

SUMMARY

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STUDY TITLE

Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border
Sequences

DATA REQUIREMENTS

N/A

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STUDY COMPLETED ON

28 – June – 2010

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Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border Sequences

SUMMARY

A plant-optimized aryloxyalkanoate dioxygenase gene (*aad-12*), originally from the soil bacterium *Delftia acidovorans*, was integrated into soybean (*Glycine max*) by *Agrobacterium*-mediated transformation of a variety “Maverick” with plasmid pDAB4468 to produce event DAS-68416-4. The aryloxyalkanoate dioxygenase-12 (AAD-12 protein), encoded by the *aad-12* gene, provides tolerance to the herbicide 2,4-dichlorophenoxyacetic acid (2,4-D). Molecular characterization indicated that event DAS-68416-4 contained a single insert including two intact expression cassettes, AAD-12 and PAT. DNA sequences flanking the insert in event DAS-68416-4 soybean were also cloned and characterized. The DNA sequence of the insert is identical to the corresponding portion in the T-DNA insert of plasmid pDAB4468 except for an extra 9 bp insertion at the 3’ junction.

To update the characterization of the soybean genomic DNA sequences surrounding the insert location of event DAS-68416-4 soybean, the sequences of the flanking borders and parental locus were analyzed using BLAST search algorithms along with up-to-date GenBank nucleotide collection [Nucleotide collection (nr/nt)], Non-Human and Non-Mouse ESTs (est_others), and protein [Non-redundant protein sequences (nr)] databases. BLASTn and BLASTx analysis of the sequences comprising the insert of DAS-68416-4 and its 5’ and 3’ flanking border regions revealed identities only to soybean derived or pDAB4468 T-DNA derived sequences. The insert of DAS-68416-4 most likely integrated into a locus close to the 3’ end downstream of a putative peroxidase gene in the soybean genome.

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Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border Sequences

DATA REQUIREMENTS

N/A

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Title: Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border Sequences

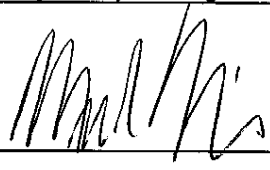
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Border Sequences


Study Initiation Date: 26/04/2010

This report represents data generated after the effective date of the EPA FIFRA Good Laboratory Practice Standards.

United States Environmental Protection Agency
Title 40 Code of Federal Regulations Part 160
FEDERAL REGISTER, August 17, 1989

Organisation for Economic Co-Operation and Development
ENV/MC/CHEM(98)17, Paris January 26, 1998

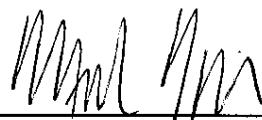
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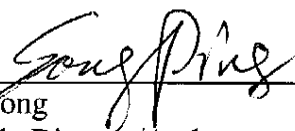
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28-June-2010

Study Completion Date

QUALITY ASSURANCE STATEMENT

Compound: Soybean aad-12 event DAS-68416-4

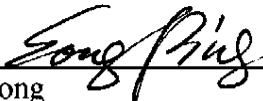
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NON-GLP STUDY

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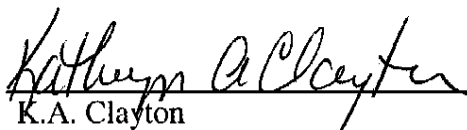
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Bioinformatics Analysis of Soybean Event DAS-68416-4 Insert and Its Flanking Border Sequences

ABSTRACT

A plant-optimized aryloxyalkanoate dioxygenase gene (*aad-12*), originally from the soil bacterium *Delftia acidovorans*, was integrated into soybean (*Glycine max*) by *Agrobacterium*-mediated transformation of a variety “Maverick” with plasmid pDAB4468 to produce event DAS-68416-4. The aryloxyalkanoate dioxygenase-12 (AAD-12 protein), encoded by the *aad-12* gene, provides tolerance to the herbicide 2,4-dichlorophenoxyacetic acid (2,4-D). Molecular characterization indicated that event DAS-68416-4 contained a single insert including two intact expression cassettes, AAD-12 and PAT. DNA sequences flanking the insert in event DAS-68416-4 soybean were also cloned and characterized. The DNA sequence of the insert is identical to the corresponding portion in the T-DNA insert of plasmid pDAB4468 except for an extra 9 bp insertion at the 3' junction.

To update the characterization of the soybean genomic DNA sequences surrounding the insert location of event DAS-68416-4 soybean, the sequences of the flanking borders and parental locus were analyzed using BLAST search algorithms along with up-to-date GenBank nucleotide collection [Nucleotide collection (nr/nt)], Non-Human and Non-Mouse ESTs (est_others), and protein [Non-redundant protein sequences (nr)] databases. BLASTn and BLASTx analysis of the sequences comprising the insert of DAS-68416-4 and its 5' and 3' flanking border regions revealed identities only to soybean derived or pDAB4468 T-DNA derived sequences. The insert of DAS-68416-4 most likely integrated into a locus close to the 3' end downstream of a putative peroxidase gene in the soybean genome.

INTRODUCTION

A plant-optimized *aad-12* gene, originally from common soil bacterium *Delftia acidovorans*, was integrated into soybean (*Glycine max*) by *Agrobacterium*-mediated transformation of a variety “Maverick” with plasmid pDAB4468 to produce event DAS-68416-4. Aryloxyalkanoate dioxygenase-12 (AAD-12 protein), encoded by the *aad-12* gene, provides tolerance to the herbicide 2,4-dichlorophenoxyacetic acid (2,4-D). Molecular characterization indicated that the event DAS-68416-4 contained a single insert including two intact expression cassettes, AAD-12 and PAT (1). In addition, DNA sequences flanking the insert in event DAS-68416-4 soybean as well as the parental locus have been cloned and characterized (2). The DNA sequence of the insert is identical to the corresponding portion in the T-DNA insert of plasmid pDAB4468 except for an extra 9 bp insertion at the 3' border junction.

Considering the nature of random integration through conventional *Agrobacterium*-mediated transformation, insertion of an exogenous gene into soybean genome could disrupt an existing gene, open reading frame, or regulatory element. The purpose of this study is to characterize the location of the insert within the soybean genome and the nature of the flanking border sequences using BLASTn and BLASTx algorithms and up-to-date nucleotide and protein databases, thus evaluating if the transgenic insert in soybean event DAS-68416-4 had integrated into an endogenous gene or genetic element.

METHODS

Query Sequence Preparation

The whole insert and its flanking border sequences were divided into 3 regions according to the previous analysis (Figure 1). DNA sequence from Region 2 includes the full-length insert of the T-DNA in pDAB4468, and the rest of the regions represent the flanking borders. The query sequences were prepared in FASTA format for the BLASTn and BLASTx search programs. The

parental locus represents the sequences from the soybean genomic region prior to insertion of the transgene.

Sequence Search and Databases

Query sequences of Region 1, 2, and the parental locus were searched for sequence similarities against the GenBank nucleotide database [Nucleotide collection (nr/nt)] (<http://www.ncbi.nlm.nih.gov>, update to February 12, 2010) and GenBank Non-mouse and Non-human ESTs (est_others) (update to February 12, 2010) using BLASTn (Basic Local Alignment Search Tool, Version 2.2.21). The 6-frame translations of the DNA sequences were also searched against the non-redundant protein dataset (Non-redundant Protein Sequences “nr”) including non-redundant GenBank CDS translation along with protein sequences from SWISS-PROT (<http://www.expasy.org/sprot/>), PIR (<http://pir.georgetown.edu/>), PRF (<http://www.prf.or.jp/aboutdb-e.html>), and PDB (<http://www.wwpdb.org/>) (update to February 12, 2010) using BLASTx (version 2.2.21). BLASTn and BLASTx searches were performed in an internal UNIX computer using the default setting of algorithm parameters (BLASTn: Expect = 10, Gap Costs = Existence: 5, Extension: 2; BLASTx: Expectation = 10, Matrix = BLOSUM 62, Gap Costs: Existence: 11, Extension: 1; Word Size =3).

RESULTS AND DISCUSSION

Sequence similarity search results from BLASTn and BLASTx and descriptions are summarized in Table 1.

Region 1 consists of 2730 bp, representing the 5' border. BLASTn search of Region 1 returned several significant alignments ($E()=0\sim3\times10^{-87}$) in a complement orientation with a soybean mRNA sequence (Accession #: BT093225.1; Table 1). These alignments cover Nucleotides (Nt) 508 – 2332 of the 5' border sequence, corresponding the Nt 96 – 1272 in the unknown soybean mRNA. According to the annotation on BT093225.1, its complement strand (Nt 247 – 1209) encodes an unknown protein (Accession #: ACU17608.1). Furthermore, the nucleotides from

508 to 2281 in the 5' border are also aligned in a sense orientation with another soybean mRNA sequences ($E()=0\sim3\times10^{-75}$; Accession #: BT093496.1; Table 1) in which the sequence of Nt 61-1023 encodes an unknown soybean protein (Accession #: ACU17865.1). One of the other top scoring alignments is with a peroxidase (PRX1) mRNA from *Medicago truncatula* in a sense orientation (Accession #: EF456703.1; $E()=8\times10^{-14} \sim 4\times10^{-40}$; APPENDIX 2). Amino acid sequence alignment of the peroxidase (Accession #: ABO77632) encoded by the mRNA from *Medicago truncatula* and the 2 undefined soybean proteins (Accession ACU17608.1 and ACU17865.1) displays a 78% identity (data not shown); indicating that the unknown function of the soybean proteins might be a peroxidase. Thus, the 5' border sequence possibly contains the coding sequence for a peroxidase gene. Similar to the search of nucleotide database, the search against the EST database returned several identical alignments with soybean cDNAs, including soybean cDNAs (Accession #: CX703225.1; CX709633.1) isolated from the water-stressed (5h and 48h) soybean root libraries, but in a complement orientation (Table 1). Nt 1495 -2332 in the 5' border also displays significant alignments with a soybean mRNA (Accession #: CF807990.1) and other plant cDNAs that may encode a peroxidase. Apparently, the unaligned regions located in the Nt 508 – 2332 of the 5' border presumably represent introns in a gene. The BLASTx search of Region 1 returned significant alignments with unknown soybean proteins (Accession #: ACU17608.1 and ACU17865.1) encoded by the aforementioned unknown mRNAs (Accession #: BT093225.1 and BT093496.1), *Medicago truncatula* peroxidase encoded by the mRNA (Accession #: EF456703.1), and peroxidase from other plant species. The BLASTx search result perfectly matched the BLASTn search results, clearly demonstrating that the 5' border sequence encodes a putative peroxidase gene. Global sequence alignment of the 5' border with GenBank Accession # BT093496.1, BT093225.1 (complement), and EF456703.1 indicates the alignment is terminated at Nt 2416 of the 5' end border, while the match position of the stop codon is located at Nt 2181 (APPENDIX 1), which is far away from the start (Nt 2731) of the transgene insert. Considering the 550 bp distance between the stop codon and the start position of the insert, the insert in DAS-68416-4 is likely located outside of the sequence associated with the putative peroxidase gene.

Region 2 encompasses the T-DNA insert from pDAB4468. As described previously, the promoter, gene, and terminator sequences of the expression cassettes for AAD-12 and PAT are intact, plus a complete MAR element at the 5' end of the insert (Table 1). Further analysis identified a 9 bp short segment located between the 3' end insert and its border. Screening this 9 bp in both orientations through the whole sequence of pDAB4468 failed to identify any matches. Neither did the BLASTn search using GenBank nucleotide database and the available soybean nucleotide database (<http://soybase.org/GlycineBlastPages>).

Region 3 consists of 1082 bp of the 3' border region. BLASTn search of Region 3 returned 2 significant short alignments with the DNA sequence from a soybean genomic clone (Accession #: AC235472.1; APPENDIX 2). The alignments start at Nt 212 of the 3' border and are too short to determine the nature associated with these alignments. In addition, there are no identified coding regions available in Accession # AC235472.1 based on the information available in this GenBank accession. BLASTn search of Region 3 using the EST database only returned no-significant alignments related to sequences from various plant species including soybean. As such, BLASTx search returned nothing but very weak alignments with protein sequences from *Bombyx mori* and fruit fly. These results imply that the sequence in the 3' border is beyond the possible coding regions identified in the 5' border.

As expected, BLAST (BLASTn, BLASTx) search of the parental locus returned a close-to-identical profile as displayed in the BLAST search of the 5' border sequence. Only the portion corresponding to the 5' border showed significant alignments (Table 1), confirming the results from the search of the individual border sequences.

Taking account of all the results from sequence similarity searches using BLAST tools, the insert of DAS-68416-4 was most likely integrated into a locus close to the 3' end downstream of a putative peroxidase gene in soybean. However, the exact coding sequence is not identified due to the lack of information on the transcription as well as the location of introns and exons in this putative peroxidase gene.

REFERENCES

1. Song, P., Cruse, J., Thomas, A., 2009. Molecular Characterization of AAD-12 Soybean Event DAS-68416-4. Dow AgroSciences Study Report 081087.
2. Poorbaugh, J., Zhou, N., Mo, J., 2009. Cloning and Characterization of DNA Sequence in the Insert and the Flanking Border Regions of AAD-2 Soybean Event DAS-68416-4. Dow AgroSciences Study Report 091048.

Table 1. Description of DNA Sequences from the Insert, its Flanking Borders in DAS-68416-4 and the Parental Locus

Region	Location	Size (bp)	% Identity (Location and Orientation) and E-value	Homologue Accession #	Location in Homologous Sequences	Description
1	1-2730	2730	98 (508-784) E() $=1 \times 10^{-145}$	BT093225.1	1272-996 (complement)	Soybean clone JCVI-FLGm-17C9 unknown mRNA (Length = 1274)
			100 (1157-1348) E() $=1 \times 10^{-101}$		996-805 (complement)	
			100 (1478-1645) E() $=3 \times 10^{-87}$		804-637 (complement)	
			99 (1789-2332) E() $=0$		639-96 (complement)	
			100 (1540-1645, E() $=3 \times 10^{-50}$	CX703225	743-638 (complement)	A soybean cDNA isolated from the water-stressed (5h and 48h) soybean root libraries (Length= 743)
			99 (1789-2332) E() $=0$		640-97 (complement)	
			100 (2338-2427) E() $=7 \times 10^{-11}$		40-1 (complement)	
			93 (508-784); E() $=1 \times 10^{-111}$	BT093496.1	2-274	Soybean clone JCVI-FLGm-17I24 unknown mRNA (Length = 1217)
			96(1157-1347); E() $=1 \times 10^{-86}$		274-464	
			97 (1478-1645); E() $=3 \times 10^{-75}$		466-633	
			93(1789-2281); E() $=0$		631-1128	
			100(1495-1645); E() $=4 \times 10^{-77}$	CF807990.1	1-151	psHB031xA07f USDA IFAFS: Expression of <i>Phytophthora sojae</i> genes during infection and propagation <i>Glycine max</i> cDNA clone sHB031A07 5, mRNA sequence (Length = 708)
			99 (1789-2332); E() $=0$		149-693	
			86 (628-784); E() $=2 \times 10^{-30}$	EF456703.1	64-220	<i>Medicago truncatula</i> peroxidase (PRX1) mRNA, complete cds (Length = 969)
			83 (1157-1342); E() $=6 \times 10^{-24}$		220-405	
			86 (1478-1578); E() $=8 \times 10^{-14}$		412-512	
			80 (1795-2170); E() $=4 \times 10^{-40}$		583-958	

Region	Location	Size (bp)	% Identity (Location and Orientation) and E-value	Homologue Accession #	Location in Homologous Sequences	Description
2	2731–9121	6391	100	T-DNA insert in pDAB4468	23–6413	T-DNA insert including complete MAR, aad-12 and pat expression cassettes
	9122-9130	9	N/A	N/A		No sequence identity
3	9131–10212	1082	90 (212–263) E() $=2\times10^{-6}$	AC235472.1	77662–77713	<i>Glycine max</i> strain Williams 82 clone GM_WBc0099F2 3, complete sequence (Length = 134971)
			87 (216–256) E() $=6.6$		78023–77983 (complement)	
Parental Locus		3867	98 (508–784) E() $=1\times10^{-145}$	BT093225.1	1272–996 (complement)	Soybean clone JCVI-FLGm-17C9 unknown mRNA (Length = 1274)
			100 (1157–1348) E() $=1\times10^{-101}$		996–805 (complement)	
			100 (1478–1645) E() $=5\times10^{-87}$		804–637 (complement)	
			99 (17898–2332) E() $=0$		639–96 (complement)	
			100 (1540–1645) E() $=1\times10^{-50}$	CX703225	743–638 (complement)	gmrtDrNS01_14-B_M13R_D10_0 74.s2 Water stressed 5h segment 2 gmrtDrNS01 <i>Glycine max</i> cDNA 3', mRNA sequence (Length = 743)
			99 (1789–2332) E() $=0$		640–97 (complement)	
			100 (2338–2427) E() $=1\times10^{-10}$		40–1 (complement)	
			93 (508–784); E() $=1\times10^{-111}$	BT093496.1	2–274	Soybean clone JCVI-FLGm-17I24 unknown mRNA (Length = 1217)
			96(1157–1347); E() $=2\times10^{-86}$		274–464	
			97 (1478–1645): E() $=4\times10^{-75}$		466–633	
			93(1789–2281); E() $=0$		631–1128	
			100 (1495–1645); E() $=6\times10^{-77}$	CF807990.1	1-151	psHB031xA07f USDA IFAFS:Expression of Phytophthora sojae genes during infection and propagation
			99 (1789–2332); E() $=0$		149-693	

Region	Location	Size (bp)	% Identity (Location and Orientation) and E-value	Homologue Accession #	Location in Homologous Sequences	Description
						<i>Glycine max</i> cDNA clone sHB031A07 5, mRNA sequence (Length = 708)
			86 (628-784); E()= 2×10^{-30}	EF456703.1	64-220	<i>Medicago truncatula</i> peroxidase (PRX1) mRNA, complete cds (Length = 969)
			83 (1157-1342); E()= 8×10^{-24}		220-405	
			86 (1478-1578); E()= 1×10^{-13}		412-512	
			80 (1795-2170); E()= 6×10^{-40}		583-958	

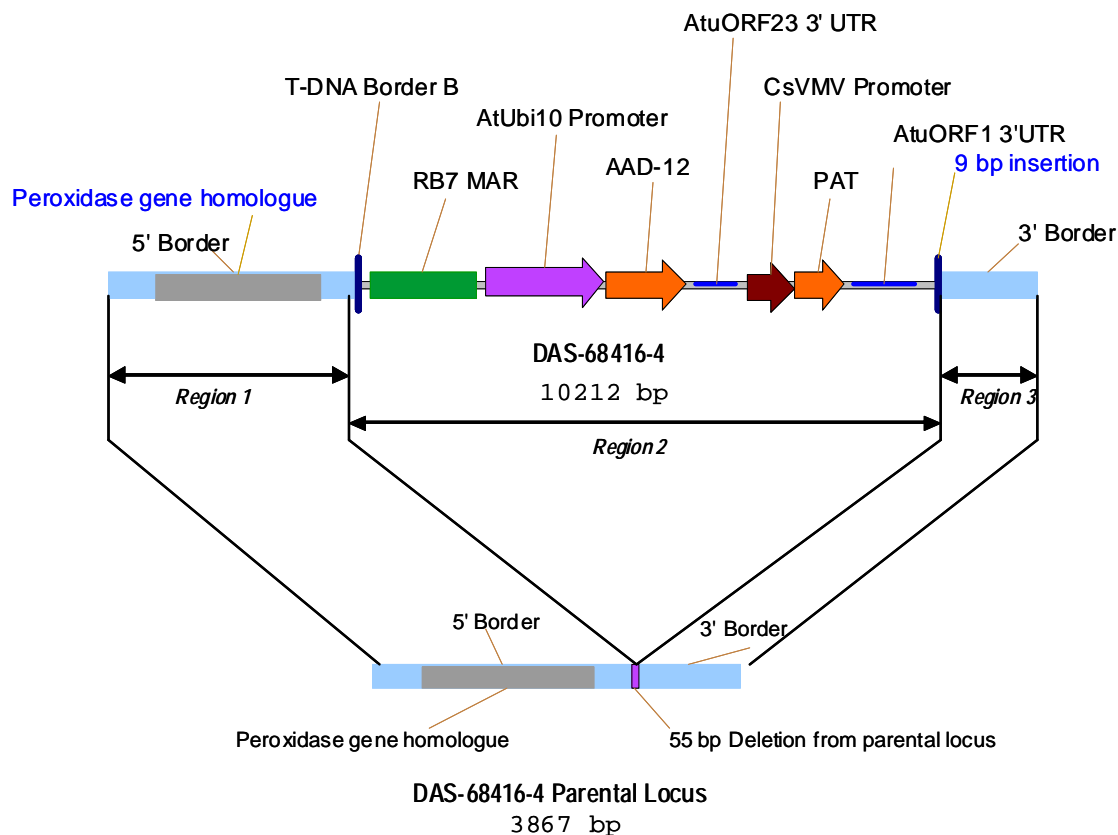


Figure 1. Diagram of the Insert, its Flanking Borders, and Parental Locus in Soybean Event DAS-68416-4

