMLDFSQKFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMYKESMALVL 2776
P L++ DFS+ F IE DA G GIG VL Q + +AYF+KAL ++S+YEKE++A++
Sbjct 994 PVALALPDFSQPFVIETDACIGIGAVLMQKGRPLAYFSKALGPKAAQSVYEKEAIAILE 1053
Query 2777 AIQHWRPYLPD*KFTIYIDQKSLRYLLDQRI 2869
A++ WR Y+ I DQ+SL+++ QR+
Sbjct 1054 ALKKWRHYILGGSLLIKTDQQLKFMMSQRL 1084

>gi|77554308|gb|ABA97104.1| retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]
Length=1412

Score = 236 bits (601), Expect (3) = 4e-131
Identities = 127/239 (53%), Positives = 161/239 (67%), Gaps = 7/239 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
F P+GLPP R DH I +KS A P +RPYR+ +K+EI+ V EML G+I+ SNS+
Sbjct 507 FDDPQGLPPKACRACDHSIPLKSHAKPVFLRPYRHNPAKDEIEKQVKEMLLSGVIOQNSA 566
Query 1878 YSSPVILVKRKDG*SRLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
+SSP +LVK+KDG+ RLC+DY+ L+ T+ KF +PV+ ELLDEL+G FSK+DL+A Y
Sbjct 567 FSSPALLVKKKDGTDWRLCIDYRQLNSITMKGKFPMPVIDELLDELSGSVFSKLDLRAGY 626
Query 2058 HQIRM-----HKPTFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFFDD 2222
HQIR+ HK TF+TH GHYE VM FGLT P TFQ AMN TL P LR++ +VFFDD

Monsanto Company

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RAR-10-071

Sbjct 627 HQIRLVEGEEHKTTFQTHSGHYEYRVMSFGLTGAPATFQAMNDTLAPVLRKFALVFFDD 686
Query 2223 ILVYSKSWEAHLHLDS*VLARLLEHYFFTNVFKKKCSFGQIKACGLGHVISKEGVLMRP 2399
ILVYS +H+ HL VL L EH + V KCSF Q + LGH+IS + V P
Sbjct 687 ILVYSPDLVSHVHHLRQVLQQLTEHQW--KVKLSKCSFAHQHLSYLGHIIISDQRVTTDP 743

Score = 149 bits (377), Expect (3) = 4e-131
Identities = 90/251 (35%), Positives = 142/251 (56%), Gaps = 8/251 (3%)
Frame = +3

Query 2898 KLLGYEFDIVYKVGASNKVVDALSR--DEDKELQGISR--PFWKDITKINEEVQKDPAL 3065
KLLG +F I Y+ G+SN +ALSR+ +E EL +S P W + +++ +D
Sbjct 917 KLLGLQFKICYRKSGSSANAANALSRKYPEELSELHVSSCSPVW--LQEVSDGYLQDVFS 974
Query 3066 AKIREELKDNLDLSDHPQYTLECDILYFRGRVLVLLASSLWIPKLLQEFQTSMLGGHSGIYIT 3245
A++ +L N +S P ++L +L F+GR+ + + K++ +S +GGHSG +T
Sbjct 975 AQLLTDLTNAESRPNFSLCNGVLRFRKGRVWIDNNPSVQDKIISALHSSPLGGHSGFPVT 1034
Query 3246 YRRITQSLYWIPIKGEITKFFVACHVQGRSKYQASSPAGLLQPLPIPNAIWEEISMNFIV 3425
Y +I W +K +I V C + ++K S GLLQPLP+P+ W+ I+M+FI
Sbjct 1035 YSKIISLFAWPKMKKQIHTAVKTCGICMQAKPDHSHKYPGLLQPLPVPDGAWQIITMDFIE 1094
Query 3426 GMLKSKGFDVILVEVDKLSKYRYFIVIKHPYFARSIVD--VKEIWLLEVPISIVSDSDL 3599
G+ KS F+ ILV VDK SKY +F + HP+ A + + + L +P I+SD D
Sbjct 1095 GLPKSGQFCILVVVDKFSKYSHFFPLSHFSAIDVAQSFMVNVYKLHGLPKFIISDRDK 1154
Query 3600 IFMSHFLQELF 3632
I SHF ++LF
Sbjct 1155 ILTSHFWEQLF 1165