APPENDIX

1. Sequence Alignments of GenBank Accession #: BT093225, BT093496, and EF456703 with the 5' Border of DAS-68416-4

	1	50
68416_5'_Border	(1) CTGTCGTTGGATTACAGAACATTGACGCCAGTTTTCACTTCGTTATCTT	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	51	100
68416_5'_Border	(51) TGAATTCATTAAAATCGAATCTCTCACCTATACCCCCCATTTTTCTAAT	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	101	150
68416_5'_Border	(101) CCATCATAATCAAATTCATAAATGAATCAGTTACCATTACCATAATACC	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	151	200
68416_5'_Border	(151) TTTTGGAAAATGAGTTTGAATAATCAGTATCTTTAGAAAATAATTAAGA	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	201	250
68416_5'_Border	(201) AATTAAATAAAAAATATTTATCATGAAGATGAGTGTAAGAAAAATTATGA	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	251	300
68416_5'_Border	(251) AAAGTATAACTTTATACATTTCTATAAAATTATTTTTCTTTTAATTCT	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	301	350
68416_5'_Border	(301) TAATTAATATCCTAAGTAAATGAGTTAATATTTATCTTTCAAAAATCTT	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	351	400
68416_5'_Border	(351) ATAGTCGCCAATTAATTTTCCCATGCAATGACAACCTTGTCGGTATTCTAC	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	401	450
68416_5'_Border	(401) GTGGTAGGTTAGGCTACCTGCCGAGACAAATTGCCTTGAGACAAATTCAA	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	451	500
68416_5'_Border	(451) TAGAGAACCCTTCCAAGGGACCATTATAAATAGAGAACTTTCATTAACCG	
BT093225_complement	(1) -----	
BT093496	(1) -----	
EF456703	(1) -----	
	501	550

68416_5'_Border	(501)	ATAAGCCACACCCCTTTCAATCAAACACAAACACTTGAAGTACTAAGTTAG	
BT093225_complement	(1)	-----GACACCCCTTTCAATCAAACACAAACACTCGAAGTACTAAGTTAG	
BT093496	(1)	-----GACACCCCTCTCAAGCAAACACAAACACTTGAAGTACTAAGTTAG	
EF456703	(1)	-----	
		551	600
68416_5'_Border	(551)	TGTGTTTGAGCAAATTAACATATGGCTTCGTT--TTGTTCTAGATTGACA	
BT093225_complement	(46)	TGTGTTTGAGCAAATTAACATATGGCTTCGTT--TTGTTCTAGATTGACA	
BT093496	(45)	TGTGTTTGAGCAAATTAACATATGGCTTCGTT--TTGTTCTAGATTGACC	
EF456703	(1)	-----ATGGCTTCGTTAAATTTGTTCTAGATTAAACC	
		601	650
68416_5'_Border	(598)	ATTT---GTTTGGCTCTGTTTGTCTTCATATGGGGAGTGCCAATGCACA	
BT093225_complement	(93)	ATTT---GTTTGGCTCTGTTTGTCTTCATATGGGGAGTGCCAATGCACA	
BT093496	(88)	ATTT---GTTTGGCTCTGTTTGTCTTCATATGGGGAGTGCCAATGCACA	
EF456703	(31)	ATGATCAGTTTAGTTCTATCTGTTCTCATAATAGGGAGTGCCAATGCACA	
		651	700
68416_5'_Border	(645)	ACTTTCTACAAACTTTTACTACCATTCATGTCCAAACCTCTTCTCCTCTG	
BT093225_complement	(140)	ACTTTCTACAAACTTTTACTACCATTCATGTCCAAACCTCTTCTCCTCTG	
BT093496	(135)	ACTTTCTACAAACTTTTACTACCATTCATGTCCAAACCTCTTCTCCTCTG	
EF456703	(81)	ACTTTCTACAAACTTTTACTCAAAAACTTGTCCAAACTCTCTACCAACAG	
		701	750
68416_5'_Border	(695)	TGAAATCCACAGTGCAATCTGCCATATCTAAGGAGACCCGCATGGGTGCT	
BT093225_complement	(190)	TGAAATCCGACAGTGCAATCTGCCATATCTAAGGAGACCCGCATGGGTGCT	
BT093496	(185)	TGAAATCCACAGTGCAATCTGCCATATCAAGGAGACCCGCATGGGTGCT	
EF456703	(131)	TGAAATCCACACTGCAACTTGCCATATCAAGGAGGCCGATGGGTGCTC	
		751	800
68416_5'_Border	(745)	TCTCTCCTTCGCTTGTCTTCCACGATTGCTTTGTCAATGTAATTTATTTT	
BT093225_complement	(240)	TCTCTCCTTCGCTTGTCTTCCACGATTGCTTTGTCAATG-----	
BT093496	(235)	TCTCTCCTTCGCTTGTCTTCCACGATTGCTTTGTCAATG-----	
EF456703	(181)	TCTATCCTTCGCTTGTCTTCCACGATTGCTTTGTCAATG-----	
		801	850
68416_5'_Border	(795)	GCACCTTCTCCACTTACATACAAATATGCTAAGCTTACATATAGCTCCT	
BT093225_complement	(280)	-----	
BT093496	(275)	-----	
EF456703	(221)	-----	
		851	900
68416_5'_Border	(845)	CTTTCTACCACTTGCATGCATCATCTAATTTTGTGTTGAAACAACACTTGT	
BT093225_complement	(280)	-----	
BT093496	(275)	-----	
EF456703	(221)	-----	
		901	950
68416_5'_Border	(895)	TCCTTTTATTATACACATCATCTTTGATAAAATTTTGTGCGTGCAACTT	
BT093225_complement	(280)	-----	
BT093496	(275)	-----	
EF456703	(221)	-----	
		951	1000
68416_5'_Border	(945)	TTTTTTAGTGTGTTAATCAGTTCTATGATGATACTATTAGTTAAGAAATT	
BT093225_complement	(280)	-----	
BT093496	(275)	-----	
EF456703	(221)	-----	
		1001	1050
68416_5'_Border	(995)	TTAATGCACTTAATAAACCATTTTAAAGTACTTTAACCCTTCAATGATATT	
BT093225_complement	(280)	-----	
BT093496	(275)	-----	
EF456703	(221)	-----	
		1051	1100
68416_5'_Border	(1045)	ATATATTTAAAGATAATAAATATTTCTGCTTTTGTCTTCTATATTAGTGTA	
BT093225_complement	(280)	-----	
BT093496	(275)	-----	
EF456703	(221)	-----	
		1101	1150
68416_5'_Border	(1095)	GTAAAGAACCTTCTTACTTCTTAGCTAGCTAAATATTAATGAGTAAACAT	

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BT093225_complement (280) -----
BT093496 (275) -----
EF456703 (221) -----
1151 1200
68416_5'_Border (1145) TAACAAATGCAGG GATGTGATGG TTCAATTCTATT GATGACACATCAAG
BT093225_complement (280) ----- GATGTGATGG TTCAATTCTATT GATGACACATCAAG
BT093496 (275) ----- GATGTGATGG TTCAATTCTATT GATGACACATCAAG
EF456703 (221) ----- GATGTGATGG ATCAATTCTCTTAGATGACACATCAAG
1201 1250
68416_5'_Border (1195) CTT CACCGG AGAGAAGAAC GCAAACCC AACAGGA ACTCT GCTCGTGGAT
BT093225_complement (317) CTT CACCGG AGAGAAGAAC GCAAACCC AACAGGA ACTCT GCTCGTGGAT
BT093496 (312) CTT CACCGG AGAGAAGAAC GCAAACCC AACAGGA ACTCT GCTCGTGGAT
EF456703 (258) CTTT ACCGGT GAGAAGAA TGCAAATCC AAATAGAA ACTC GCTCGTGGAT
1251 1300
68416_5'_Border (1245) TCGAG GTT ATT GACAACATT AAATCAGCCGT GGAGAAAGT GTGTCCAGGA
BT093225_complement (367) TCGAG GTT ATT GACAACATT AAATCAGCCGT GGAGAAAGT GTGTCCAGGA
BT093496 (362) ACGAG GTT CAT T GACAACATT AAATCAGCCGT GGAGAAAGT CATGTCCAGGA
EF456703 (308) TTGAT GTT CAT C GACAACATA AAGA CAGCCGT AGAGAA CGTATGCCCGGA
1301 1350
68416_5'_Border (1295) GTTGT TTCTGCGCAGATATCCTTGCCATC GCTGCCAGAGACTCTGTTCA
BT093225_complement (417) GTTGT TTCTGCGCAGATATCCTTGCCATC GCTGCCAGAGACTCTGTTCA
BT093496 (412) GTTGT TCCTGCGCAGATATCCTTGCCATAGCTGCCAGAGACTCTGTTCA
EF456703 (358) GTTGT ATCATGTGCTGATATCCTAGCCATGCTGCCGCAGACTCTGTTGC
1351 1400
68416_5'_Border (1345) GATT GTAAGTGGTCAAACAACCAACAAAAACACATTAAACTAAATCATTA
BT093225_complement (467) GATT -----
BT093496 (462) GATC -----
EF456703 (408) AATT -----
1401 1450
68416_5'_Border (1395) AATTGTACATATCAAAATTAATTACCAATTTAGTACCACACATGCAATTA
BT093225_complement (471) -----
BT093496 (466) -----
EF456703 (412) -----
1451 1500
68416_5'_Border (1445) AAGAGAACATTTTGTGATTTTGATCAATATAG CTTGGAGG CCCTACATG
BT093225_complement (471) ----- CTTGGAGG CCCTACATG
BT093496 (466) ----- CTTGGAGG CCCTAGTTG
EF456703 (412) ----- CTTGGAGG TCCAACTG
1501 1550
68416_5'_Border (1495) GAATGT TAAAC TTGGAAGAAGAGAC GCTAGAACTGCTAGCCAATCTGCTG
BT093225_complement (488) GAATGT TAAAC TTGGAAGAAGAGAC GCTAGAACTGCTAGCCAATCTGCTG
BT093496 (483) GAATGT TAAAG TTGGAAGAAGAGAC GCTAGAACTGCTAGCCAATCTGCTG
EF456703 (429) GAATGT TAAAC TTGGAAGAAGAGATGCTAAACGGCTAGTCAATCCGCTG
1551 1600
68416_5'_Border (1545) CTAACAATGGCATCCCTGCACCCACTTCAAACCTTAACCAACTCATCTCA
BT093225_complement (538) CTAACAATGGCATCCCTGCACCCACTTCAAACCTTAACCAACTCATCTCA
BT093496 (533) CTAACAATGGCATCCCTGCACCCACTTCAAACCTTAACCAACTCATCTCA
EF456703 (479) CTAACA CTGCATCCCTGCACCAACTTCAAACCTCAATACACTCACTCA
1601 1650
68416_5'_Border (1595) AGATT TAGCGCTCTTGGACTTTCCACCAAGGACTTGGTGGCCTTGTCCGG
BT093225_complement (588) AGATT TAGCGCTCTTGGACTTTCCACCAAGGACTTGGTGGCCTTGTCCGG
BT093496 (583) AGATT CAGCGCTCTTGGACTTTCCACCAAGGACTTGGTGGCCTTGTCCGG
EF456703 (529) ATGTT TAGCGC CGTTGGTCTTTCTAGCAAAGATTGGTCACTTGTCAAG
1651 1700
68416_5'_Border (1645) TACAAAACATATATCACATAATTTTCCAATTAATTACATTTCAATCATAT
BT093225_complement (638) T-----
BT093496 (633) T-----
EF456703 (579) T-----
1701 1750
68416_5'_Border (1695) AGTAAAATTTCTCAATTAATTAGGAACATGAGAAACTTATAGTCACACGT
BT093225_complement (639) -----

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BT093496	(634)	-----	
EF456703	(580)	-----	
		1751	1800
68416_5'_Border	(1745)	TCTTTTGTGAGGAATATTGCATGGTTAATTTTGCTTTCATTAGGT	GGT
BT093225_complement	(639)	-----	GGT
BT093496	(634)	-----	GGT
EF456703	(580)	-----	GCA
		1801	1850
68416_5'_Border	(1795)	CACACAATTGGACAAGCAAGGTGCACAACTTCAGAGCCCGCATCTACAA	
BT093225_complement	(642)	CACACAATTGGACAAGCAAGGTGCACAACTTCAGAGCCCGCATCTACAA	
BT093496	(637)	CACACAATTGGACAAGCAAGGTGCACAACTTCAGAGCCCGCATCTACAA	
EF456703	(583)	CACACAATTGGACAAGCAAGGTGTACAAATTTAGGGCAAGAACTCTACAA	
		1851	1900
68416_5'_Border	(1845)	CGAGACCAACATAGAAACCGCATTTCGCAAGGACTAGGCAGCAAAAGCTGCC	
BT093225_complement	(692)	CGAGACCAACATAGGAAACCGCATTTCGCAAGGACTAGGCAGCAAAAGCTGCC	
BT093496	(687)	CGAGACCAACATAGAACCGCATTTCGCAAGGCAAGGCAACAAAGCTGCC	
EF456703	(633)	CGAGACCAACATAAATGCTGCTATTNGCTAGCACGAGGCAATCAAAATGCC	
		1901	1950
68416_5'_Border	(1895)	CTAGAACATCAGGGTCAGGGGACAACAACTCTGGCACCCTTGATCTTCAA	
BT093225_complement	(742)	CTAGAACATCAGGGTCAGGGGACAACAACTCTGGCACCCTTGATCTTCAA	
BT093496	(737)	CAAGAACATCAGGGTCAGGGGACAATTAATCTTGCAACGCTTGATCTTCAA	
EF456703	(683)	CAAGGCATCAGGATCAGGTGACAACAACTTGGCACCTCTTGATCTTCAAG	
		1951	2000
68416_5'_Border	(1945)	ACTCCAAACAGCTTTGACAACACTACTTCAAGAACCTCGTTTCAGAAAGAA	
BT093225_complement	(792)	ACTCCAAACAGCTTTGACAACACTACTTCAAGAACCTCGTTTCAGAAAGAA	
BT093496	(787)	ACTCCAAACGAATTCGACAACACTACTTCAAGAACTCTTGTTTCAGAAAGAA	
EF456703	(733)	ACTCCTAGTTCCTTTTGACAACAACACTACTTCAAGAACCTTGTTTCAGAAAGAA	
		2001	2050
68416_5'_Border	(1995)	GGGTCTCTCCACTCTGATCAGCAACTCTTCAACGGTGGGTCCACCGACT	
BT093225_complement	(842)	GGGTCTCTCCACTCTGATCAGCAACTCTTCAACGGTGGGTCCACCGACT	
BT093496	(837)	GGGTCTCTCCACTCTGATCAGCAACTCTTCAATGGTGGGTCCACCGACT	
EF456703	(783)	GGGTCTCTCCATTGAGACCAACAACCTTTTAAACGGCGGGTCCACCAACT	
		2051	2100
68416_5'_Border	(2045)	CCATTGTGCGTGGCTACAGCACCAACCCGGGCACCTTCTCCTCTGATTTTC	
BT093225_complement	(892)	CCATTGTGCGTGGCTACAGCACCAACCCGGGCACCTTCTCCTCTGATTTTC	
BT093496	(887)	CCATTGTGCGTGGCTACAGCACCAACCCAGCTCCTTCTCCTCTGACTTC	
EF456703	(833)	CAATAGTGAGTGGTTATAGTACTAGCCCAAGCTCTTTTCTCCTGATTTT	
		2101	2150
68416_5'_Border	(2095)	GCCGCCGCCATGATCAAGATGGGAGACATTAGTCCTCTCACATGGCTCCAA	
BT093225_complement	(942)	GCCGCCGCCATGATCAAGATGGGAGACATTAGTCCTCTCACATGGCTCCAA	
BT093496	(937)	GCCGCCGCCATGATCAAGATGGGAGACATTAGTCCTCTCACATGGCTCCAA	
EF456703	(883)	GCCGCTGCTATGATCAAGATGGGAATATTAAACCTCTCACCGGATCCAA	
		2151	2200
68416_5'_Border	(2145)	TGGAGAAATCAGGAAGAAATGTAGAAAGATTAACTAAATT--TGATTGAGT	
BT093225_complement	(992)	TGGAGAAATCAGGAAGAAATGTAGAAAGATTAACTAAATT--TAATTGAGT	
BT093496	(987)	CGGAGAAATCAGGAAGAAATGTAGAAAGATTAACTAAATTACTAATTGAGT	
EF456703	(933)	TGGAGAGATTAGGAAGAACTGTAGAAAAACCAACTAA-----	
		2201	2250
68416_5'_Border	(2193)	CTTGAATATTAAGGGTCCTA---CACATACGCAAGCAATTTAATTGTGTT	
BT093225_complement	(1040)	CTTGAATATTAAGGGTCCTA---CACATACGCAAGCAATTTAATTGTGTT	
BT093496	(1037)	CTCCAAATATTAAGGGTCCTACTACACATACGCAAGCAATTTAATTGTGTT	
EF456703	(970)	-----	
		2251	2300
68416_5'_Border	(2240)	TAATAAGTTGTTAAAACATGTTTTGGTTGTATTTTGGATTCCCTAGTGTAG	
BT093225_complement	(1087)	TAATAAGTTGTTAAAACATGTTTTGGTTGTATTTTGGATTCCCTAGTGTAG	
BT093496	(1087)	TAATAAGTTGTTAAAACATGTTTTGGTTGTGTTTTGGATTCCCGTGTGGG	
EF456703	(970)	-----	
		2301	2350
68416_5'_Border	(2290)	TTTCGGTGATCAATGCCGTCTACTTTAGTGTGTTCTACTTCCCTTTATTT	
BT093225_complement	(1137)	TTTCGGTGATCAATGCCGTCTACTTTAGTGTGTTCTACTTCCCTTTATTT	
BT093496	(1137)	TTAATTTCCTAGTGTAGTTGCTGTTATCAATGCGGTATACGTTAGTGTGT	

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EF456703      (970) -----
                2351                                     2400
68416_5'_Border (2340) TTGTTTCTTTTCTTACTTTTCCTTAACTATATTGTAGG-AAAAAAAAAAT
BT093225_complement (1187) TTGTTTCTTTTCTTACTTTTCCTTAACTATATTGTAGG-AAAAAAAAAAT
BT093496      (1187) GTTC TACTT CAAA AAAAAAAAAA AAAAAA -----
EF456703      (970) -----
                2401                                     2450
68416_5'_Border (2389) CCTTTATCAAGCATTAT CAA GAA CGGA GTTTGCTTTTAAATTTCCCTT
BT093225_complement (1237) CCTTTATCAAGCATTAT CAAAAA AAAAAA -----
BT093496      (1218) -----
EF456703      (970) -----
                2451                                     2500
68416_5'_Border (2439) CATAACATTCCATCAGAATTCAGTTTGTCTTTGTCTTCTAAATTACGTTC
BT093225_complement (1275) -----
BT093496      (1218) -----
EF456703      (970) -----
                2501                                     2550
68416_5'_Border (2489) AAATCAGGGATGATAATCGGTTAGGTAATATATACAGTACCCCTTGCATA
BT093225_complement (1275) -----
BT093496      (1218) -----
EF456703      (970) -----
                2551                                     2600
68416_5'_Border (2539) GTCACGTTTGAAAAATATAATCATACTTAGTTCGGTAACAATTTAAATTA
BT093225_complement (1275) -----
BT093496      (1218) -----
EF456703      (970) -----
                2601                                     2650
68416_5'_Border (2589) TCATTCTCGTAATCATTAGCTACTTATGCACTCATATCCGTATCCGTAC
BT093225_complement (1275) -----
BT093496      (1218) -----
EF456703      (970) -----
                2651                                     2700
68416_5'_Border (2639) TTGCTCTTGTCGTAAGTCAATAAATTAATATAAAAAAATACTTAAACTT
BT093225_complement (1275) -----
BT093496      (1218) -----
EF456703      (970) -----
                2701                                     2742
68416_5'_Border (2689) GTTACAATAAATTAATAATTTATTTTAAATCATTCAGCA
BT093225_complement (1275) -----
BT093496      (1218) -----
EF456703      (970) -----

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2. BLASTn Search Output of the 5' End Border Sequence in Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nr/nt)
3. BLASTn Search Output of the 5' End Border Sequence in Soybean Event DAS-68416-4 against GenBank No-mouse and No-human EST s (est_others)
4. BLASTx Search Outputs of the 5' END Border Sequence in Soybean Event DAS-68416-4 against GenBank Non-redundant Protein Sequences "nr"

5. BLASTn Search Output of the 3' End Border Sequence in Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nr/nt)
6. BLASTn Search Output of the 3' End Border Sequence in Soybean Event DAS-68416-4 against GenBank No-mouse and No-human ESTs (est_others)
7. BLASTx Search Outputs of the 3' End Border Sequence in Soybean Event DAS-68416-4 against GenBank Non-redundant Proteins Sequences "nr"
8. BLASTn Search Output of the DNA sequence at the Parental Locus of Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nr/nt)
9. BLASTn Search Output of the DNA sequences at the Parental Locus of Soybean Event DAS-68416-4 against GenBank No-mouse and No-human ESTs (est_others)
10. BLASTx Search Outputs of the DNA sequence at the Parental Locus of Soybean Event DAS-68416-4 against GenBank Non-redundant Proteins Sequences "nr"

NOTE: All The BLAST search output files are electronically stored in a secured computer in Dow AgroSciences and available for view in PDF format.

BLASTn Output of the 5' Border Sequence Flanking the Insert in Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nt/nr)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 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.

Query= 68416_5_border
(2730 letters)

Database: /usr/local/blast/db/blastlibs/nt
10,930,266 sequences; 30,212,464,392 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
gb BT093225.1	Soybean clone JCVI-FLGm-17C9 unknown mRNA	1039	0.0
gb BT093496.1	Soybean clone JCVI-FLGm-17I24 unknown mRNA	731	0.0
gb EF456703.1	Medicago truncatula peroxidase (PRX1) mRNA, compl...	176	4e-40
gb BT098008.1	Soybean clone JCVI-FLGm-22H8 unknown mRNA	174	2e-39
emb CU137662.1	Medicago truncatula chromosome 5 clone mth2-155l...	172	7e-39
emb CR938710.1	Medicago truncatula chromosome 5 clone mth2-170k...	172	7e-39
gb AF149281.1	AF149281 Phaseolus vulgaris clone pBPERB5 peroxida...	163	7e-36
ref XM_002520789.1	Ricinus communis Peroxidase 52 precursor, pu...	129	9e-26
gb BT052838.1	Medicago truncatula clone MTYFH_FI_FJ_FK1G-0-8 un...	111	2e-20
gb AY311597.1	Gossypium hirsutum class III peroxidase (pod7) mR...	105	1e-18
emb FP100639.1	Phyllostachys edulis cDNA clone: bphyem110n02, f...	103	5e-18
emb FP099994.1	Phyllostachys edulis cDNA clone: bphyem210i11, f...	103	5e-18
dbj AB027752.1	Nicotiana tabacum mRNA for peroxidase, complete ...	96	1e-15
gb AY837788.2	Catharanthus roseus clone Prx4 putative secretory...	90	8e-14
gb FJ644943.1	Sesuvium portulacastrum peroxidase 1 (POD1) mRNA,...	88	3e-13
dbj AK242814.1	Oryza sativa Japonica Group cDNA, clone: J090061...	86	1e-12
ref NM_001072100.1	Oryza sativa (japonica cultivar-group) Os1lg...	86	1e-12
tpe BN000659.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	86	1e-12
dbj AB019228.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	86	1e-12
emb BX000512.1	Oryza sativa chromosome 11, . BAC OSJNBa0025K19 ...	86	1e-12
gb EF661875.2	Catharanthus roseus putative secretory peroxidase...	84	5e-12
ref NM_125225.1	Arabidopsis thaliana peroxidase, putative (AT5G...	80	8e-11
dbj AK117722.1	Arabidopsis thaliana At5g58390 mRNA for putative...	80	8e-11
gb AY085030.1	Arabidopsis thaliana clone 124846 mRNA, complete ...	80	8e-11
gb EZ329073.1	TSA: Artemisia annua strain Madagascar Contig1561...	76	1e-09

ref XM_002450087.1	Sorghum bicolor hypothetical protein, mRNA	76	1e-09
ref XM_002269882.1	PREDICTED: Vitis vinifera hypothetical prote...	76	1e-09
emb AM447728.2	Vitis vinifera contig VV78X018697.9, whole genom...	76	1e-09
ref XM_002278960.1	PREDICTED: Vitis vinifera hypothetical prote...	72	2e-08
gb AY206413.1	Ipomoea batatas anionic peroxidase swpb2 mRNA, co...	72	2e-08
gb EZ399860.1	TSA: Artemisia annua strain Uganda Contig16355, m...	70	7e-08
gb EZ145065.1	TSA: Artemisia annua strain Artemis Contig4471, m...	70	7e-08
gb EZ141680.1	TSA: Artemisia annua strain Artemis Contig1086, m...	70	7e-08
ref XM_002489001.1	Sorghum bicolor hypothetical protein (SORBID...	70	7e-08
ref XM_002441657.1	Sorghum bicolor hypothetical protein, mRNA	70	7e-08
emb AM456467.1	Vitis vinifera, whole genome shotgun sequence, c...	70	7e-08
gb GU230149.1	Ipomoea batatas anionic peroxidase mRNA, complete...	68	3e-07
ref XM_002268223.1	PREDICTED: Vitis vinifera hypothetical prote...	68	3e-07
gb FJ099755.1	Pinus taeda isolate 1286 anonymous locus 2_6350_0...	68	3e-07
emb CU231251.1	Populus EST from mild drought-stressed leaves	68	3e-07
gb AY206412.1	Ipomoea batatas anionic peroxidase swpb1 mRNA, co...	68	3e-07
dbj AK322204.1	Solanum lycopersicum cDNA, clone: LEFL1035AA07, ...	66	1e-06
ref XM_002328955.1	Populus trichocarpa predicted protein, mRNA	66	1e-06
ref XM_002319932.1	Populus trichocarpa predicted protein, mRNA	66	1e-06
gb AC214418.1	Populus trichocarpa clone POP106-D21, complete se...	66	1e-06
gb BT096974.1	Soybean clone JCVI-FLGm-21M8 unknown mRNA	64	5e-06
gb FJ596178.1	Capsicum annuum peroxidase (POD) mRNA, complete cds	64	5e-06
gb EF433455.1	Ipomoea batatas basic peroxidase swpb4 mRNA, comp...	64	5e-06
gb AC235385.1	Glycine max strain Williams 82 clone GM_WBb0113B1...	62	2e-05
gb GQ258782.1	Brassica rapa peroxidase 52 mRNA, partial cds	60	7e-05
gb FJ099770.1	Pinus taeda isolate 1299 anonymous locus 2_6350_0...	60	7e-05
gb FJ099768.1	Pinus taeda isolate 1282 anonymous locus 2_6350_0...	60	7e-05
gb FJ099767.1	Pinus taeda isolate 1292 anonymous locus 2_6350_0...	60	7e-05
gb FJ099766.1	Pinus taeda isolate 1285 anonymous locus 2_6350_0...	60	7e-05
gb FJ099765.1	Pinus taeda isolate 1288 anonymous locus 2_6350_0...	60	7e-05
gb FJ099762.1	Pinus taeda isolate 1298 anonymous locus 2_6350_0...	60	7e-05
gb FJ099761.1	Pinus taeda isolate 1289 anonymous locus 2_6350_0...	60	7e-05
gb FJ099760.1	Pinus taeda isolate 1297 anonymous locus 2_6350_0...	60	7e-05
gb FJ099759.1	Pinus taeda isolate 1283 anonymous locus 2_6350_0...	60	7e-05
gb FJ099758.1	Pinus taeda isolate 1287 anonymous locus 2_6350_0...	60	7e-05
gb FJ099757.1	Pinus taeda isolate 1291 anonymous locus 2_6350_0...	60	7e-05
gb EF433456.1	Ipomoea batatas basic peroxidase swpb5 mRNA, comp...	60	7e-05
gb AC226196.1	Musa acuminata clone BAC MA4-125A12, complete seq...	60	7e-05
ref XM_001754018.1	Physcomitrella patens subsp. patens predicte...	60	7e-05
emb AM449831.1	Vitis vinifera, whole genome shotgun sequence, c...	60	7e-05
gb AY206414.1	Ipomoea batatas anionic peroxidase swpb3 mRNA, co...	60	7e-05
gb AF485265.1	Gossypium hirsutum class III peroxidase (pod3) mR...	60	7e-05
gb EZ328614.1	TSA: Artemisia annua strain Madagascar Contig1516...	58	3e-04
gb EZ256818.1	TSA: Artemisia annua strain Artemis Contig23488, ...	58	3e-04
gb EZ397212.1	TSA: Artemisia annua strain Uganda Contig13707, m...	58	3e-04
dbj AK328734.1	Solanum lycopersicum cDNA, clone: LEFL3035G12, H...	58	3e-04
emb AJ544515.1	Asparagus officinalis partial mRNA for peroxidas...	58	3e-04
ref XM_002521820.1	Ricinus communis Lignin-forming anionic pero...	56	0.001
ref XM_002521805.1	Ricinus communis Lignin-forming anionic pero...	56	0.001

ref XM_002521804.1	Ricinus communis Peroxidase 30 precursor, pu...	56	0.001
gb FJ529216.1	Cucumis sativus 1-aminocyclopropane-1-carboxylate...	56	0.001
ref XM_002450088.1	Sorghum bicolor hypothetical protein, mRNA	56	0.001
gb FJ050772.1	Pinus taeda isolate 4650 anonymous locus 0_13032_...	56	0.001
gb FJ050764.1	Pinus taeda isolate 4651 anonymous locus 0_13032_...	56	0.001
gb FJ050758.1	Pinus taeda isolate 4655 anonymous locus 0_13032_...	56	0.001
gb FJ050757.1	Pinus taeda isolate 4653 anonymous locus 0_13032_...	56	0.001
gb AF149278.1	AF149278 Phaseolus vulgaris peroxidase 3 precursor...	56	0.001
dbj AK320453.1	Solanum lycopersicum cDNA, clone: LEFL1009CA06, ...	54	0.004
dbj AK320190.1	Solanum lycopersicum cDNA, clone: LEFL1006BD07, ...	54	0.004
gb AC235342.1	Glycine max strain Williams 82 clone GM_WBb0088H1...	54	0.004
emb CT832689.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.004
emb CT832688.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.004
emb CT832687.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.004
ref NM_001072503.1	Oryza sativa (japonica cultivar-group) Os12g...	54	0.004
tpe BN000664.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	54	0.004
dbj AK069456.1	Oryza sativa Japonica Group cDNA clone:J023019E0...	54	0.004
emb X91172.1	R. sativus prxK1 gene	54	0.004
emb BX000510.1	Oryza sativa chromosome 12, . BAC OJ1769_D07 of ...	54	0.004
gb EZ315890.1	TSA: Artemisia annua strain Madagascar Contig2436...	52	0.018
gb EZ359220.1	TSA: Artemisia annua strain Uganda Contig6381, mR...	52	0.018
gb EZ166433.1	TSA: Artemisia annua strain Artemis Contig25839, ...	52	0.018
gb BT106781.1	Picea glauca clone GQ03010_F17 mRNA sequence	52	0.018
ref XM_002285606.1	PREDICTED: Vitis vinifera hypothetical prote...	52	0.018
gb AC235417.1	Glycine max strain Williams 82 clone GM_WBb0135A0...	52	0.018
ref XM_002334206.1	Populus trichocarpa predicted protein, mRNA	52	0.018
ref NM_001157951.1	Zea mays peroxidase 2 (LOC100285056), mRNA >...	52	0.018
gb BT044614.1	Arabidopsis thaliana unknown protein (At4g33420) ...	52	0.018
gb FJ099764.1	Pinus taeda isolate 1294 anonymous locus 2_6350_0...	52	0.018
gb FJ099763.1	Pinus taeda isolate 1290 anonymous locus 2_6350_0...	52	0.018
gb BT042071.1	Zea mays full-length cDNA clone ZM_BFb0125B03 mRN...	52	0.018
emb AM450885.2	Vitis vinifera contig VV78X220288.8, whole genom...	52	0.018
ref NM_119496.3	Arabidopsis thaliana peroxidase, putative (AT4G...	52	0.018
emb AM446475.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.018
emb AM436560.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.018
emb AM429435.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.018
ref NM_101322.1	Arabidopsis thaliana anionic peroxidase, putati...	52	0.018
gb AF453791.1	Ipomoea batatas anionic peroxidase (POD) gene, pr...	52	0.018
dbj AB193816.1	Pisum sativum mRNA for peroxidase, complete cds,...	52	0.018
dbj AK176812.1	Arabidopsis thaliana mRNA for peroxidase ATP17a ...	52	0.018
gb AY089094.1	Arabidopsis thaliana clone 32346 mRNA, complete s...	52	0.018
gb AC108072.3	Homo sapiens BAC clone RP11-704A16 from 2, comple...	52	0.018
gb AF451951.1	Arabidopsis thaliana class III peroxidase ATP32 m...	52	0.018
emb AL161583.2	Arabidopsis thaliana DNA chromosome 4, contig fr...	52	0.018
gb AC010657.3	AC010657 Genomic sequence for Arabidopsis thaliana...	52	0.018
emb AL035678.1	Arabidopsis thaliana DNA chromosome 4, BAC clone...	52	0.018
gb AC012188.2	F14L17 Sequence of BAC F14L17 from Arabidopsis tha...	52	0.018
gb EZ395724.1	TSA: Artemisia annua strain Uganda Contig12219, m...	50	0.069
gb EZ362599.1	TSA: Artemisia annua strain Uganda Contig9760, mR...	50	0.069

gb BT066765.1	Zea mays full-length cDNA clone ZM_BFb0066D03 mRNA...	50	0.069
gb BT055307.1	Zea mays full-length cDNA clone ZM_BFc0167H14 mRNA...	50	0.069
gb EU962146.1	Zea mays clone 240603 mRNA sequence	50	0.069
gb FJ070719.1	Pinus taeda isolate 7938 anonymous locus 0_3458_0...	50	0.069
gb FJ070718.1	Pinus taeda isolate 7947 anonymous locus 0_3458_0...	50	0.069
gb FJ070717.1	Pinus taeda isolate 7943 anonymous locus 0_3458_0...	50	0.069
gb FJ070716.1	Pinus taeda isolate 7950 anonymous locus 0_3458_0...	50	0.069
gb FJ070715.1	Pinus taeda isolate 7940 anonymous locus 0_3458_0...	50	0.069
gb FJ070714.1	Pinus taeda isolate 7948 anonymous locus 0_3458_0...	50	0.069
gb FJ070713.1	Pinus taeda isolate 7949 anonymous locus 0_3458_0...	50	0.069
gb FJ070712.1	Pinus taeda isolate 7952 anonymous locus 0_3458_0...	50	0.069
gb FJ070711.1	Pinus taeda isolate 7941 anonymous locus 0_3458_0...	50	0.069
gb FJ070710.1	Pinus taeda isolate 7951 anonymous locus 0_3458_0...	50	0.069
gb FJ070709.1	Pinus taeda isolate 7942 anonymous locus 0_3458_0...	50	0.069
gb FJ070708.1	Pinus taeda isolate 7953 anonymous locus 0_3458_0...	50	0.069
gb FJ070707.1	Pinus taeda isolate 7937 anonymous locus 0_3458_0...	50	0.069
gb FJ070706.1	Pinus taeda isolate 7946 anonymous locus 0_3458_0...	50	0.069
gb FJ070705.1	Pinus taeda isolate 7945 anonymous locus 0_3458_0...	50	0.069
gb FJ070703.1	Pinus taeda isolate 7939 anonymous locus 0_3458_0...	50	0.069
ref NM_001137528.1	Zea mays hypothetical protein LOC100192105 (...)	50	0.069
gb DQ244260.1	Zea mays clone 3973 mRNA sequence	50	0.069
tpe BN000615.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	50	0.069
dbj AP004731.3	Oryza sativa Japonica Group genomic DNA, chromos...	50	0.069
dbj AB007645.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	50	0.069
emb Y10465.1	S. oleracea mRNA for peroxidase, clone PC44	50	0.069
gb CP000102.1	Methanosphaera stadtmanae DSM 3091, complete genome	50	0.069
emb FP012230.5	Pig DNA sequence from clone CH242-162F1 on chrom...	48	0.27
gb EZ275595.1	TSA: Artemisia annua strain Madagascar Contig1982...	48	0.27
gb EZ286664.1	TSA: Artemisia annua strain Madagascar Contig1305...	48	0.27
gb EZ342046.1	TSA: Artemisia annua strain Uganda Contig9262, mR...	48	0.27
gb EZ321242.1	TSA: Artemisia annua strain Madagascar Contig7788...	48	0.27
gb EZ318330.1	TSA: Artemisia annua strain Madagascar Contig4876...	48	0.27
gb EZ247069.1	TSA: Artemisia annua strain Artemis Contig13739, ...	48	0.27
gb EZ258457.1	TSA: Artemisia annua strain Madagascar Contig1560...	48	0.27
gb EZ396283.1	TSA: Artemisia annua strain Uganda Contig12778, m...	48	0.27
gb EZ220993.1	TSA: Artemisia annua Contig18004	48	0.27
gb EZ366681.1	TSA: Artemisia annua strain Uganda Contig132, mRN...	48	0.27
gb EZ196247.1	TSA: Artemisia annua strain Artemis Contig9804, m...	48	0.27
gb EZ355157.1	TSA: Artemisia annua strain Uganda Contig2318, mR...	48	0.27
gb EZ173232.1	TSA: Artemisia annua strain Artemis Contig32638, ...	48	0.27
gb BT102799.1	Picea glauca clone GQ02016_E21 mRNA sequence	48	0.27
gb BT101612.1	Picea glauca clone GQ01308_P23 mRNA sequence	48	0.27
gb AC212861.3	Pongo abelii BAC clone CH276-236D6 from chromosom...	48	0.27
ref XM_002451803.1	Sorghum bicolor hypothetical protein, mRNA	48	0.27
gb AC235800.1	Solanum lycopersicum chromosome 3 clone C03HBa013...	48	0.27
ref XM_002285687.1	PREDICTED: Vitis vinifera hypothetical prote...	48	0.27
ref XM_002269022.1	PREDICTED: Vitis vinifera hypothetical prote...	48	0.27
dbj AK323976.1	Solanum lycopersicum cDNA, clone: LEFL1068DD08, ...	48	0.27
ref XM_002320381.1	Populus trichocarpa predicted protein, mRNA	48	0.27

gb CP001098.1	Halothermothrix orenii H 168, complete genome	48	0.27
gb EF677600.1	Picea sitchensis clone WS02771_I11 unknown mRNA	48	0.27
gb FJ050773.1	Pinus taeda isolate 4643 anonymous locus 0_13032_...	48	0.27
gb FJ050771.1	Pinus taeda isolate 4657 anonymous locus 0_13032_...	48	0.27
gb FJ050770.1	Pinus taeda isolate 4649 anonymous locus 0_13032_...	48	0.27
gb FJ050769.1	Pinus taeda isolate 4648 anonymous locus 0_13032_...	48	0.27
gb FJ050768.1	Pinus taeda isolate 4659 anonymous locus 0_13032_...	48	0.27
gb FJ050767.1	Pinus taeda isolate 4658 anonymous locus 0_13032_...	48	0.27
gb FJ050766.1	Pinus taeda isolate 4644 anonymous locus 0_13032_...	48	0.27
gb FJ050765.1	Pinus taeda isolate 4645 anonymous locus 0_13032_...	48	0.27
gb FJ050763.1	Pinus taeda isolate 4660 anonymous locus 0_13032_...	48	0.27
gb FJ050762.1	Pinus taeda isolate 4647 anonymous locus 0_13032_...	48	0.27
gb FJ050761.1	Pinus taeda isolate 4654 anonymous locus 0_13032_...	48	0.27
gb FJ050760.1	Pinus taeda isolate 4646 anonymous locus 0_13032_...	48	0.27
gb FJ050759.1	Pinus taeda isolate 4656 anonymous locus 0_13032_...	48	0.27
gb FJ050756.1	Pinus taeda isolate 4652 anonymous locus 0_13032_...	48	0.27
gb EF083074.1	Picea sitchensis clone WS02728_C07 unknown mRNA	48	0.27
gb EU024896.1	Uncultured bacterium clone tgutfos2_Contig107 gen...	48	0.27
emb BX548174.1	Prochlorococcus marinus MED4 complete genome	48	0.27
gb CP000647.1	Klebsiella pneumoniae subsp. pneumoniae MGH 78578...	48	0.27
emb AM454579.2	Vitis vinifera contig VV78X062755.15, whole geno...	48	0.27
emb AM428729.2	Vitis vinifera contig VV78X273545.5, whole genom...	48	0.27
emb AM462968.1	Vitis vinifera, whole genome shotgun sequence, c...	48	0.27
emb AM453059.1	Vitis vinifera, whole genome shotgun sequence, c...	48	0.27
emb AM481723.1	Vitis vinifera contig VV78X090480.3, whole genom...	48	0.27
dbj AP006865.1	Lotus japonicus genomic DNA, chromosome 2, clone...	48	0.27
dbj AB049589.1	Avicennia marina PER mRNA for secretory peroxida...	48	0.27
emb BX828399.1	Arabidopsis thaliana Full-length cDNA Complete s...	48	0.27
emb BX832751.1	Arabidopsis thaliana Full-length cDNA Complete s...	48	0.27
dbj AB010692.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	48	0.27
emb Y10467.1	S. oleracea mRNA for peroxidase, clone PC23	48	0.27
ref XM_670091.1	Plasmodium berghei strain ANKA hypothetical pro...	48	0.27
gb AF109124.1	AF109124 Ipomoea batatas anionic peroxidase swpa2 ...	48	0.27
gb EZ295716.1	TSA: Artemisia annua strain Madagascar Contig1601...	46	1.1
gb EZ256521.1	TSA: Artemisia annua strain Artemis Contig23191, ...	46	1.1
gb EZ360402.1	TSA: Artemisia annua strain Uganda Contig7563, mR...	46	1.1
gb EZ150610.1	TSA: Artemisia annua strain Artemis Contig10016, ...	46	1.1
gb AC239433.3	Solanum lycopersicum strain Heinz 1706 chromosome...	46	1.1
ref NW_003037936.1	Schistosoma mansoni genome sequence supercon...	46	1.1
gb BT095984.1	Soybean clone JCVI-FLGm-20M19 unknown mRNA	46	1.1
gb BT093602.1	Soybean clone JCVI-FLGm-17D17 unknown mRNA	46	1.1
gb AC237089.1	Oryza granulata clone OG_ABa0096023, complete seq...	46	1.1
ref XM_002448761.1	Sorghum bicolor hypothetical protein, mRNA	46	1.1
emb FN357570.1	Schistosoma mansoni genome sequence supercontig ...	46	1.1
emb FN357441.1	Schistosoma mansoni genome sequence supercontig ...	46	1.1
gb BT086529.1	Zea mays full-length cDNA clone ZM_BFc0177005 mRN...	46	1.1
gb EZ053600.1	TSA: Zea mays contig54722, mRNA sequence	46	1.1
emb AL844509.2	Plasmodium falciparum 3D7 chromosome 13	46	1.1
gb AC235371.1	Glycine max strain Williams 82 clone GM_WBb0104B0...	46	1.1