Score = 133 bits (334), Expect (3) = 4e-131
Identities = 73/162 (45%), Positives = 103/162 (63%), Gaps = 1/162 (0%)
Frame = +2

Query 2393 EAIL*WPMKPTKTLRGFLELTGYIKRSICNYGKIARPLIDLLK*G-NFKWNEDSIKASI 2569
E ++ W +PK K LRGFL L GYY++ + +G + RPL +LLK F W+ ++ +A
Sbjct 747 EEVVNNAVVPKFVKLRLGFLGLAGYYRKFKVQFGILCRPLTNLLKDVFPVWSVEADQAFK 806
Query 2570 QLQQAITTIPTLSMLDFSQKFSIECDASGKGIGVVLTDQRKQIAYFNKALKDLTSLKSMY 2749
L+QA+ + P LS+ DFS F+IE DAS +GIG VL+Q IA+ +KAL T S Y
Sbjct 807 ALKQALVSAVPLSLPDFSLPFTTIETDASDEGIGAVLSQCCHPIAFLSKALGVTKGLSTY 866
Query 2750 EKESMALVLAIQHWRPYLPD*KFTIYIDQKSLRYLLDQRIIT 2875
EKE +A++LA+ HWR YL +F I D SL +L +QR+ T
Sbjct 867 EKEYLAILLAVDHWRSYLLQEQEFVILTDHHSMLHNEQLRHT 908

>gi|147775005|emb|CAN70471.1| hypothetical protein [Vitis vinifera]
Length=1122

Score = 246 bits (629), Expect (3) = 7e-131
Identities = 117/235 (49%), Positives = 163/235 (69%), Gaps = 7/235 (2%)
Frame = +3

Query 1698 FSGPKGLPPSREVDHKAIAKSGAYPDNVRPYRPHLQKNEIKTLVVEML*LGIIRLSNSS 1877
F P LPP+RE+DH+I +K G P NVRPYR+ QK EI+ V +ML LG+I+ S S
Sbjct 175 FQKPNQLPPAREIDHRITLKEGTEPVNVRPYRYAYFQKAEIEKQVCDMLGLGIKASTSL 234
Query 1878 YSSPVILVKRKDG*SRLCMDYQALSKATVPDKFLIPVMKELLDELNGPIHFSKIDLKARY 2057
+SSPV+LVK+KDG+ R C DY+AL+ T+ D+F IP + ++LDEL+G +F+K+DL+A Y

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Sbjct  235  FSSPVLVKKKDGTRFCTDYRALNAVTIKDRFPIPTVDDMLDELHGATYFTKLDLRAGY  294

Query  2058  HQIRMHKP-----TFRTHQGHYESPVMPFGLTNTPTTFQ*AMNATLKPFLRRYVVVFFDD  2222
           H +R+H P      FRTH GHYE VMPFGL+N P+TFQ  MN+  +P+L ++V+VFF D
Sbjct  295  HYVRVHPPDIPKTAFRTHNGHYEYLVMPFGLSNAPSTFQAIMNSIFRPYLGKFVLVFFXD  354

Query  2223  ILVYSKSWEAHLDHLS*VLARLLEHYFFTNVFKKKCSFGQIKAGCLGHVISKEGV  2387
           IL+YS +  HL+H+      L +H FF  +  KC+FGQ +  LGH+++  GV
Sbjct  355  ILIYSPNXNMHLEHVKAFAEILRQHQFFVKI--SKCAFGQXELEYLGHIVTXXGV  407

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Lambda      K      H
      0.318      0.134      0.401

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Gapped
Lambda      K      H
      0.267      0.0410      0.140

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Effective search space used: 2097114074532

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Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
excluding environmental samples from WGS projects
Posted date: Dec 31, 2009  5:42 PM
Number of letters in database: 3,505,279,183
Number of sequences in database: 10,272,453

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Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Neighboring words threshold: 12
Window for multiple hits: 40

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