gb AC235196.1	Glycine max strain Williams 82 clone GM_WBb0014G1...	46	1.1
gb AC235187.1	Glycine max strain Williams 82 clone GM_WBb0010C0...	46	1.1
gb AC235182.1	Glycine max strain Williams 82 clone GM_WBb0008C1...	46	1.1
ref XM_002319931.1	Populus trichocarpa predicted protein, mRNA	46	1.1
ref NM_001158468.1	Zea mays peroxidase 52 (LOC100285577), mRNA ...	46	1.1
gb EU954765.1	Zea mays clone 1482328 mRNA sequence	46	1.1
gb EU951047.1	Zea mays clone 687198 mRNA sequence	46	1.1
gb FJ088527.1	Pinus taeda isolate 6658 anonymous locus 2_10243_...	46	1.1
gb FJ088526.1	Pinus taeda isolate 6661 anonymous locus 2_10243_...	46	1.1
gb FJ088525.1	Pinus taeda isolate 6650 anonymous locus 2_10243_...	46	1.1
gb FJ088524.1	Pinus taeda isolate 6653 anonymous locus 2_10243_...	46	1.1
gb FJ088523.1	Pinus taeda isolate 6663 anonymous locus 2_10243_...	46	1.1
gb FJ088522.1	Pinus taeda isolate 6662 anonymous locus 2_10243_...	46	1.1
gb FJ088521.1	Pinus taeda isolate 6654 anonymous locus 2_10243_...	46	1.1
gb FJ088520.1	Pinus taeda isolate 6655 anonymous locus 2_10243_...	46	1.1
gb FJ088519.1	Pinus taeda isolate 6657 anonymous locus 2_10243_...	46	1.1
gb FJ088518.1	Pinus taeda isolate 6664 anonymous locus 2_10243_...	46	1.1
gb FJ088517.1	Pinus taeda isolate 6651 anonymous locus 2_10243_...	46	1.1
gb FJ088516.1	Pinus taeda isolate 6649 anonymous locus 2_10243_...	46	1.1
gb FJ088515.1	Pinus taeda isolate 6666 anonymous locus 2_10243_...	46	1.1
gb FJ088514.1	Pinus taeda isolate 6660 anonymous locus 2_10243_...	46	1.1
gb FJ088513.1	Pinus taeda isolate 6665 anonymous locus 2_10243_...	46	1.1
gb FJ088512.1	Pinus taeda isolate 6656 anonymous locus 2_10243_...	46	1.1
gb FJ088511.1	Pinus taeda isolate 4039 anonymous locus 2_10243_...	46	1.1
gb FJ088510.1	Pinus taeda isolate 4033 anonymous locus 2_10243_...	46	1.1
gb FJ088509.1	Pinus taeda isolate 4024 anonymous locus 2_10243_...	46	1.1
gb FJ088508.1	Pinus taeda isolate 4026 anonymous locus 2_10243_...	46	1.1
gb FJ088507.1	Pinus taeda isolate 4025 anonymous locus 2_10243_...	46	1.1
gb FJ088506.1	Pinus taeda isolate 4031 anonymous locus 2_10243_...	46	1.1
gb FJ088505.1	Pinus taeda isolate 4032 anonymous locus 2_10243_...	46	1.1
gb FJ088504.1	Pinus taeda isolate 4037 anonymous locus 2_10243_...	46	1.1
gb FJ088503.1	Pinus taeda isolate 4022 anonymous locus 2_10243_...	46	1.1
gb FJ088502.1	Pinus taeda isolate 4028 anonymous locus 2_10243_...	46	1.1
gb FJ088501.1	Pinus taeda isolate 4034 anonymous locus 2_10243_...	46	1.1
gb FJ088500.1	Pinus taeda isolate 4038 anonymous locus 2_10243_...	46	1.1
gb FJ088499.1	Pinus taeda isolate 4030 anonymous locus 2_10243_...	46	1.1
gb FJ088498.1	Pinus taeda isolate 4035 anonymous locus 2_10243_...	46	1.1
gb FJ088497.1	Pinus taeda isolate 4036 anonymous locus 2_10243_...	46	1.1
gb FJ088496.1	Pinus taeda isolate 4029 anonymous locus 2_10243_...	46	1.1
gb FJ088495.1	Pinus taeda isolate 4027 anonymous locus 2_10243_...	46	1.1
gb FJ088494.1	Pinus taeda isolate 4023 anonymous locus 2_10243_...	46	1.1
gb AC189631.2	Brassica rapa subsp. pekinensis clone KBrS003K07,...	46	1.1
dbj AP010414.1	Lotus japonicus genomic DNA, chromosome 6, clone...	46	1.1
dbj AP009714.1	Lotus japonicus genomic DNA, clone: Ljt08001, TM...	46	1.1
gb CP001056.1	Clostridium botulinum B str. Eklund 17B, complete...	46	1.1
ref XM_001751456.1	Physcomitrella patens subsp. patens predicte...	46	1.1
gb EF087739.1	Picea sitchensis clone WS02740_P19 unknown mRNA	46	1.1
gb AC213540.1	Populus trichocarpa clone POP053-A08, complete se...	46	1.1
gb EU060241.1	Uncultured bacterium clone LMOABA27ZD09RM1 genom...	46	1.1

gb EF645823.1	Manihot esculenta cultivar MTAI8 cationic peroxid...	46	1.1
emb AM489166.2	Vitis vinifera contig VV78X028632.7, whole genom...	46	1.1
emb AM444565.2	Vitis vinifera contig VV78X153928.11, whole geno...	46	1.1
emb AM436965.2	Vitis vinifera contig VV78X063704.11, whole geno...	46	1.1
ref NM_117724.3	Arabidopsis thaliana peroxidase 40 (PER40) (P40...	46	1.1
emb BX293980.2	Mycoplasma mycoides subsp. mycoides SC str. PG1...	46	1.1
ref NM_001097269.1	Xenopus (Silurana) tropicalis hypothetical p...	46	1.1
gb EF055261.1	Sesbania rostrata peroxidase 1 (prx1) mRNA, compl...	46	1.1
ref XM_623898.2	PREDICTED: Apis mellifera similar to Muscle pro...	46	1.1
ref NM_120616.2	Arabidopsis thaliana peroxidase, putative (AT5G...	46	1.1
gb BT017949.1	Zea mays clone EL01N0522B07.c mRNA sequence	46	1.1
gb BT013033.1	Lycopersicon esculentum clone 114281R, mRNA sequence	46	1.1
gb BT011747.1	Arabidopsis thaliana At4g16270 gene, complete cds	46	1.1
gb AY065270.1	Arabidopsis thaliana putative peroxidase (At5g053...	46	1.1
emb AJ809342.1	Picea abies mRNA for peroxidase (px7 gene)	46	1.1
emb AJ809341.1	Picea abies mRNA for peroxidase (px6 gene)	46	1.1
gb AC084740.5	Homo sapiens BAC clone RP11-423E20 from 4, comple...	46	1.1
gb AC099520.2	Homo sapiens chromosome 5 clone RP11-6N13, comple...	46	1.1
gb AC012602.4	Homo sapiens chromosome 5 clone CTC-328N13, compl...	46	1.1
emb BX005227.12	Zebrafish DNA sequence from clone CH211-286C23 ...	46	1.1
dbj AK175982.1	Arabidopsis thaliana mRNA, complete cds, clone: ...	46	1.1
dbj AK175661.1	Arabidopsis thaliana mRNA, complete cds, clone: ...	46	1.1
emb BX826801.1	Arabidopsis thaliana Full-length cDNA Complete s...	46	1.1
emb BX537286.4	Zebrafish DNA sequence from clone DKEY-28J4 in l...	46	1.1
dbj AP006135.1	Lotus japonicus genomic DNA, chromosome 1, clone...	46	1.1
gb AC008970.4	AC008970 Homo sapiens chromosome 5 clone CTD-2374C...	46	1.1
emb AL161543.2	Arabidopsis thaliana DNA chromosome 4, contig fr...	46	1.1
emb AL132978.1	Arabidopsis thaliana DNA chromosome 3, BAC clone...	46	1.1
emb Z97340.2	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA ...	46	1.1
emb Z82992.1	A. thaliana FCA gene encoding FCA alpha, beta, gamm...	46	1.1
gb AC166091.3	Glycine max clone gmw1-11j16, complete sequence	46	1.1
gb AY108407.1	Zea mays PC0110242 mRNA sequence	46	1.1
emb AL157764.12	Human DNA sequence from clone RP11-562E17 on ch...	46	1.1
gb AF145349.1	AF145349 Glycine max peroxidase (Prx3) mRNA, parti...	46	1.1
gb AF078691.1	AF078691 Manihot esculenta peroxidase gene, partia...	46	1.1
gb AF067188.1	AF067188 Beta vulgaris cell wall peroxidase mRNA, ...	46	1.1
gb L36231.1	SSNPX12A Stylosanthes humilis peroxidase (px12) mRNA...	46	1.1
gb L36110.1	SSNPEROXIA Stylosanthes humilis peroxidase mRNA	46	1.1
emb FN554766.1	Escherichia coli 042 complete genome	44	4.3
gb EZ396827.1	TSA: Artemisia annua strain Uganda Contig13322, m...	44	4.3
gb AC239575.2	Solanum lycopersicum strain Heinz 1706 clone hba-...	44	4.3
ref NG_016144.1	Homo sapiens inositol 1,4,5-triphosphate recept...	44	4.3
gb BT106566.1	Picea glauca clone GQ03005_B15 mRNA sequence	44	4.3
gb FJ415216.1	Gossypium hirsutum clone Ghpox5 class III peroxid...	44	4.3
emb CU633361.7	Pig DNA sequence from clone CH242-1G8 on chromos...	44	4.3
gb AE014187.2	Plasmodium falciparum 3D7 chromosome 14, complete...	44	4.3
gb DQ676955.1	Ipomoea batatas anionic peroxidase (swpa4) gene, ...	44	4.3
emb FP099688.1	Phyllostachys edulis cDNA clone: bphylf045i10, f...	44	4.3
emb FP094559.1	Phyllostachys edulis cDNA clone: bphylf061m22, f...	44	4.3

emb	FP093329.1	Phyllostachys edulis cDNA clone: bphyst031i16, f...	44	4.3
emb	FP092972.1	Phyllostachys edulis cDNA clone: bphylf025d09, f...	44	4.3
emb	FP091819.1	Phyllostachys edulis cDNA clone: bphyem202n22, f...	44	4.3
emb	FP101172.1	Phyllostachys edulis cDNA clone: bphyem105e15, f...	44	4.3
ref	XM_002442921.1	Sorghum bicolor hypothetical protein, mRNA	44	4.3
ref	XM_002455522.1	Sorghum bicolor hypothetical protein, mRNA	44	4.3
ref	XM_002455521.1	Sorghum bicolor hypothetical protein, mRNA	44	4.3
ref	XM_002432395.1	Pediculus humanus corporis conserved hypothe...	44	4.3
gb	EU725468.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb	EU725467.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb	EU725466.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb	EU725465.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb	EU725464.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	4.3
gb	EU725463.1	Triticum aestivum class III peroxidase (Prx109-A)...	44	4.3
gb	AC216032.2	Oryza minuta clone OM_Ba0196N15, complete sequence	44	4.3
gb	EZ063624.1	TSA: Zea mays contig64746, mRNA sequence	44	4.3
emb	AL844507.2	Plasmodium falciparum 3D7 chromosome 8	44	4.3
dbj	AK329676.1	Solanum lycopersicum cDNA, clone: LEFL3153D08, H...	44	4.3
gb	AC235246.1	Glycine max strain Williams 82 clone GM_WBb0033G1...	44	4.3
gb	AC235231.1	Glycine max strain Williams 82 clone GM_WBb0026L1...	44	4.3
gb	AC235115.1	Glycine max strain Williams 82 clone GM_WBa0021N1...	44	4.3
gb	AE013600.1	Mus musculus piebald deletion region complete seq...	44	4.3
ref	XM_002338588.1	Populus trichocarpa predicted protein, mRNA	44	4.3
ref	XM_002336305.1	Populus trichocarpa predicted protein, mRNA	44	4.3
ref	XM_002303984.1	Populus trichocarpa predicted protein, mRNA	44	4.3
gb	BT061140.1	Zea mays full-length cDNA clone ZM_BFb0114015 mRN...	44	4.3
emb	CU928163.2	Escherichia coli UMN026 chromosome, complete genome	44	4.3
emb	CU928164.2	Escherichia coli IAI39 chromosome, complete genome	44	4.3
dbj	AK245281.1	Glycine max cDNA, clone: GMFL01-25-021	44	4.3
gb	EU960147.1	Zea mays clone 222156 mRNA sequence	44	4.3
gb	EU945238.1	Zea mays clone 245264 mRNA sequence	44	4.3
gb	AC232892.1	Oryza officinalis clone 00_Ba0082D20, complete s...	44	4.3
gb	FJ078274.1	Pinus taeda isolate 5928 anonymous locus 0_6659_0...	44	4.3
gb	FJ078266.1	Pinus taeda isolate 5925 anonymous locus 0_6659_0...	44	4.3
gb	FJ078265.1	Pinus taeda isolate 5919 anonymous locus 0_6659_0...	44	4.3
gb	FJ078264.1	Pinus taeda isolate 5914 anonymous locus 0_6659_0...	44	4.3
gb	FJ078263.1	Pinus taeda isolate 5916 anonymous locus 0_6659_0...	44	4.3
gb	FJ078262.1	Pinus taeda isolate 5915 anonymous locus 0_6659_0...	44	4.3
gb	FJ078261.1	Pinus taeda isolate 5922 anonymous locus 0_6659_0...	44	4.3
gb	BT038706.1	Zea mays full-length cDNA clone ZM_BFb0310H17 mRN...	44	4.3
gb	BT037971.1	Zea mays full-length cDNA clone ZM_BFb0205C16 mRN...	44	4.3
ref	NM_001143045.1	Zea mays hypothetical protein LOC100216632 (...)	44	4.3
ref	NM_001137329.1	Zea mays hypothetical protein LOC100191905 (...)	44	4.3
gb	EU795178.1	Uncultured bacterium HF0010_09016 genomic sequence	44	4.3
gb	CP000970.1	Escherichia coli SMS-3-5, complete genome	44	4.3
emb	CU570896.5	Zebrafish DNA sequence from clone DKEY-194E13 in...	44	4.3
gb	EF444530.1	Oryza sativa Japonica Group putative peroxidase m...	44	4.3
gb	AC216704.1	Solanum lycopersicum chromosome 2 clone C02HBa023...	44	4.3
emb	CU570678.3	M.truncatula DNA sequence from clone MTH2-16J21 ...	44	4.3

gb AC215650.1	Populus trichocarpa clone POP108-K22, complete se...	44	4.3
gb AC215390.1	Solanum lycopersicum chromosome 2 clone C02HBa012...	44	4.3
gb AC210491.1	Oryza glaberrima clone OG_BB0088K23, complete se...	44	4.3
ref XM_001553571.1	Botryotinia fuckeliana B05.10 60S ribosomal ...	44	4.3
gb EF533695.1	Glycine max clone BAC GM_WBb098N15, complete sequ...	44	4.3
emb AM483376.2	Vitis vinifera contig VV78X083975.15, whole geno...	44	4.3
emb AM466347.2	Vitis vinifera contig VV78X176098.3, whole genom...	44	4.3
emb AM464800.2	Vitis vinifera contig VV78X220659.11, whole geno...	44	4.3
emb AM445395.2	Vitis vinifera contig VV78X136138.6, whole genom...	44	4.3
emb AM434275.2	Vitis vinifera contig VV78X203901.6, whole genom...	44	4.3
emb CT025903.11	Zebrafish DNA sequence from clone DKEY-66H5 in ...	44	4.3
emb AM432525.2	Vitis vinifera contig VV78X143782.10, whole geno...	44	4.3
emb AM451582.2	Vitis vinifera contig VV78X210575.8, whole genom...	44	4.3
ref XM_001446891.1	Paramecium tetraurelia hypothetical protein ...	44	4.3
ref XM_001428564.1	Paramecium tetraurelia hypothetical protein ...	44	4.3
ref NM_129711.3	Arabidopsis thaliana electron carrier/ heme bin...	44	4.3
ref NM_126037.4	Arabidopsis thaliana peroxidase 72 (PER72) (P72...	44	4.3
gb EF421197.1	Nelumbo nucifera cationic peroxidase (CP) mRNA, c...	44	4.3
emb AM463654.1	Vitis vinifera contig VV78X012147.8, whole genom...	44	4.3
emb AM464677.1	Vitis vinifera contig VV78X194278.8, whole genom...	44	4.3
emb AM475805.1	Vitis vinifera contig VV78X097027.7, whole genom...	44	4.3
gb AE014298.4	Drosophila melanogaster chromosome X, complete se...	44	4.3
gb CP000551.1	Prochlorococcus marinus str. AS9601, complete genome	44	4.3
gb AC120193.5	Homo sapiens chromosome 8, clone RP11-10H17, comp...	44	4.3
gb AC185364.2	Populus trichocarpa clone Pop1-63B23, complete se...	44	4.3
emb CT830771.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	4.3
emb CT836342.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	4.3
emb CT828052.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	4.3
dbj AK243473.1	Oryza sativa Japonica Group cDNA, clone: J100072...	44	4.3
ref NM_001071707.1	Oryza sativa (japonica cultivar-group) Os10g...	44	4.3
ref NM_001071706.1	Oryza sativa (japonica cultivar-group) Os10g...	44	4.3
ref NM_001061107.1	Oryza sativa (japonica cultivar-group) Os05g...	44	4.3
ref NM_001055328.1	Oryza sativa (japonica cultivar-group) Os03g...	44	4.3
ref NM_001052935.1	Oryza sativa (japonica cultivar-group) Os02g...	44	4.3
ref NM_001049442.1	Oryza sativa (japonica cultivar-group) Os01g...	44	4.3
emb AM293547.1	Picea abies mRNA for properoxidase (pxl7 gene), ...	44	4.3
tpe BN000657.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000656.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000598.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000562.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000559.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000544.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
tpe BN000535.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	4.3
dbj AK227717.1	Arabidopsis thaliana mRNA for peroxidase, comple...	44	4.3
gb AY206411.1	Ipomoea batatas anionic peroxidase swpa6 mRNA, co...	44	4.3
gb AY206409.1	Ipomoea batatas anionic peroxidase swpa4 mRNA, co...	44	4.3
gb AC102440.12	Mus musculus chromosome 1, clone RP24-146C18, co...	44	4.3
gb AC087552.3	Oryza sativa Japonica Group chromosome 5 clone P0...	44	4.3
gb AE017263.1	Mesoplasma florum L1 complete genome	44	4.3

gb	AC123834.4	Mus musculus BAC clone RP24-132N9 from chromosome...	44	4.3
gb	AC133523.3	Mus musculus BAC clone RP23-34E20 from 19, comple...	44	4.3
gb	AC126691.3	Mus musculus BAC clone RP23-221H11 from 14, compl...	44	4.3
gb	AC069248.4	Homo sapiens chromosome 3 clone RP11-6I21 map 3p,...	44	4.3
gb	AC113010.10	Mus musculus chromosome 18, clone RP23-172F6, co...	44	4.3
gb	AC155955.2	Xenopus (Silurana) tropicalis clone CH216-151P9, ...	44	4.3
dbj	AP007151.1	Aspergillus oryzae RIB40 DNA, SC005	44	4.3
gb	BT008727.1	Arabidopsis thaliana At2g41480 gene, complete cds	44	4.3
gb	BT008314.1	Arabidopsis thaliana At5g66390 gene, complete cds	44	4.3
emb	BX546477.9	Zebrafish DNA sequence from clone DKEYP-79C5 in ...	44	4.3
emb	BX842700.35	Zebrafish DNA sequence from clone DKEY-2P18 in ...	44	4.3
gb	AC161005.4	Pan troglodytes BAC clone CH251-668M6 from chromo...	44	4.3
gb	AC161283.2	Pan troglodytes BAC clone CH251-354N8 from chromo...	44	4.3
dbj	AK081398.1	Mus musculus 16 days embryo head cDNA, RIKEN ful...	44	4.3
gb	AY139994.1	Arabidopsis thaliana putative peroxidase (At2g414...	44	4.3
gb	AC074196.14	Oryza sativa chromosome 10 BAC OSJNBa0040D23 gen...	44	4.3
gb	AC105363.2	Oryza sativa Japonica Group chromosome 3 clone OJ...	44	4.3
gb	AC004625.3	Arabidopsis thaliana chromosome 2 clone T26J13 ma...	44	4.3
gb	AC021006.7	Homo sapiens chromosome 11, clone RP11-124G5, com...	44	4.3
gb	AC093154.2	Homo sapiens chromosome 1 clone RP3-445010, compl...	44	4.3
gb	AF455807.1	AF455807 Nicotiana tomentosiformis anionic peroxid...	44	4.3
gb	AC024958.8	Homo sapiens, clone RP11-561E1, complete sequence	44	4.3
gb	AC092697.6	Oryza sativa chromosome 10 BAC OSJNBb0060I05 geno...	44	4.3
emb	AL160288.21	Human DNA sequence from clone RP11-160P20 on ch...	44	4.3
gb	AC021956.8	Homo sapiens chromosome 11, clone RP11-447I3, com...	44	4.3
emb	AL121584.24	Human DNA sequence from clone RP11-388K2 on chr...	44	4.3
gb	AC158774.6	Mus musculus chromosome 18, clone RP23-427N16, co...	44	4.3
gb	AC156828.8	Medicago truncatula clone mth2-18j19, complete se...	44	4.3
gb	AC142260.6	Mus musculus BAC clone RP24-508M8 from chromosome...	44	4.3
emb	CR937028.1	Zebrafish DNA sequence from clone DKEYP-79C5 in ...	44	4.3
dbj	AP004358.5	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
emb	AL935302.7	Zebrafish DNA sequence from clone DKEY-13N1 in l...	44	4.3
emb	BX629350.6	Zebrafish DNA sequence from clone CH211-155E13 i...	44	4.3
emb	BX571960.6	Zebrafish DNA sequence from clone DKEY-165I8 in ...	44	4.3
emb	BX832014.1	Arabidopsis thaliana Full-length cDNA Complete s...	44	4.3
emb	BX831693.1	Arabidopsis thaliana Full-length cDNA Complete s...	44	4.3
dbj	AP005613.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
emb	BX323818.8	Zebrafish DNA sequence from clone DKEY-48H7 in l...	44	4.3
dbj	BS000099.1	Pan troglodytes chromosome 22 clone:PTB-047E13, ...	44	4.3
dbj	AK108037.1	Oryza sativa Japonica Group cDNA clone:002-137-C...	44	4.3
dbj	AK105708.1	Oryza sativa Japonica Group cDNA clone:001-201-E...	44	4.3
dbj	AK103660.1	Oryza sativa Japonica Group cDNA clone:J033135H0...	44	4.3
dbj	AK099187.1	Oryza sativa Japonica Group cDNA clone:J023107P1...	44	4.3
dbj	AK073847.1	Oryza sativa Japonica Group cDNA clone:J033069F0...	44	4.3
dbj	AK070715.1	Oryza sativa Japonica Group cDNA clone:J023058L0...	44	4.3
dbj	AK060028.1	Oryza sativa Japonica Group cDNA clone:006-303-F...	44	4.3
dbj	AK059977.1	Oryza sativa Japonica Group cDNA clone:006-212-B...	44	4.3
dbj	AP006427.1	Lotus japonicus genomic DNA, chromosome 1, clone...	44	4.3
emb	AJ544516.1	Asparagus officinalis mRNA for peroxidase (prx3 ...	44	4.3

emb	AL596024.5	Zebrafish DNA sequence from clone BUSM1-199M19 i...	44	4.3
gb	AC093380.6	Homo sapiens BAC clone RP11-329G2 from 2, complet...	44	4.3
gb	AC012373.14	AC012373 Drosophila melanogaster, chromosome X, r...	44	4.3
gb	AC012098.9	AC012098 Drosophila melanogaster, chromosome X, re...	44	4.3
dbj	AP002971.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
dbj	AP002820.2	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
dbj	AP002482.1	Oryza sativa Japonica Group genomic DNA, chromos...	44	4.3
dbj	AB042103.1	Asparagus officinalis AoPOX1 mRNA for peroxidase...	44	4.3
emb	AL115668.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL114300.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL113536.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL113375.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL112173.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL111555.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL111377.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL111140.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL111098.1	Botrytis cinerea strain T4 cDNA library	44	4.3
emb	AL110651.1	Botrytis cinerea strain T4 cDNA library	44	4.3
dbj	AB013389.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	44	4.3
emb	AL021684.1	Arabidopsis thaliana DNA chromosome 5, BAC clone...	44	4.3
dbj	AB010075.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	44	4.3
emb	X98774.1	A. thaliana mRNA for peroxidase ATP6a, EST clone 15...	44	4.3
emb	X98320.1	A. thaliana mRNA for peroxidase, prxr8	44	4.3
emb	BX908747.25	Zebrafish DNA sequence from clone DKEY-58J15 in...	44	4.3
gb	AC157575.1	Mus musculus BAC clone RP23-16D16 from 9, complet...	44	4.3
gb	AC155233.2	Mus musculus BAC clone RP24-381F23 from 12, compl...	44	4.3
gb	AY923052.1	Homo sapiens PDZ and LIM domain 1 (elfin) (PDLIM1...	44	4.3
gb	AC102393.8	Mus musculus chromosome 18, clone RP24-125H9, com...	44	4.3
emb	BX649473.8	Zebrafish DNA sequence from clone CH211-65G16 in...	44	4.3
emb	BX548017.3	Mouse DNA sequence from clone RP23-335I21 on chr...	44	4.3
emb	AL935181.5	Zebrafish DNA sequence from clone CH211-162K9, c...	44	4.3
emb	AL807770.17	Mouse DNA sequence from clone RP23-206L14 on ch...	44	4.3
dbj	AP005626.2	Homo sapiens genomic DNA, chromosome 8q24, clone...	44	4.3
gb	AY108615.1	Zea mays PC0132912 mRNA sequence	44	4.3

>gb|BT093225.1| Soybean clone JCVI-FLGm-17C9 unknown mRNA

Length = 1274

Score = 1039 bits (524), Expect = 0.0

Identities = 539/544 (99%)

Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

|||||

Sbjct: 639 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 580

Query: 1849 accaacaatagaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908

|||||
Sbjct: 579 accaacataggaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 520

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||

Sbjct: 519 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 460

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 459 tacttcaagaacctcggttcagaagaagggtttcctccactctgatcagcaactgttcaac 400

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 399 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttcccctct 340

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||

Sbjct: 339 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 280

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtcttgaatattaagggt 2208
|||

Sbjct: 279 gaagtcaggaagaattgtagaaggattaactaatttaattcagtcttgaatattaagggt 220

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 2268
|||||

Sbjct: 219 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 160

Query: 2269 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 2328
|||||

Sbjct: 159 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 100

Query: 2329 tccc 2332
|||

Sbjct: 99 tccc 96

Score = 525 bits (265), Expect = e-145
Identities = 274/277 (98%)
Strand = Plus / Minus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567
|||||
Sbjct: 1272 acaccctttcaatcaaacacaaacactcgaagtactaagttagtgtgttcgagcaaatta 1213

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
|||||
Sbjct: 1212 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 1153

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
|||||
Sbjct: 1152 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 1093

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcatgggtgcttct 747
|||||
Sbjct: 1092 tcctctgtgaaatccgagtgcaatctgccatatctaaggagaccgcatgggtgcttct 1033

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 1032 ctcttcgcttggttcttccacgattgctttgtcaatg 996

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 996 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 937

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 936 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 877

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 876 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 817

Query: 1337 tctgttcagatt 1348
|||||

Score = 333 bits (168), Expect = 3e-87
Identities = 168/168 (100%)
Strand = Plus / Minus

Query: 1538 tctgtgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 744 tctgtgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 685

>gb|BT093496.1| Soybean clone JCVI-FLGm-17I24 unknown mRNA
Length = 1217

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 631 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 690

```
Query: 1849  accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
              | ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 691   agcaacatagacaccgcatttgcaagggaaggcaacaaagctgccaagaacatcaggg 750
```

```
Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
          ||||| ||||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 751 tcaggggacaataatcttgcaacgcttgatcttcaaactccaaccgaattcgacaactac 810
```

Query: 1969 t a c t t t c a a g a a c c t c g t t c a g a a g a g g t c t c t c c a c t c t g a t c a g c a a c t g t t c a a c 2028

Sbjct: 811 tacttcaagaatcttggtcagaagaagggtctcctccactctgatcagcaactgttcaat 870

Sbjct: 871 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgagctccttctcctct 930

Sbjct: 931 gacttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaacgga 990

Sbjct: 991 gaaatcaggaagaattgtagaaggattaactaattactaattgagtcctccaatattaagg 1050

Sbjct: 1051 gtcctactacacatacgcaagcaattttaattgtgtttaataagttgttaaaacatgtttt 1110

Sbjct: 1111 ggttgtgttttggattcc 1128

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567

Sbjct: 2 acaccctctcaagcaaacacaaacacttgaagtactaagttagtgtttttgagcaa-- 58

Sbjct: 59 -ctatggcttcgttttgttctagattgaccatttgtttggctctgtttgtcctcatattg 117

Sbjct: 118 gggagtgccaatgcccaactttctacaaacttctactaccattcgtgtccaaacctcttc 177

Query: 688 tcctctgtgaaatccacagtgaatctgccatatctaaggagacccgcatgggtgcttct 747
||| |||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct: 178 tccactgtgaaatccacagtgaatctgccatatcaaaggagacccgcatgggtgcttct 237

Query: 748 ctctctcgcttgtttcttccacgattgctttgtcaatg 784
|||| | ||||||||||||||||||||
Sbjct: 238 ctctccgcccgttcttccacgattgctttgtcaatg 274

Score = 331 bits (167), Expect = 1e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 274 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||||||||||||||||||| ||||| ||||||||||||||||||||
Sbjct: 334 aaccccaacaggaactctgctcgtggatacagggtcattgacaacattaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctcctgcgcagatatccttgccatcgctgccagagac 1336
||||| |||||||||||| |||||||||||||||||||| |||||||||
Sbjct: 394 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 453

Query: 1337 tctgttcagat 1347
|||||||
Sbjct: 454 tctgttcagat 464

Score = 293 bits (148), Expect = 3e-75
Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||||||| ||||||||||||||||||||
Sbjct: 466 cttggaggccctagtgtgaatgttaaagttggaagaagagacgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||||||||||||||| ||||||||||||||||||||

Sbjct: 526 tctgctgctaacaatggcatccctccaccacttcaaaccttaaccaactcatctcaaga 585

Sbjct: 586 ttcagegctcttggactttccaccaaggacttggtcgccttgtccggt 633

Score = 176 bits (89), Expect = 4e-40
Identities = 304/376 (80%)
Strand = Plus / Plus

Sbjct: 583 cacacaattggacaagcaaggtgtacaaat ttttagggcacgaatctacaacgagaccaac 642

Sbjct: 643 ataaatgctgcatngctagcacgaggcaatcaaattgcccaaaggcatcaggatcaggt 702

Sbjct: 703 gacaacaatttggcacctcttgatcttcagactcctagttcttttgacaacaactacttc 762

Sbjct: 763 aagaaccttgttcagaacaagggtcttctccattcagaccaacaactttttaacggcggg 822

Sbjct: 823 tccaccaactcaatagtgagtggttatagtactagcccaagctcttttctctgatttt 882

Sbjct: 883 gccgctgctatgatcaagatgggaaatattaaacctctcaccggatcaaattggagagatt 942

Sbjct: 943 aggaagaactgtagaa 958

Score = 145 bits (73), Expect = 2e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
|||||
Sbjct: 64 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgccccaaactctct 123

Query: 688 tctctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcgcatgggtgcttct 747
|||
Sbjct: 124 accacagtgaatccacactgcaaactgccatatcaaaggaggcccgaatgggtgcctct 183

Query: 748 ctctctcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 184 atctccgcttggttcttccacgattgctttgtcaatg 220

Score = 123 bits (62), Expect = 6e-24
Identities = 155/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 220 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 279

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||
Sbjct: 280 aatccaaatagaaactccgctcgtggatttgatgtcatcgacaacataaagacagccgta 339

Query: 1277 gagaaagtgtgtccaggagttgttctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 340 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 399

Query: 1337 tctgtt 1342
|||||
Sbjct: 400 tctgtt 405

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
 ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 412 cttggaggtccaacctggaatgtaaaacttggagaagagatgctaaaacggctagtcaa 471

>gb|BT098008.1| Soybean clone JCVI-FLGm-22H8 unknown mRNA
Length = 1324

Query: 1792 ggtcacacaattggacaagcaaggatgcacaaacttcagagcccgcatctacaacgagacc 1851
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 678 ggtcatacaattggacaagcaaggatgcacaaccttttagagcccgaatctacaacgagagc 619

```
Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactac 1971
           |||||
Sbjct: 558 ggggacaacaaccttgacccattgactttgccactccactttctttgacaaccactac 499
```

```
Query: 2032 ggggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctgat 2091
           || ||||| ||||| | ||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 438  gggtccactgactccttagtgggtacctacagcaccaaccgggctcctttttcgccgat 379
```


Sbjct: 915 aaagtgtgtccgggtgtggttttcttgcgctgacattcttgccatcgctgccagagactct 856

Query: 1340 gttcagat 1347

||| |||

Sbjct: 855 gttgagat 848

Score = 121 bits (61), Expect = 2e-23

Identities = 85/93 (91%)

Strand = Plus / Minus

Query: 692 ctgtgaaatccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctcc 751

||||||| ||||||| |||| ||||||||| |||||||||||||||||||||||||

Sbjct: 1130 ctgtgaaacgcacagtgaatcggccatatcaaaggagacccgcatgggtgcttctctcc 1071

Query: 752 ttcgcttgcttctccacgattgctttgtcaatg 784

| || ||||||||||||||||||||| |||

Sbjct: 1070 tacgtttgttcttccacgattgctttgttaatg 1038

>emb|CU137662.1| Medicago truncatula chromosome 5 clone mth2-15518, COMPLETE SEQUENCE
Length = 111929

Score = 172 bits (87), Expect = 7e-39

Identities = 150/171 (87%)

Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535

||||||||||| |||||| | ||| ||||||||||||||||| || ||||| |||||

Sbjct: 97958 agcttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagta 98017

Query: 1536 aatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaa 1595

|||| ||||| |||||| | ||||| ||||||||||||| || |||||||||||||

Sbjct: 98018 aatcagctgcaaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaa 98077

Query: 1596 gatttagcgctcttggactttccaccaaggacttggctgccttgctccgta 1646

| |||| | |||||| | ||||||||||||| ||||||| ||||| |||||

Sbjct: 98078 ggtttaatgctcttggctcttccaccaaggatttggctgcattgtctggta 98128

Score = 157 bits (79), Expect = 4e-34

Identities = 172/203 (84%)
Strand = Plus / Plus

Query: 1152 tgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 97540 tgcagggatgtgatggttcaattctctcgatgacacatcaagcttcaccggagagaaaa 97599

Query: 1212 acgcaaaccacaacaggaactctgctcgtggattcgaggttattgacaacattaaatcag 1271
|||
Sbjct: 97600 ctgccaatcccaacaaaaattcgcccggtggattcgaagtgatcgacaaaatcaaatcag 97659

Query: 1272 ccgtggagaaagtgtgtccaggagttgttctcgcgcagatatccttgccatcgctgcca 1331
|
Sbjct: 97660 cagtggagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgcta 97719

Query: 1332 gagactctgttcagattgtaagt 1354
|||
Sbjct: 97720 gagactctgttgagatcgtaagt 97742

Score = 119 bits (60), Expect = 9e-23
Identities = 288/364 (79%)
Strand = Plus / Plus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
|||
Sbjct: 98322 tagggggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacg 98381

Query: 1847 agaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcag 1906
|
Sbjct: 98382 actccaacatagatacttctttgctcgcacaaggcaatcagggtgcccgaagacatcgg 98441

Query: 1907 ggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaact 1966
|||
Sbjct: 98442 gttccggggacaataatttgccacccttgatcttgcaacaccaacatcctttgacaacc 98501

Query: 1967 actacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttca 2026
|
Sbjct: 98502 attacttcaagaacctagtgtgacagtaagggtactccactccgaccaacaactcttta 98561

Query: 2027 acggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcct 2086
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 98562 atggtggatccaccgattccatagtgcacgaatatagcttgatccaagctcttttctct 98621

```
Query: 2147  gaga 2150
        |||
Sbjct: 98682 gaga 98685
```

```

Query: 709   caatctgccatatctaaggagaccgcgatgggtgcttctctctcttcgcttgttcttccac 768
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 96891 caatctgccatatcaaaagagactcgcgatgggtgcttctctctcttcgcttgttcttccac 96950

```

>emb|CR938710.1| Medicago truncatula chromosome 5 clone mth2-170k9, COMPLETE SEQUENCE
Length = 123977

```
Query: 1476   agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535
             |||||
Sbjct: 113949 agcttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagta 113890
```


Query: 1596 gatttagcgtcttggactttccaccaaggacttggtcgccttgtccggta 1646
| |||| ||||||| ||||||||||||| ||||||| ||||| ||||
Sbjct: 113829 ggtttaatgctcttggctttccaccaaggatttggtcgcattgtcttgta 113779

Score = 157 bits (79), Expect = 4e-34
Identities = 172/203 (84%)
Strand = Plus / Minus

Query: 1152 tgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||||||||||||||||||| | |||||||||||||||||||||||||
Sbjct: 114367 tgcagggatgtgatggttcaattctctcgatgacacatcaagcttcaccggagagaaaa 114308

Query: 1212 acgcaaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcag 1271
|| || ||||||| || || || ||||||||||| || || ||||| || |||||||
Sbjct: 114307 ctgccaatcccaacaaaaattcggcccggtgattcgaaagtgcgacaaaatcaaatcag 114248

Query: 1272 ccgtggagaaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgcca 1331
| ||||||||||| ||||||| | ||||| ||||| || ||||||| ||||| |||||
Sbjct: 114247 cagtggagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgcta 114188

Query: 1332 gagactctgttcagattgtaagt 1354
||||||||||| |||| |||||||
Sbjct: 114187 gagactctgttgagatcgtaagt 114165

Score = 119 bits (60), Expect = 9e-23
Identities = 288/364 (79%)
Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacg 1846
|||| ||||||||||||||||||||||||| | || ||||||| ||| |||||||
Sbjct: 113586 tagggggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacg 113527

Query: 1847 agaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcag 1906
| ||||||||||| || | ||||| | || ||||| | ||||||| | |||||
Sbjct: 113526 actccaacatagatacttcctttgctcgcacaaggcaatcagggtgcccccaagacatcgg 113467

Query: 1907 ggtcaggggacacaatctggcaccacttgatcttcaaactccaaccagctttgacaact 1966

Query: 1152 tgcagggatgtgatgggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||| ||||||| || |||||| | ||||| ||||||||||||||||||||
Sbjct: 359 tgcagggtgtgatgggtcgattctacttgatgatacatcaagcttcaccggagagaaga 418

Query: 1212 acgcaaaccaccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcag 1271
||||| || ||||| ||||||||||||||||||| || || || ||||| || || |||||
Sbjct: 419 acgcacgtcctaacaagaactctgctcgtggatttgatgtgatcgacaaaatcaagtcag 478

Query: 1272 ccgtggagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgcca 1331
| ||||||| ||||||| ||||| || || ||||| || || ||||||||||||| |||||||
Sbjct: 479 ctgtggaggaagtgtgccagggtgtggtctcctgtgctgatatccttgccattgctgcca 538

Query: 1332 gagactctgttcagattgtaag 1353
|||| ||||||||| || |||||
Sbjct: 539 gagattctgttcacatcgtaag 560

Score = 133 bits (67), Expect = 6e-27
Identities = 124/143 (86%)
Strand = Plus / Plus

Query: 1493 tggaaatgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||| || ||||||||||||||||| | || || || ||||||||||||| |||||||
Sbjct: 679 tggaaacgtgaaacttggagaagagattcgaggacagcaagccaatctgctgccaacaat 738

Query: 1553 ggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612
||||||| ||||||||||||| | ||||||||||||| ||||| | | |||||||
Sbjct: 739 ggcatcccaccacccacttcaaacgtcaaccaactcatctccagattcaactctcttgga 798

Query: 1613 ctttccaccaaggacttggtcgc 1635
||||| |||||||||||||
Sbjct: 799 ctttctcccaaggacttggtcgc 821

>ref|XM_002520789.1| Ricinus communis Peroxidase 52 precursor, putative, mRNA
Length = 957

Score = 129 bits (65), Expect = 9e-26
Identities = 110/125 (88%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
|||||
Sbjct: 421 tggaatgttaaacttgaagaagagatgctagaactgcaagccttctgctgccaataat 480

Query: 1553 ggcattccagctccaacttctaacttgaaccaactcatctcaagatttagcgctcttggc 1612
|||||
Sbjct: 481 ggcattccagctccaacttctaacttgaaccaactcatctcaagatttagtgctcttggc 540

Query: 1613 ctttc 1617
|||||
Sbjct: 541 ctttc 545

Score = 54.0 bits (27), Expect = 0.004
Identities = 33/35 (94%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatc 1191
|||||
Sbjct: 214 ggatgtgatggttcaattctacttgatgacacatc 248

Score = 50.1 bits (25), Expect = 0.069
Identities = 31/33 (93%)
Strand = Plus / Plus

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 182 ttcgcttggttcttccacgactgctttgttaatg 214

Score = 50.1 bits (25), Expect = 0.069
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaa 1823
|||||
Sbjct: 577 cacacaatcgacaagcaaggtgcacaaa 605

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattag 2126
|||||||
Sbjct: 879 catgatcaagatgggagacattag 902

>gb|BT052838.1| Medicago truncatula clone MTYFH_FI_FJ_FK1G-0-8 unknown mRNA
Length = 773

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Minus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| | ||||| ||| ||||| ||||| |||
Sbjct: 464 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccg 405

Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||| ||| ||||| || ||||| || | ||| |||||
Sbjct: 404 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 345

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatattccttgccatcgctgccagagactc 1338
|| || || ||||| || || || ||||| ||||| |||||
Sbjct: 344 gtatgccccggagttgtatcatgtgtgatattccttgccattgctgccacagactc 289

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Minus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||||| ||||| ||||| | || || ||||| ||||| |||||
Sbjct: 549 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 490

Query: 765 ccacgattgctttgtcaatg 784
|||||||
Sbjct: 489 ccacgattgctttgtcaatg 470

Score = 79.8 bits (40), Expect = 8e-11
Identities = 133/164 (81%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| |||||||||||||||| || | ||||||| |||
Sbjct: 278 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 219

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || ||||||| || |||||| ||||||| ||||| |||||
Sbjct: 218 tctgatgcgaacactgccatcccaagaccaacttccaaccttaataactcacctcaatg 159

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgct 1641
|||| | |||| |||||||||||||||| ||||| |||||
Sbjct: 158 tttagaatgttggtctttccaccaaggacttagtcgcattgct 115

Score = 63.9 bits (32), Expect = 5e-06
Identities = 62/72 (86%)
Strand = Plus / Minus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| |||||||||||||||||||| ||||||| || ||| || ||||||| |||
Sbjct: 114 agtgctcacacaattggacaagcaaagtgcaaacatttaggtacgaatctacaatga 55

Query: 1848 gaccaacataga 1859
|||||||||||
Sbjct: 54 gaccaacataga 43

>gb|AY311597.1| Gossypium hirsutum class III peroxidase (pod7) mRNA, complete cds
Length = 1282

Score = 105 bits (53), Expect = 1e-18
Identities = 238/297 (80%), Gaps = 2/297 (0%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| |||||| |||| ||||||||||||||| |||||| |||||| | |||||||
Sbjct: 732 ctgccaagaacaacaggctcaggggacaacaacttggcacctcttgatatccaaactcc 791

Query: 1950 aaccagctttgacaactactacttcaagaacctcggttcagaagaag-ggtctcctccact 2008
||| ||||| ||||| ||||| ||||| ||| ||| ||| |||||
Sbjct: 792 aacatcttttgacaacaactacttcaagaacct-aatcagtc aaaggacttctccact 850

Query: 2009 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 2068
||||| || ||||| ||||| ||||| || ||||| || ||| ||| ||| |||
Sbjct: 851 ctgatcaacagttgttcaatgggtggatccacggattccatcgttcgcggttacggaaca 910

Query: 2069 acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 2128
||| || ||||| || ||||| | || ||||| ||||| ||||| ||||| |||||
Sbjct: 911 gcccaagctccttcaattcgattttgtggctgccatgatcaagatgggagacattagtc 970

Query: 2129 ctctcactgggtccaatggagaaatcaggaagaattgtagaaggattaactaatttg 2185
| ||||| || ||| || ||||| || ||||| | ||||| |||||
Sbjct: 971 ccctcactggatcacgtggggagatcaggaagaactgcagaagggtgaactaatttg 1027

Score = 85.7 bits (43), Expect = 1e-12
Identities = 109/131 (83%)
Strand = Plus / Plus

Query: 1502 aaacttggaagaagagacgctagaactgtagccaatctgctgctaacaatggcatccct 1561
||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 490 aaacttggaagaagagatgcaagaagtgtagccagtctgcggctaataatggcattcct 549

Query: 1562 gcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||| ||||| ||| | |||| ||||| || ||| | ||||| ||||| |||||
Sbjct: 550 ccaccaacttcgaacttgaaccgactcacttcagggtcaatgctcttggactctccacc 609

Query: 1622 aaggacttggt 1632
| |||||
Sbjct: 610 aaggacttggt 620

Score = 75.8 bits (38), Expect = 1e-09
Identities = 50/54 (92%)
Strand = Plus / Plus

Query: 731 cccgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784

Sbjct: 221 cccgaatgggtgcttctctgcttcgattgttcttccacgactgctttgtcaatg 274

Score = 61.9 bits (31), Expect = 2e-05
Identities = 118/147 (80%)
Strand = Plus / Plus

Query: 1196 ttcaccggagagaagaacgcaaaccccaacaggaactctgtctgtggattcgaggttatt 1255
 ||||||||||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 313 ttcaccggagagaaaaatgctaaccggaatcggaactcgtctcgcggattcgatgttgtt 372

Query: 1256 gacaacattaaatcagccgtggagaaaagtgtgtccaggagtgtttctgcgcagatatc 1315
|| ||| | | | | | | | | | | | | | | | | |
Sbjct: 373 gataacatcaagtcagctgttgagaatgttgcctggtgtagtttcttgtgtgatatc 432

```

Query: 1316 cttgccatcgctgccagagactctgtt 1342
          | |||| | |||| ||||| |||||
Sbjct: 433  ttggccattgctgctagagactctgtt 459

```

>emb|FP100639.1| Phyllostachys edulis cDNA clone: bphyem110n02, full insert sequence
Length = 1307

Score = 103 bits (52), Expect = 5e-18
Identities = 157/192 (81%)
Strand = Plus / Plus

```
Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||||| || || ||||| | ||||||||| ||||| | ||||| |||||
Sbjct: 710 tcacaccatagccaagcacgctgcacaaacttcagagcccacgtatacaacgacaccaa 769
```

Query: 1854 catagaaaccgcatttgcaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
 ||| || ||| |||| |||| |||| | | ||||| ||||| |||||
 Sbjct: 770 catcgacggcgccctttgcgaggacgaggcagtcaggttgccctaggacatcaggctcagg 829

```
Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
          ||||| ||||| || || || ||||| ||||| ||| || ||| |||||
Sbjct: 830  tgacaacaacctggcgctctggaccttcaaaccccaacgctcttcgagaacaactacta 889
```

Query: 1974 caagaacctcgt 1985

|||||||
Sbjct: 890 caagaacctcgt 901

Score = 54.0 bits (27), Expect = 0.004
Identities = 78/95 (82%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| |||| |||||||||||||||||||| | | || | || ||||||||||||
Sbjct: 1005 gatttcgtggccggcatgatcaagatgggagacgtcacgccgttgacgggctccaatgga 1064

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt 2183
| ||||||||| || |||||||||
Sbjct: 1065 caggtcaggaagaactgcagaagggttaactaatt 1099

>emb|FP099994.1| Phyllostachys edulis cDNA clone: bphyem210i11, full insert sequence
Length = 1213

Score = 103 bits (52), Expect = 5e-18
Identities = 157/192 (81%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||| || || ||||||| | ||||||||||||||||||| | || ||||||||| |||||
Sbjct: 688 tcacaccataggccaagcacgctgcacaaacttcagagcccacgtatacaacgacaccaa 747

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || ||| ||||| ||||| ||||| | | ||||||||| ||||||||| |||||
Sbjct: 748 catcgacggcgcctttgcgaggacgaggcagtcaggttgccctaggacatcagggtcagg 807

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||| ||||| || || || ||||||||| ||||| ||| || ||| |||||
Sbjct: 808 tgacaacaacctggcgcctctggaccttcaaaccccaaccgtcttcgagaacaactacta 867

Query: 1974 caagaacctcgt 1985
|||||||
Sbjct: 868 caagaacctcgt 879

Score = 54.0 bits (27), Expect = 0.004
Identities = 78/95 (82%)
Strand = Plus / Plus

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| |||| ||||||||||||||||||| | | || | || |||||||||||||
Sbjct: 983 gatttcgtggccggcatgatcaagatgggagacgtcacgccgttgacgggctccaatgga 1042

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt 2183
| ||||||||| || ||||||| |||||||||
Sbjct: 1043 caggtcaggaagaactgcagaagggttaactaatt 1077

>dbj|AB027752.1| Nicotiana tabacum mRNA for peroxidase, complete cds, clone:tpoxC1
Length = 1356

Score = 95.6 bits (48), Expect = 1e-15
Identities = 111/132 (84%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||||| ||||| ||||||| ||||||||||||||||| ||||||||||||||||| |||||||||
Sbjct: 719 ctgcccagaagttcaggtcaggggacaacaatttggcaccacttgatcttcaaactcc 778

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactc 2009
| | ||||||||| | || ||||||||| || ||| | || ||||||||| || |||||||
Sbjct: 779 taacaaatttgacaacaattatttcaagaatctgttgacaaaagggtcttcttccactc 838

Query: 2010 tgatcagcaact 2021
||||||| |||||
Sbjct: 839 tgatcaacaact 850

Score = 54.0 bits (27), Expect = 0.004
Identities = 60/71 (84%)
Strand = Plus / Plus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
||||||| | ||||| || ||||||||||||| || |||||| | ||||||||||||||||| ||
Sbjct: 333 tctgctagaggatttgaagttattgacaatatcaaactctgctgtggagaaagtgtgcctc 392

Query: 1292 ggagttgtttc 1302
|| |||||
Sbjct: 393 ggtgtgtttc 403

Score = 50.1 bits (25), Expect = 0.069
Identities = 43/49 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctcttcgcttggttcttccacgattgctttgtcaatg 784
||||||| |||| | ||||| ||||| |||||
Sbjct: 210 atgggtgcttctcttcttcgtctattcttccatgattgcttcgtcaatg 258

Score = 46.1 bits (23), Expect = 1.1
Identities = 104/131 (79%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||| | ||||| ||||| || ||| ||||| || |
Sbjct: 465 tggaatgtaaaattgggaagaagagattctagaactgcaagtcaaagtgctgccaatagt 524

Query: 1553 ggcattccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612
||||| || | | ||||| ||||| ||||| || || ||| |||||
Sbjct: 525 ggcattcctcctgctacttctaaccttaatagactcatctcaagtttcagtgtgttggc 584

Query: 1613 ctttccaccaa 1623
||||| |||||
Sbjct: 585 ctttctaccaa 595

>gb|AY837788.2| Catharanthus roseus clone Prx4 putative secretory peroxidase mRNA,
complete cds
Length = 1055

Score = 89.7 bits (45), Expect = 8e-14
Identities = 126/153 (82%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||||| ||||| || | ||||| ||||| ||||| |||||
Sbjct: 459 tggaatgtgaaacttggaagaagagatgcaacaactgcaagccaagctgctgctaacaat 518

Score = 67.9 bits (34), Expect = 3e-07

Identities = 49/54 (90%)

Strand = Plus / Plus

Age Group	Percentage
18-24	10%
25-34	15%
35-44	20%
45-54	25%
55-64	30%
65-74	35%
75-84	40%
85+	45%

Score = 60.0 bits (30), Expect = 7e-05

Identities = 54/62 (87%)

Strand = Plus / Plus

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Score = 46.1 bits (23), Expect = 1.1

Identities = 50/59 (84%)

Strand = Plus / Plus

[illegible]

Subjct: 336 ggatttgaggtggttgacaacattaaatccgccgtggaaaatgtttgtccgggcgttgt 394

>gb|FJ644943.1| Sesuvium portulacastrum peroxidase 1 (POD1) mRNA, complete cds
Length = 1293

Score = 87.7 bits (44), Expect = 3e-13
Identities = 71/80 (88%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| ||||| | ||||| ||||| | ||||| ||||| ||||| |||||
Sbjct: 937 atgatcaagatgggtgacatcaaacctcttactggttcaaatggagaaattaggaagaat 996

Query: 2164 tgtagaaggattaactaatt 2183
|| ||||| ||||| |||||
Sbjct: 997 tgcagaaggattaactaatt 1016

Score = 61.9 bits (31), Expect = 2e-05
Identities = 61/71 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 457 cttggaggaccaacatgggatgtgaaactaggaagaagagatgccagaacagctaaccaa 516

Query: 1538 tctgctgctaa 1548
|||||||
Sbjct: 517 gctgctgctaa 527

Score = 54.0 bits (27), Expect = 0.004
Identities = 51/59 (86%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 622 ggtggccactcaataggacaagcaaggtgcacaaatttcagggtcacatataacaacga 680

>dbj|AK242814.1| Oryza sativa Japonica Group cDNA, clone: J090061H15, full insert
sequence
Length = 1215

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||||||| | || ||||||| |||||
Sbjct: 662 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 721

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | | ||||| | || ||||| | ||||||| | | ||||| |||||
Sbjct: 722 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 781

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||||||||||| | ||||||| || ||||| || || || || |||||
Sbjct: 782 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 841

Query: 1974 caagaacctcggttcagaagaagggtctcctccactctgatcag 2016
||||||||||| ||||||| ||||| |||||||||
Sbjct: 842 caagaacctcgctcgtcaagaagggtctcctgcactctgatcag 884

>ref|NM_001072100.1| Oryza sativa (japonica cultivar-group) Os11g0112400 (Os11g0112400)
mRNA, complete cds
Length = 975

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||||||| | || ||||||| |||||
Sbjct: 588 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 647

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | | ||||| | || ||||| | ||||||| | | ||||| |||||
Sbjct: 648 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 707

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||||||||||| | ||||||| || ||||| || || || || |||||
Sbjct: 708 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 767

Query: 1974 caagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| |||||
Sbjct: 768 caagaacctcgtcgtcaagaagggtcctgcactctgatcag 810

>tpe|BN000659.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx130 gene for
class III peroxidase 130 precursor, exons 1-4
Length = 2195

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||| | ||||||| ||||| | || ||||||| |||||
Sbjct: 1808 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 1867

Query: 1854 catagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| || ||||| | ||||||| | ||||| |||||
Sbjct: 1868 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 1927

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||| ||||||| | ||||||| || ||||| || || || |||||
Sbjct: 1928 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 1987

Query: 1974 caagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| |||||
Sbjct: 1988 caagaacctcgtcgtcaagaagggtcctgcactctgatcag 2030

>dbj|AB019228.1| Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCK7
Length = 87090

Score = 85.7 bits (43), Expect = 1e-12
Identities = 52/55 (94%)
Strand = Plus / Minus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787
||||||| ||||||| ||||| |||||||
Sbjct: 74225 cgcatgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatgtaa 74171

>emb|BX000512.1| Oryza sativa chromosome 11, . BAC OSJNBa0025K19 of library OSJNBa from

chromosome 11 of cultivar Nipponbare of ssp. japonica of
Oryza sativa (rice), complete sequence
Length = 181322

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||| ||| ||||||| |||||
Sbjct: 158955 tcacaccattggacaagcacgatgcacaaacttcagagctcacatatacaacgaaaccaa 158896

Query: 1854 catagaaaccgcatttgcaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| || ||||| | ||||||| | ||||| |||||
Sbjct: 158895 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 158836

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||||||| | ||||||| || ||||| || || || |||||
Sbjct: 158835 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 158776

Query: 1974 caagaacctcggttcagaagaagggtctctctccactctgatcag 2016
||||||| || ||||| ||||| |||||||||
Sbjct: 158775 caagaacctcgctcgaagaagggtctctctccactctgatcag 158733

>gb|EF661875.2| Catharanthus roseus putative secretory peroxidase (Prx3) mRNA,
complete cds
Length = 1233

Score = 83.8 bits (42), Expect = 5e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctctctgattttgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
|||| ||||||| || ||||||||||||||||||| ||||||| | |||||
Sbjct: 924 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 983

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||||| | ||||| ||||||| || |||||
Sbjct: 984 tcaaatggagaggttaggaaaaattgtaggagggttaa 1021

Score = 46.1 bits (23), Expect = 1.1
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 639 cacacaattggtcaagcaaggtgcaca 665

>ref|NM_125225.1| Arabidopsis thaliana peroxidase, putative (AT5G58390) mRNA,
 complete cds
 Length = 1220

Score = 79.8 bits (40), Expect = 8e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 229 cgcattgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>dbj|AK117722.1| Arabidopsis thaliana At5g58390 mRNA for putative peroxidase,
 complete cds, clone: RAFL17-40-J20
 Length = 656

Score = 79.8 bits (40), Expect = 8e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 226 cgcattgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 277

>gb|AY085030.1| Arabidopsis thaliana clone 124846 mRNA, complete sequence
 Length = 1220

Score = 79.8 bits (40), Expect = 8e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 229 cgcattgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>gb|EZ329073.1| TSA: Artemisia annua strain Madagascar Contig15619, mRNA sequence
Length = 698

Score = 75.8 bits (38), Expect = 1e-09
Identities = 56/62 (90%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 169 ctgccaagaacctcagggtcaggagacaacaatttggcaccactagatctccaaactcc 228

Query: 1950 aa 1951
 ||
Sbjct: 229 aa 230

>ref|XM_002450087.1| Sorghum bicolor hypothetical protein, mRNA
Length = 996

Score = 75.8 bits (38), Expect = 1e-09
Identities = 80/94 (85%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 704 gctgccctagaacctcaggttcaggtgacaacaatttggcgctcttgaccttcaaacc 763

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982
 ||||| ||||| ||| ||||| ||||| |||||
Sbjct: 764 caaccgtctttgagaacaactactacaagaacct 797

Score = 50.1 bits (25), Expect = 0.069
Identities = 40/45 (88%)
Strand = Plus / Plus

Query: 2137 ggctccaatggagaaatcaggaagaattgtagaaggattaactaa 2181
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 952 ggctccaatggacagatcaggaagaactgcagaatgattaactaa 996

>ref|XM_002269882.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257005
(LOC100257005), mRNA
Length = 1180

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||||||
Sbjct: 754 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 813

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 814 tactacaagaacct 827

Score = 58.0 bits (29), Expect = 3e-04
Identities = 47/53 (88%)
Strand = Plus / Plus

Query: 732 cegcatgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
||||||||| ||||||||||| || | ||||||| |||||||||||||
Sbjct: 225 cegcatgggcgcttctctccttcgcttcttccatgattgctttgtcaatg 277

>emb|AM447728.2| Vitis vinifera contig VV78X018697.9, whole genome shotgun sequence
Length = 22220

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||||||
Sbjct: 11004 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 10945

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 10944 tactacaagaacct 10931

Score = 65.9 bits (33), Expect = 1e-06
Identities = 51/57 (89%)
Strand = Plus / Minus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaat 788
||||||| ||||||||| || | ||||||| |||||||||
Sbjct: 12714 ccgcatgggcgcttctctcctccgtctcttcttccatgattgctttgtcaatgtaat 12658

>ref|XM_002278960.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257059
(LOC100257059), mRNA
Length = 966

Score = 71.9 bits (36), Expect = 2e-08
Identities = 101/120 (84%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
||||||| |||| | | ||||||| || ||||| || || |
Sbjct: 694 tcaggggacaacaacttggccctctggatcttcaaactcctac-agcttttgagaacaa 752

Query: 1968 ctacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaa 2027
||||| ||||||| | |||||| | | ||||||| |||||||
Sbjct: 753 ctactacaagaacctgatcaagaagaagggtctcctccactctgatcagcagctgttcaa 812

Score = 67.9 bits (34), Expect = 3e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||||| ||||| ||||||| ||||| ||||| |||
Sbjct: 580 cacacaattgggaagcaaggtgcacatccttcagggcccgcatatacaatgagacaaac 639

Query: 1855 at 1856
||
Sbjct: 640 at 641

Score = 65.9 bits (33), Expect = 1e-06
Identities = 129/161 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| |||| ||||| || ||||| || ||||| || || || |||||
Sbjct: 409 cttggaggccttagctggaacgtaaaacttgggcgaagagacgcccggaccgcaagccag 468

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||| ||||| || || ||||| || ||||| || ||||| ||
Sbjct: 469 gctgctgcaaacaacagcatccctcctccaacttcaaacctgaaccaactaatctctaga 528

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgcctt 1638
|| ||||| || || ||||| ||||| |||||
Sbjct: 529 ttccaagctcttggcctctcaaccaggacttggcgcctt 569

Score = 58.0 bits (29), Expect = 3e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| ||||| || || || ||||| || ||||| || ||||| ||
Sbjct: 889 atgatcaagatgggagatatcagccactcactggatcaaatggagagattaggaagaac 948

Query: 2164 tgtagaagg 2172
|| |||||
Sbjct: 949 tgcagaagg 957

>gb|AY206413.1| Ipomoea batatas anionic peroxidase swpb2 mRNA, complete cds
Length = 1263

Score = 71.9 bits (36), Expect = 2e-08
Identities = 57/64 (89%)
Strand = Plus / Plus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaaga 2161
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 989 ccatgatcaagatggccaacatttcgcctctcactggctccaaggagaaatcaggaaga 1048

Query: 2162 attg 2165
|||
Sbjct: 1049 attg 1052

>gb|EZ399860.1| TSA: Artemisia annua strain Uganda Contig16355, mRNA sequence
Length = 1170

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||||| ||||||| || ||||| |||||||||
Sbjct: 518 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctccaaactcc 459

Query: 1950 aac 1952
|||
Sbjct: 458 aac 456

>gb|EZ145065.1| TSA: Artemisia annua strain Artemis Contig4471, mRNA sequence
Length = 1332

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||||| ||||||| || ||||| |||||||||
Sbjct: 713 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctccaaactcc 772

Query: 1950 aac 1952
|||
Sbjct: 773 aac 775

Score = 58.0 bits (29), Expect = 3e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||| ||||||||||||| ||| ||||| |||||||||||||
Sbjct: 207 atgggcgcttctctccttcgcttgcttgcacttccatgattgctttgtcaatg 255

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaaga 1513
||||||| ||||||||||||| ||||| |||||
Sbjct: 447 cttggaggacctacatggaatgtgaaactgggaaga 482

>gb|EZ141680.1| TSA: Artemisia annua strain Artemis Contig1086, mRNA sequence
Length = 456

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||| ||||||| || ||||| |||||||
Sbjct: 224 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctcaaactcc 283

Query: 1950 aac 1952
|||
Sbjct: 284 aac 286

>ref|XM_002489001.1| Sorghum bicolor hypothetical protein (SORBIDRAFT_0246s002010) mRNA,
complete cds
Length = 1045

Score = 69.9 bits (35), Expect = 7e-08
Identities = 200/255 (78%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaagggtcacaaacttcagagcccgcatctacaacgag 1848
|||| | ||||| || || ||||| | ||||| ||||||||| || |||||||||
Sbjct: 653 ggtgctcacaccataggccaagcacgctgcaccaacttcagagaccacatctacaacgac 712

Query: 1849 accaacatagaaacgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
||||| | || || ||||||||| ||||| | || ||||| || |||||
Sbjct: 713 accaacgtcgacggagcctttgcaaggacaaggcaatcaggttgctcctagcacctcagga 772

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||
Sbjct: 773 acaggtgacaacaacttggcaccattggaccttcaaacaccaaccgtctttgagaacgac 832

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||| ||||| ||||| || || || ||||| ||||| || || |||||

Sbjct: 833 tactacaagaaccttgttagcaacatggggctcctacactctgaccaagagctcttcaac 892

Query: 2029 ggtgggtccaccgac 2043

||||| |||||

Sbjct: 893 ggtggcgccaccgac 907

Score = 46.1 bits (23), Expect = 1.1

Identities = 62/75 (82%)

Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

||||| ||||| || || || ||||| || || |||||

Sbjct: 967 catgatcaagatgggtgacattacaccgttgacgggctccgctggggagatcaggaagaa 1026

Query: 2163 ttgtagaaggattaa 2177

|| |||||

Sbjct: 1027 ctgcagaaggattaa 1041

>ref|XM_002441657.1| Sorghum bicolor hypothetical protein, mRNA

Length = 588

Score = 69.9 bits (35), Expect = 7e-08

Identities = 200/255 (78%)

Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacgag 1848

||||| ||||| || || ||||| || ||||| ||||| || |||||

Sbjct: 4 ggtgctcacacataggccaagcacgctgcaccaacttcagagaccacatctacaacgac 63

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaaactgcccctagaacatcaggg 1908

||||| || || || ||||| ||||| || || || ||||| || |||||

Sbjct: 64 accaacgtcgacggagcctttgcaaggacaaggcaatcaggttgctcctagcacctcagg 123

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||
Sbjct: 124 acaggtgacaacaacttggcaccattggaccttcaaacaccaaccgtctttgagaacgac 183

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028

||||| ||||| ||||| || || || ||||| ||||| || || || |||||
Sbjct: 184 tactacaagaaccttgttagcaacatggggctcctacactctgaccaagagctcttcaac 243

Query: 2029 ggtgggtccaccgac 2043

||||| |||||
Sbjct: 244 ggtggcgccaccgac 258

Score = 46.1 bits (23), Expect = 1.1
Identities = 62/75 (82%)
Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

||||| ||||| || || || ||||| || || || |||||
Sbjct: 318 catgatcaagatgggtgacattacaccgttgacgggctccgctggggagatcaggaagaa 377

Query: 2163 ttgtagaaggattaa 2177

|| ||||| |||||
Sbjct: 378 ctgcagaaggattaa 392

>emb|AM456467.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X246626.10,
clone ENTAV 115
Length = 52838

Score = 69.9 bits (35), Expect = 7e-08
Identities = 131/163 (80%)
Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagcc 1535

||||| ||||| ||||| || ||||| ||||| || || || |||||
Sbjct: 14928 agcttggagggcctagctggaacgtaaaacttgggcgaagagacgcccggaccgcaagcc 14987

Query: 1536 aatctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaa 1595

| ||||| ||||| ||||| || || ||||| ||||| |||||
Sbjct: 14988 aggctgctgcaaacaacagcatccctcctccaacttcaaacctgaaccaactaatctcta 15047

Query: 1596 gatttagcgctcttggactttccaccaaggacttggtcgcctt 1638
|||| | ||||| | | | ||| ||||| |||||
Sbjct: 15048 gattccaagctcttggcctctcaaccagggacttggttcctt 15090

Score = 67.9 bits (34), Expect = 3e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 15195 cacacaattgggcaagcaaggtgcacatccttcagggcccgcatatacaatgagacaaac 15254

Query: 1855 at 1856
||
Sbjct: 15255 at 15256

Score = 67.9 bits (34), Expect = 3e-07
Identities = 100/120 (83%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
||| ||||| ||| | | ||||| ||||| || ||||| || ||| |
Sbjct: 15309 tcargggacaacaacttggccctctggatcttcaaactcctac-agcttttgagaacaa 15367

Query: 1968 ctacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaa 2027
|||| ||||| | | ||||| || | ||||| ||||| |||||
Sbjct: 15368 ctactacaagaacctgatcaagaagaagggtctcctccactctgatcagcagctgttcaa 15427

Score = 58.0 bits (29), Expect = 3e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| ||||| || | ||||| || ||||| || |||||
Sbjct: 15504 atgatcaagatgggagatatcagccactcactggatcaaatggagagattaggaagaac 15563

Query: 2164 tgtagaagg 2172

|| |||||
Sbjct: 15564 tgcagaagg 15572

>gb|GU230149.1| Ipomoea batatas anionic peroxidase mRNA, complete cds
Length = 1125

Score = 67.9 bits (34), Expect = 3e-07
Identities = 46/50 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctctcttcgcttgttcttccacgattgctttgt 779
|||||||
Sbjct: 289 acccgcatgggtgcttccctcattcgcttgttcttccatgactgctttgt 338

>ref|XM_002268223.1| PREDICTED: Vitis vinifera hypothetical protein LOC100263665
(LOC100263665), mRNA
Length = 1002

Score = 67.9 bits (34), Expect = 3e-07
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttc 1827
|||||||
Sbjct: 516 tcacacaattggacaagcaaggtgcacaaacttc 549

>gb|FJ099755.1| Pinus taeda isolate 1286 anonymous locus 2_6350_01 genomic sequence
Length = 410

Score = 67.9 bits (34), Expect = 3e-07
Identities = 61/70 (87%)
Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||| ||||| ||||| | |||||
Sbjct: 308 taggtgctcatacaattggccaagcacggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>emb|CU231251.1| Populus EST from mild drought-stressed leaves
Length = 584

Score = 67.9 bits (34), Expect = 3e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || |||||||||||||||| ||| |||| | |||| | ||||| |||||
Sbjct: 138 cacacaatcgggcaagcaaggtgcacaagctttagagctcgcataatacaatgagaccaac 197

Query: 1855 at 1856
||
Sbjct: 198 at 199

>gb|AY206412.1| Ipomoea batatas anionic peroxidase swpb1 mRNA, complete cds
Length = 1257

Score = 67.9 bits (34), Expect = 3e-07
Identities = 37/38 (97%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaagaattg 2165
||||||| ||||||||||||||||||||
Sbjct: 1002 cctctcactggtccaatggagaaatcaggaagaattg 1039

Score = 44.1 bits (22), Expect = 4.3
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1217 aaccccaacaggaactctgctcgtgg 1242
||||||| ||||||||||||
Sbjct: 348 aaccccaacagaaactctgctcgtgg 373

>dbj|AK322204.1| Solanum lycopersicum cDNA, clone: LEFL1035AA07, HTC in leaf
Length = 1170

Score = 65.9 bits (33), Expect = 1e-06
Identities = 48/53 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcacatgggtgcttctctccttcgcttggttcttcacgattgctt 776
||||| ||||| ||||||||| ||||||| | |||||||||
Sbjct: 213 aaggaaaccgaatgggtgcttcctccttcgcctattcttcacgattgctt 265

Score = 58.0 bits (29), Expect = 3e-04
Identities = 47/53 (88%)
Strand = Plus / Plus

Query: 1801 attggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||| ||||||| ||||| | ||||| |||||||||
Sbjct: 642 attggacaagcaaggtgcacaagtttcaggggacgcatatacacgagaccaa 694

Score = 56.0 bits (28), Expect = 0.001
Identities = 70/84 (83%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||||| ||||||| || || ||||| ||||||| || ||||||| |||||||
Sbjct: 945 gccatgattaagatgggtgatatcctccctcactgggttctaattggagagatcaggaag 1004

Query: 2161 aattgtagaaggattaactaat 2184
|| || || || || || || || || ||
Sbjct: 1005 aactgcaggagaatcaactaat 1028

Score = 50.1 bits (25), Expect = 0.069
Identities = 100/125 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||||| ||||||| ||||||| ||||| | || || || || || || || ||
Sbjct: 747 tcaggatcaggggataacaatttggcacctcttgatttacagaccctacgcgcttcgac 806

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
|| ||||||| ||||| || | || ||||| || ||||||| ||||||| ||
Sbjct: 807 aatcactacttcataaaccttgtaacaaaaagggactgctccattctgatcagcagctt 866

Query: 2023 ttcaa 2027

|||||

Sbjct: 867 ttcaa 871

>ref|XM_002328955.1| Populus trichocarpa predicted protein, mRNA

Length = 1047

Score = 65.9 bits (33), Expect = 1e-06

Identities = 57/65 (87%)

Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854

|||||||

Sbjct: 633 cacacaattggacaagcaagatgcacaaactttagggcacgcatatataatgagaccacc 692

Query: 1855 ataga 1859

|||||

Sbjct: 693 ataga 697

Score = 54.0 bits (27), Expect = 0.004

Identities = 66/79 (83%)

Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

|||||||

Sbjct: 941 catgatcaagatgggagatatcaggcctctcactggatccagaggagagattagaaataa 1000

Query: 2163 ttgtagaaggattaactaa 2181

||| || ||||| |||||

Sbjct: 1001 ttgcaggaggatcaactaa 1019

Score = 44.1 bits (22), Expect = 4.3

Identities = 34/38 (89%)

Strand = Plus / Plus

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactcc 1949

|||||||

Sbjct: 750 ggggacaacaacttggcaccacttgattgcaaactcc 787

>ref|XM_002319932.1| Populus trichocarpa predicted protein, mRNA
Length = 1220

Score = 65.9 bits (33), Expect = 1e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||| |||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 592 cacacaatcgggcaagcaaggtgtacaagctttagagctcgcatatacaatgagaccaac 651

Query: 1855 ataga 1859
|||||
Sbjct: 652 ataga 656

Score = 48.1 bits (24), Expect = 0.27
Identities = 39/44 (88%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctctcttcgcttggttcttccacgattgctttgt 779
||||||||||||| ||||||||||||| || ||||| |||||
Sbjct: 178 atgggtgcttctcttgttcgcttggttcttcatgattgtttgt 221

>gb|AC214418.1| Populus trichocarpa clone POP106-D21, complete sequence
Length = 88637

Score = 65.9 bits (33), Expect = 1e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||| |||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 88236 cacacaatcgggcaagcaaggtgtacaagctttagagctcgcatatacaatgagaccaac 88295

Query: 1855 ataga 1859
|||||
Sbjct: 88296 ataga 88300

Score = 52.0 bits (26), Expect = 0.018
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtca 781
|||||
Sbjct: 86397 atgggtgcttctcttggttcgcttggttcttcatgattgtttgtca 86442

>gb|BT096974.1| Soybean clone JCVI-FLGm-21M8 unknown mRNA
Length = 1201

Score = 63.9 bits (32), Expect = 5e-06
Identities = 44/48 (91%)
Strand = Plus / Plus

Query: 1810 gcaaggtgcacaaacttcagagcccgcatctacaacgagaccaacata 1857
|||||
Sbjct: 639 gcaaggtgcactaccttcagagaccgcatctacaacgacaccaacata 686

>gb|FJ596178.1| Capsicum annuum peroxidase (POD) mRNA, complete cds
Length = 1353

Score = 63.9 bits (32), Expect = 5e-06
Identities = 59/68 (86%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||||
Sbjct: 646 aggtgctcacacaattggacaagcaaggtgcacatcattcagggcacgtatatacaatga 705

Query: 1848 gaccaaca 1855
|||||
Sbjct: 706 gaccaaca 713

Score = 61.9 bits (31), Expect = 2e-05
Identities = 55/63 (87%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
|||||

Sbjct: 965 atgatcaagatgggtgacaatcgccacttactggatctaattggagaaattaggaagaat 1024

Query: 2164 tgt 2166

|||

Sbjct: 1025 tgt 1027

Score = 54.0 bits (27), Expect = 0.004

Identities = 48/55 (87%)

Strand = Plus / Plus

Query: 1157 ggatgtgatgggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211

||||||| ||| | | | | ||||||||||||||||||| |||||||||

Sbjct: 290 ggatgtgatggatcactgctccttgatgacacatcaagcttcactggagagaaga 344

Score = 44.1 bits (22), Expect = 4.3

Identities = 43/50 (86%)

Strand = Plus / Plus

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttggactttc 1617

||||| ||||||| ||||||||| || ||||| ||| ||| |||||

Sbjct: 572 acttctaaccttaataactcatctctagtttttagtgctgttggcctttc 621

>gb|EF433455.1| Ipomoea batatas basic peroxidase swpb4 mRNA, complete cds

Length = 1369

Score = 63.9 bits (32), Expect = 5e-06

Identities = 47/52 (90%)

Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784

||||||| || ||||||||||||| | ||||||||||| |||||||||

Sbjct: 180 cgcatgggcgcctctctccttcgcctcttcttccacgactgctttgtcaatg 231

Score = 60.0 bits (30), Expect = 7e-05

Identities = 63/74 (85%)

Strand = Plus / Plus

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
||||||| ||||||||||||||||| || || | || ||||||| |||||
Sbjct: 888 gatttcgcagccgccatgatcaagatgggtgatatcaagcccctcactgggaacaatgga 947

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||
Sbjct: 948 gagatcaggaagaa 961

Score = 44.1 bits (22), Expect = 4.3
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaa 1209
||||||| ||||||| ||||| || ||||| |||||||||||||
Sbjct: 234 tgtgatggatcaattctcttggacgatacatcttccttcaccggagagaa 283

>gb|AC235385.1| Glycine max strain Williams 82 clone GM_WBb0113B18, complete sequence
Length = 137121

Score = 61.9 bits (31), Expect = 2e-05
Identities = 37/39 (94%)
Strand = Plus / Minus

Query: 277 aaattatTTTTCTTTtaatttcttaattaatatacctaa 315
|||| ||||||||||||||| |||||||||||||
Sbjct: 62660 aaataatTTTTCTTTtaattttttaattaatatacctaa 62622

>gb|GQ258782.1| Brassica rapa peroxidase 52 mRNA, partial cds
Length = 1113

Score = 60.0 bits (30), Expect = 7e-05
Identities = 147/186 (79%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| || ||||| ||||| | ||||||||||||||||| || ||||| | |||||
Sbjct: 172 ggatgcgacggttctattctactagatgacacatcaagctttacgggagaacaaaacgcg 231

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| ||| | || ||||||||| || | || | ||||||||| ||||| ||

Sbjct: 232 aacccaaaccgcaattctgctcgtgggtttaatgtgatagacaacattaaaacagcggtt 291

Sbjct: 292 gaagcagcatgtcccggggttggtgtcttgctgatatcttagccatcgcagctagagac 351

Sbjct: 352 tctggtt 357

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Sbjct: 248 aatccaacat 239

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Subject: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcattctacaacg 249

Sbjct: 248 aatccaacat 239

>gb|FJ099767.1| Pinus taeda isolate 1292 anonymous locus 2_6350_01 genomic sequence
Length = 439

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099766.1| Pinus taeda isolate 1285 anonymous locus 2_6350_01 genomic sequence
Length = 434

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099765.1| Pinus taeda isolate 1288 anonymous locus 2_6350_01 genomic sequence
Length = 438

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099762.1| Pinus taeda isolate 1298 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 taggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 307 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 248

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 247 aatccaacat 238

>gb|FJ099761.1| Pinus taeda isolate 1289 anonymous locus 2_6350_01 genomic sequence
Length = 360

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 taggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099760.1| Pinus taeda isolate 1297 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| |||| | ||||||| | |||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099759.1| Pinus taeda isolate 1283 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| |||| | ||||||| | |||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099758.1| Pinus taeda isolate 1287 anonymous locus 2_6350_01 genomic sequence
Length = 449

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| |||| | ||||||| | |||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099757.1| Pinus taeda isolate 1291 anonymous locus 2_6350_01 genomic sequence
Length = 358

Score = 60.0 bits (30), Expect = 7e-05
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 taggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|EF433456.1| Ipomoea batatas basic peroxidase swpb5 mRNA, complete cds
Length = 1331

Score = 60.0 bits (30), Expect = 7e-05
Identities = 36/38 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaagaattg 2165
||||||||||| ||| |||||||||||||||||||
Sbjct: 1038 cctctcactggttcccatggagaaatcaggaagaattg 1075

>gb|AC226196.1| Musa acuminata clone BAC MA4-125A12, complete sequence
Length = 110853

Score = 60.0 bits (30), Expect = 7e-05
Identities = 51/58 (87%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||| ||||||||| ||| |||| | ||||||||| || |||||||||||||||
Sbjct: 32082 cagggtgtgatggatcagttctgctggatgacacgtccagcttcaccggagagaaga 32139

Score = 46.1 bits (23), Expect = 1.1
Identities = 71/87 (81%)
Strand = Plus / Plus

Query: 1960 gacaactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaa 2019
||||||| ||||||||| |||| | || || ||||||||| || || ||||| || |||||

Sbjct: 32773 gacaacttctacttcaggaacttggtgaagaagaaggcctgctgcactcggaccagcag 32832

Query: 2020 ctgttcaacggtgggtccaccgactcc 2046

||||||| || |||||||||||||

Sbjct: 32833 ctgttcagtgaggatccaccgactcc 32859

>ref|XM_001754018.1| Physcomitrella patens subsp. patens predicted protein
(PHYPADRAFT_115024) mRNA, complete cds
Length = 1095

Score = 60.0 bits (30), Expect = 7e-05

Identities = 36/38 (94%)

Strand = Plus / Plus

Query: 741 tgcttctctccttcgcttggttcttccacgattgctttg 778

|||| |||| ||||||||||||||||||||||||||||

Sbjct: 273 tgctgctctgcttcgcttggttcttccacgattgctttg 310

>emb|AM449831.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X191828.16,
clone ENTAV 115
Length = 47040

Score = 60.0 bits (30), Expect = 7e-05

Identities = 33/34 (97%)

Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttc 1827

|||||||||||||||||||||||||||||| ||||

Sbjct: 34025 tcacacaattggacaagcaaggtgcacaagcttc 33992

>gb|AY206414.1| Ipomoea batatas anionic peroxidase swpb3 mRNA, complete cds
Length = 1290

Score = 60.0 bits (30), Expect = 7e-05

Identities = 63/74 (85%)

Strand = Plus / Plus

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggetccaatgga 2148

||||||| |||||||||||||||||||| || || | || ||||||| |||||||

Sbjct: 918 gatttcgcagccgcatgatcaagatgggtgatatcaagccactcactgggaacaatgga 977

Query: 2149 gaaatcaggaagaa 2162
|| |||||
Sbjct: 978 gagatcaggaagaa 991

Score = 56.0 bits (28), Expect = 0.001
Identities = 46/52 (88%)
Strand = Plus / Plus

Query: 733 cgcattgggtctctctcttcgcttgttcttccacgattgctttgtcaatg 784
||||| || ||||| | ||||| || |||||
Sbjct: 210 cgcattgggcctctctcttcgcttcttccatgactgctttgtcaatg 261

>gb|AF485265.1| Gossypium hirsutum class III peroxidase (pod3) mRNA, complete cds
Length = 1336

Score = 60.0 bits (30), Expect = 7e-05
Identities = 42/46 (91%)
Strand = Plus / Plus

Query: 737 tgggtgcttctctcttcgcttgttcttccacgattgctttgtcaa 782
||||| ||||| || || |||||
Sbjct: 257 tgggtgcttctctcttcgcttgttcttccatgactgctttgtcaa 302

Score = 52.0 bits (26), Expect = 0.018
Identities = 53/62 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||| ||||| || || ||||| |||||
Sbjct: 979 atgataaagatgggagatattaagccactcaccgatcaaattggtgaaatcaggaagaat 1038

Query: 2164 tg 2165
||
Sbjct: 1039 tg 1040

>gb|EZ328614.1| TSA: Artemisia annua strain Madagascar Contig15160, mRNA sequence
Length = 324

Score = 58.0 bits (29), Expect = 3e-04

Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||| ||| ||||||| |||||||||||||||
Sbjct: 202 atgggcgcttctctccttcgtttgcaattccatgattgctttgtcaatg 250

>gb|EZ256818.1| TSA: Artemisia annua strain Artemis Contig23488, mRNA sequence
Length = 426

Score = 58.0 bits (29), Expect = 3e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||| ||| ||||||| |||||||||||||||
Sbjct: 204 atgggcgcttctctccttcgtttgcaattccatgattgctttgtcaatg 252

>gb|EZ397212.1| TSA: Artemisia annua strain Uganda Contig13707, mRNA sequence
Length = 491

Score = 58.0 bits (29), Expect = 3e-04
Identities = 44/49 (89%)
Strand = Plus / Minus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||| ||| ||||||| |||||||||||||||
Sbjct: 167 atgggcgcttctctccttcgtttgcaattccatgattgctttgtcaatg 119

>dbj|AK328734.1| Solanum lycopersicum cDNA, clone: LEFL3035G12, HTC in root
Length = 1222

Score = 58.0 bits (29), Expect = 3e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 1215 caaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccg 1274
||||| ||||||||||||||| ||||||||||| || || ||||| | ||||||| ||
Sbjct: 354 caaaccccaacaggaactcggtcgtggatttgatgtcattgatgatattaaatctgcac 413

Query: 1275 tggagaaag 1283

|||||||
Sbjct: 414 tggagaaag 422

>emb|AJ544515.1| Asparagus officinalis partial mRNA for peroxidase (prx2 gene)
Length = 1041

Score = 58.0 bits (29), Expect = 3e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||||
Sbjct: 826 gccatgatcaagatgggagatattagccccctcactgggtctaaaggagagattaggaag 885

Query: 2161 a 2161
|
Sbjct: 886 a 886

>ref|XM_002521820.1| Ricinus communis Lignin-forming anionic peroxidase precursor,
putative, mRNA
Length = 978

Score = 56.0 bits (28), Expect = 0.001
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcgatatccttgc 1320
|||||
Sbjct: 343 aaatctgcagtggagaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>ref|XM_002521805.1| Ricinus communis Lignin-forming anionic peroxidase precursor,
putative, mRNA
Length = 978

Score = 56.0 bits (28), Expect = 0.001
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcgatatccttgc 1320
|||||
Sbjct: 343 aaatctgcagtggagaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>ref|XM_002521804.1| Ricinus communis Peroxidase 30 precursor, putative, mRNA
Length = 891

Score = 56.0 bits (28), Expect = 0.001
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatataccttgc 1320
||||| || |||||||| | ||||| ||||||||||||||||| |||||||||
Sbjct: 343 aaatctgcagtgagagaagatatgtcctggagttgtttcctgcgctgatataccttgc 398

>gb|FJ529216.1| Cucumis sativus 1-aminocyclopropane-1-carboxylate synthase (ACS2) gene,
ACS2-M allele and putative peroxidase gene, complete cds
Length = 52751

Score = 56.0 bits (28), Expect = 0.001
Identities = 34/36 (94%)
Strand = Plus / Minus

Query: 751 cttegcttgttcttccacgattgctttgtcaatgta 786
||||| ||||||||||||||||||| |||||
Sbjct: 50350 cttegcatgttcttccacgattgctttgtaaatgta 50315

>ref|XM_002450088.1| Sorghum bicolor hypothetical protein, mRNA
Length = 1265

Score = 56.0 bits (28), Expect = 0.001
Identities = 58/68 (85%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||| ||||| ||||| ||||| | ||||| ||||||||||||| || |||||||
Sbjct: 686 ggtgctcacaccattgggcaagcacggtgcaccaacttcagagcccacatatatacaacgac 745

Query: 1849 accaacat 1856
||| ||||
Sbjct: 746 accgacat 753

>gb|FJ050772.1| Pinus taeda isolate 4650 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.001
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050764.1| Pinus taeda isolate 4651 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.001
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050758.1| Pinus taeda isolate 4655 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.001
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacacgataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050757.1| Pinus taeda isolate 4653 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.001
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|AF149278.1|AF149278 Phaseolus vulgaris peroxidase 3 precursor (FBP3) mRNA, complete cds
Length = 1850

Score = 56.0 bits (28), Expect = 0.001
Identities = 46/52 (88%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttcacgattgctttgtcaatg 784
||||||| ||||||||| ||||| || || |||||||||
Sbjct: 981 cgcatgggagcttctctccttcgcctcttctttcatgactgctttgtcaatg 1032

>dbj|AK320453.1| Solanum lycopersicum cDNA, clone: LEFL1009CA06, HTC in leaf
Length = 1260

Score = 54.0 bits (27), Expect = 0.004
Identities = 57/67 (85%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||| ||||||||| ||||| || || || || || ||
Sbjct: 649 ggtgctcacacaattggacaagcaagatgcacaacatttagggcacgtatatacaatgag 708

Query: 1849 accaaca 1855
|||||
Sbjct: 709 accaaca 715

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||||| || ||| ||| || ||||| || ||||| ||||| |||||
Sbjct: 967 atgatcaagatgggcgatattcgtccacttactggatcgaatggtgaaattaggaagaa 1025

>dbj|AK320190.1| Solanum lycopersicum cDNA, clone: LEFL1006BD07, HTC in leaf
Length = 1236

Score = 54.0 bits (27), Expect = 0.004
Identities = 48/55 (87%)
Strand = Plus / Plus

Query: 1215 caaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatc 1269
||||||| || ||||| ||||| || ||||| ||||| |||||
Sbjct: 354 caaaccccaacaggaattcagctcgtggattcgaagtccttgacgagattaaatc 408

>gb|AC235342.1| Glycine max strain Williams 82 clone GM_WBb0088H14, complete sequence
Length = 183165

Score = 54.0 bits (27), Expect = 0.004
Identities = 33/35 (94%)
Strand = Plus / Plus

Query: 281 tattttttcttttaatttcttaattaatcctaa 315
||||||| ||||| |||||
Sbjct: 50421 tattttttcttttaatttctcaattaatgtcctaa 50455

>emb|CT832689.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCRN133B17, full
insert sequence
Length = 1270

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaaggaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853

||||| ||||| ||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 717 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 776

Query: 1854 cat 1856

|||
Sbjct: 777 cat 779

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| | ||||||||| || ||||||||| || ||||| || ||
Sbjct: 826 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 885

Query: 1963 aactactacttcaagaacctcggtcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| || ||||||| ||||| || |||||||||
Sbjct: 886 aacaactactacaagaacctcgctcgtaagaagggtcctgcattctgatcag 939

>emb|CT832688.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA237B02, full
insert sequence
Length = 2326

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 1773 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 1832

Query: 1854 cat 1856

|||
Sbjct: 1833 cat 1835

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 1882 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 1941

Query: 1963 aactactacttcaagaacctcggtcagaagaagggctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1942 aacaactactacaagaacctcgctcgtaagaagggctcctgcattctgatcag 1995

>emb|CT832687.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA219E15, full
insert sequence
Length = 1331

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| || ||||| ||||| ||||| || ||||| |||||
Sbjct: 783 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 842

Query: 1854 cat 1856
|||
Sbjct: 843 cat 845

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 892 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 951

Query: 1963 aactactacttcaagaacctcggtcagaagaagggctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 952 aacaactactacaagaacctcgctcgtaagaagggctcctgcattctgatcag 1005

>ref|NM_001072503.1| Oryza sativa (japonica cultivar-group) Os12g0112000 (Os12g0112000)
mRNA, complete cds
Length = 1318

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 719 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 778

Query: 1854 cat 1856
|||
Sbjct: 779 cat 781

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||||||| || ||||||||| || ||||| || ||
Sbjct: 828 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 887

Query: 1963 aactactacttcaagaacctcgcttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| || ||||||| ||||| || |||||||
Sbjct: 888 aacaactactacaagaacctcgctcgtaagaagggtctcctgcattctgatcag 941

>tpe|BN000664.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx135 gene for
class III peroxidase 135 precursor, exons 1-4
Length = 2198

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 1811 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 1870

Query: 1854 cat 1856
|||
Sbjct: 1871 cat 1873

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 1920 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 1979

Query: 1963 aactactacttcaagaacctcgcttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| || ||||| |||||
Sbjct: 1980 aacaactactacaagaacctcgctcgtaagaagggtctcctgcattctgatcag 2033

>dbj|AK069456.1| Oryza sativa Japonica Group cDNA clone:J023019E08, full insert
sequence
Length = 1319

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||| ||||| || || ||||| |||||
Sbjct: 720 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 779

Query: 1854 cat 1856
|||
Sbjct: 780 cat 782

Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 829 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 888

Query: 1963 aactactacttcaagaacctcgcttcagaagaagggtctcctccactctgatcag 2016

Sbjct: 889 aacaactactacaagaacctcgctcgtaagaaggggctctgcattctgatcag 942

```
>emb|X91172.1| R. sativus prxK1 gene
      Length = 3190
```

Score = 54.0 bits (27), Expect = 0.004
Identities = 39/43 (90%)
Strand = Plus / Plus

```
Query: 2023 ttcaacggtgggtccaccgactccattgtgcgtggctacagca 2065
          ||| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 2635 ttcaacggtggetccaccgactccatagtccgtggttacagca 2677
```

Score = 46.1 bits (23), Expect = 1.1
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctcttcgcttggtcttccacgattgctttgtcaa 782
 ||||| || ||||| | |||||
 Sbjct: 1344 atgggtgcattctatccttcgcttttcttccacgattgcttcgtcaa 1390

>emb|BX000510.1| Oryza sativa chromosome 12, . BAC OJ1769_D07 of library Monsanto from
chromosome 12 of cultivar Nipponbare of ssp. japonica of
Oryza sativa (rice), complete sequence
Length = 115859

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
 ||||| ||||| ||||| | ||||||||| ||| | ||||| |||||
 Sbjct: 24329 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 24270

```
Query: 1854  cat 1856
      |||
Sbjct: 24269 cat 24267
```

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Score = 52.0 bits (26), Expect = 0.018
Identities = 92/114 (80%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || |||||||| || |||||||| || ||||| || ||
Sbjct: 24220 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 24161

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| || ||||||| ||||| || |||||||||
Sbjct: 24160 aacaactactacaagaacctcgtcgtcaagaagggtcctgcattctgatcag 24107

>gb|EZ315890.1| TSA: Artemisia annua strain Madagascar Contig2436, mRNA sequence
Length = 309

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Minus

Query: 2089 gatttcgccgccgccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || ||||||||||||||||| || ||||||||| || |||||
Sbjct: 265 gatttcgccgctgccatgatcaagatgggtgatattagtcacttactgg 216

>gb|EZ359220.1| TSA: Artemisia annua strain Uganda Contig6381, mRNA sequence
Length = 492

Score = 52.0 bits (26), Expect = 0.018
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 1907 ggtcaggggacaacaatctggcaccacttgatcttcaaactccaac 1952
||||||| ||||||||| ||||||| || ||||| |||||||||
Sbjct: 11 ggtcaggagacaacaatttggcaccgctagatctcaaactccaac 56

>gb|EZ166433.1| TSA: Artemisia annua strain Artemis Contig25839, mRNA sequence
Length = 448

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcgcccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || ||||||||||||||||| || ||||||| || |||||
Sbjct: 164 gatttcgcggctgccatgatcaagatgggtgatattagtcacttactgg 213

>gb|BT106781.1| Picea glauca clone GQ03010_F17 mRNA sequence
Length = 722

Score = 52.0 bits (26), Expect = 0.018
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 1957 tttgacaactactacttcaagaacct 1982
|||||||||||||||||||||||
Sbjct: 192 tttgacaactactacttcaagaacct 217

>ref|XM_002285606.1| PREDICTED: Vitis vinifera hypothetical protein LOC100253646
(LOC100253646), mRNA
Length = 1032

Score = 52.0 bits (26), Expect = 0.018
Identities = 50/58 (86%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatataccttgccatcgctgccagagactctgttc 1343
||||||||||||||||||| || || || ||||| || || ||||||| |||||
Sbjct: 382 tgtccaggagttgtttcctgcgctgacatactagccatagccgcccgagactccgttc 439

>gb|AC235417.1| Glycine max strain Williams 82 clone GM_WBb0135A07, complete sequence
Length = 184957

Score = 52.0 bits (26), Expect = 0.018
Identities = 35/38 (92%)
Strand = Plus / Plus

Query: 279 attatTTTTtctTTtaatttcttaattaatatcctaag 316
||||||||| ||||||||| ||||||||| |||||
Sbjct: 56366 attatTTTTtatttTaatttatttaattaatattctaag 56403

>ref|XM_002334206.1| Populus trichocarpa predicted protein, mRNA
Length = 954

Score = 52.0 bits (26), Expect = 0.018

Identities = 35/38 (92%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||| ||||| |||||
Sbjct: 874 gccatgatcaaaatgggagacatcagtcactcactgg 911

>ref|NM_001157951.1| Zea mays peroxidase 2 (LOC100285056), mRNA
>gi|195646697|gb|EU970699.1| Zea mays clone 349100
peroxidase 2 precursor, mRNA, complete cds
Length = 1360

Score = 52.0 bits (26), Expect = 0.018
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 2092 ttgccgccgccatgatcaagatggg 2117
||||||| ||||| ||||| |||||
Sbjct: 956 ttgccgccgccatgatcaagatggg 981

>gb|BT044614.1| Arabidopsis thaliana unknown protein (At4g33420) mRNA, complete cds
Length = 978

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
||||||| || ||||| ||||| ||||| |||||
Sbjct: 373 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 422

>gb|FJ099764.1| Pinus taeda isolate 1294 anonymous locus 2_6350_01 genomic sequence
Length = 414

Score = 52.0 bits (26), Expect = 0.018
Identities = 59/70 (84%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||| ||||| ||||| | ||||| ||||| |||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagtcgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099763.1| Pinus taeda isolate 1290 anonymous locus 2_6350_01 genomic sequence
Length = 448

Score = 52.0 bits (26), Expect = 0.018
Identities = 59/70 (84%)
Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | ||||||||| |||||
Sbjct: 307 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatTTacaacg 248

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 247 aatccaacat 238

>gb|BT042071.1| Zea mays full-length cDNA clone ZM_BFb0125B03 mRNA, complete cds
Length = 1342

Score = 52.0 bits (26), Expect = 0.018
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 2092 ttcgccgccgcatgatcaagatggg 2117
|||||||||||||||||||
Sbjct: 1003 ttcgccgccgcatgatcaagatggg 1028

>emb|AM450885.2| Vitis vinifera contig VV78X220288.8, whole genome shotgun sequence
Length = 12944

Score = 52.0 bits (26), Expect = 0.018
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 1797 cacaattggacaagcaaggtgcacaa 1822
|||||||||||||||||||
Sbjct: 1055 cacaattggacaagcaaggtgcacaa 1080

>ref|NM_119496.3| Arabidopsis thaliana peroxidase, putative (AT4G33420) mRNA, complete
cds
Length = 1197

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 401 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 450

>emb|AM446475.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X020658.13,
clone ENTAV 115
Length = 18355

Score = 52.0 bits (26), Expect = 0.018
Identities = 50/58 (86%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactctgttc 1343
|||||
Sbjct: 15894 tgtccaggagttgtttcctgcgcgtgacatactagccatagccgcccagactccgttc 15951

>emb|AM436560.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X083975.17,
clone ENTAV 115
Length = 6769

Score = 52.0 bits (26), Expect = 0.018
Identities = 50/58 (86%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 5849 cagggatgtgatgcttctatattattggacgacactgcaagctttaccggagagaaga 5792

Score = 44.1 bits (22), Expect = 4.3
Identities = 49/58 (84%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| || ||||| ||| ||| |||||
Sbjct: 1513 cagggatgtgatgcttctatattattggatgacactgcaaactttactggagagaaga 1456

>emb|AM429435.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X154826.4,
clone ENTAV 115
Length = 7609

Score = 52.0 bits (26), Expect = 0.018
Identities = 50/58 (86%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| || ||||| ||| ||||| |||||
Sbjct: 2278 cagggatgtgatgcttctatattattggacgacactgcaaactttaccggagagaaga 2221

>ref|NM_101322.1| Arabidopsis thaliana anionic peroxidase, putative (AT1G14550) mRNA,
complete cds
Length = 966

Score = 52.0 bits (26), Expect = 0.018
Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
||||||| ||||| ||||| |||||
Sbjct: 913 cctctcactggctctaattggagaaatcagaaaga 946

>gb|AF453791.1| Ipomoea batatas anionic peroxidase (POD) gene, promoter region and
partial cds
Length = 3741

Score = 52.0 bits (26), Expect = 0.018
Identities = 47/54 (87%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgta 786
||||||| ||||| ||| ||||| | ||||| |||||
Sbjct: 2101 cgcattggggcttcctcattcgtctcttcttccacgattgctttgtcgatgta 2154

>dbj|AB193816.1| Pisum sativum mRNA for peroxidase, complete cds, clone:PsPOX11
Length = 1217

Score = 52.0 bits (26), Expect = 0.018
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 739 ggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
 ||||||| | ||||||||||||||| | ||||||| |||
Sbjct: 197 ggtgcttctatacttcgcttggttcttccatgactgctttgttaatg 242

Score = 44.1 bits (22), Expect = 4.3
Identities = 61/74 (82%)
Strand = Plus / Plus

Query: 1477 gcttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagcca 1536
 ||||||| || ||||||| ||| ||||||||||||||| || ||||| || |||||
Sbjct: 433 gcttggaggaccacatggatggttccacttggaagaagagatgcaagaacagcaagcca 492

Query: 1537 atctgctgctaaca 1550
 | ||||| |||||
Sbjct: 493 aagtctgccaaca 506

>dbj|AK176812.1| Arabidopsis thaliana mRNA for peroxidase ATP17a like protein, partial
 cds, clone: RAFL25-36-D17
 Length = 1203

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttctgcgcagatataccttgccatcgctgccagaga 1335
 ||||||||||||| || ||||||||||| ||||||| ||||| |||||
Sbjct: 397 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 446

>gb|AY089094.1| Arabidopsis thaliana clone 32346 mRNA, complete sequence
 Length = 1179

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 395 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 444

>gb|AC108072.3| Homo sapiens BAC clone RP11-704A16 from 2, complete sequence
Length = 36787

Score = 52.0 bits (26), Expect = 0.018
Identities = 29/30 (96%)
Strand = Plus / Minus

Query: 1045 atatatttaaagataataaatatttctgct 1074
|||||
Sbjct: 31744 atatatttaaagttaataaatatttctgct 31715

>gb|AF451951.1| Arabidopsis thaliana class III peroxidase ATP32 mRNA, complete cds
Length = 1082

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 373 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 422

>emb|AL161583.2| Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
Length = 199536

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 113403 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 113452

>gb|AC010657.3|AC010657 Genomic sequence for Arabidopsis thaliana BAC T5E21 from chromosome I,
complete sequence
Length = 83351

Score = 52.0 bits (26), Expect = 0.018

Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 17743 cctctcactggctcctaattggagaaatcagaaaga 17776

>emb|AL035678.1| Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)
Length = 96475

Score = 52.0 bits (26), Expect = 0.018
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 48624 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 48673

>gb|AC012188.2|F14L17 Sequence of BAC F14L17 from Arabidopsis thaliana chromosome 1, complete
sequence
Length = 111686

Score = 52.0 bits (26), Expect = 0.018
Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 111350 cctctcactggctcctaattggagaaatcagaaaga 111383

>gb|EZ395724.1| TSA: Artemisia annua strain Uganda Contig12219, mRNA sequence
Length = 273

Score = 50.1 bits (25), Expect = 0.069
Identities = 55/65 (84%)
Strand = Plus / Minus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 221 gccatgatcaagatgggtgatattagtcacttactggacgtaatggtgagatcaggaag 162

Query: 2161 aattg 2165
 |||||
Sbjct: 161 aattg 157

>gb|EZ362599.1| TSA: Artemisia annua strain Uganda Contig9760, mRNA sequence
Length = 346

Score = 50.1 bits (25), Expect = 0.069
Identities = 55/65 (84%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
 ||||||| ||||||||||||| ||||| ||||| | ||| | || ||||| |||||
Sbjct: 216 cttggaggacctacatggaatgtgaaactgggaagacgtgactcaaggactgcgagccaa 275

Query: 1538 tctgc 1542
 |||||
Sbjct: 276 gctgc 280

>gb|BT066765.1| Zea mays full-length cDNA clone ZM_BFb0066D03 mRNA, complete cds
Length = 1217

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
 ||||| ||||||||||||| ||||||||||| ||| |||||
Sbjct: 665 tgcaccaacttcagagcccacatctacaacgacaccgacat 705

>gb|BT055307.1| Zea mays full-length cDNA clone ZM_BFc0167H14 mRNA, complete cds
Length = 1194

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
 ||||| ||||||||||||| ||||||||||| ||| |||||
Sbjct: 640 tgcaccaacttcagagcccacatctacaacgacaccgacat 680

>gb|EU962146.1| Zea mays clone 240603 mRNA sequence
Length = 1299

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
||||| ||||||||||||| ||||||||||| ||| |||||
Sbjct: 737 tgcaccaacttcagagcccacatctacaacgacaccgacat 777

>gb|FJ070719.1| Pinus taeda isolate 7938 anonymous locus 0_3458_02 genomic sequence
Length = 364

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||
Sbjct: 269 ccatgataaagatgggaaacattagccctctcactgg 233

>gb|FJ070718.1| Pinus taeda isolate 7947 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070717.1| Pinus taeda isolate 7943 anonymous locus 0_3458_02 genomic sequence
Length = 359

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||||| ||||||||| |||||||||||

Sbjct: 263 ccatgataaagatgggaaacattagccctctcactgg 227

>gb|FJ070716.1| Pinus taeda isolate 7950 anonymous locus 0_3458_02 genomic sequence
Length = 350

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070715.1| Pinus taeda isolate 7940 anonymous locus 0_3458_02 genomic sequence
Length = 366

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 270 ccatgataaagatgggaaacattagccctctcactgg 234

>gb|FJ070714.1| Pinus taeda isolate 7948 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070713.1| Pinus taeda isolate 7949 anonymous locus 0_3458_02 genomic sequence
Length = 438

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 293 ccatgataaagatgggaaacattagccctctcactgg 257

>gb|FJ070712.1| Pinus taeda isolate 7952 anonymous locus 0_3458_02 genomic sequence
Length = 349

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 253 ccatgataaagatgggaaacattagccctctcactgg 217

>gb|FJ070711.1| Pinus taeda isolate 7941 anonymous locus 0_3458_02 genomic sequence
Length = 350

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070710.1| Pinus taeda isolate 7951 anonymous locus 0_3458_02 genomic sequence
Length = 360

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 264 ccatgataaagatgggaaacattagccctctcactgg 228

>gb|FJ070709.1| Pinus taeda isolate 7942 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.069

Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070708.1| Pinus taeda isolate 7953 anonymous locus 0_3458_02 genomic sequence
Length = 349

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070707.1| Pinus taeda isolate 7937 anonymous locus 0_3458_02 genomic sequence
Length = 420

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 275 ccatgataaagatgggaaacattagccctctcactgg 239

>gb|FJ070706.1| Pinus taeda isolate 7946 anonymous locus 0_3458_02 genomic sequence
Length = 297

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 191 ccatgataaagatgggaaacattagccctctcactgg 155

>gb|FJ070705.1| Pinus taeda isolate 7945 anonymous locus 0_3458_02 genomic sequence

Length = 350

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 255 ccatgataaagatgggaaacattagccctctcactgg 219

>gb|FJ070703.1| Pinus taeda isolate 7939 anonymous locus 0_3458_02 genomic sequence
Length = 355

Score = 50.1 bits (25), Expect = 0.069
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 259 ccatgataaagatgggaaacattagccctctcactgg 223

>ref|NM_001137528.1| Zea mays hypothetical protein LOC100192105 (LOC100192105), mRNA
>gi|194690673|gb|BT034416.1| Zea mays full-length cDNA
clone ZM_BFc0170D07 mRNA, complete cds
Length = 1217

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
||||| ||||||||| ||||||||| ||| |||||
Sbjct: 665 tgcaccaacttcagagcccacatctacaacgacaccgacat 705

>gb|DQ244260.1| Zea mays clone 3973 mRNA sequence
Length = 1224

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856

||||| ||||||||||||| ||||||||||| ||| |||||
Sbjct: 672 tgcaccaacttcagagcccacatctacaacgacaccgacat 712

>tpc|BN000615.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx86 gene for
class III peroxidase 86 precursor, exons 1-3
Length = 1188

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
||||||| | ||||||||| ||||||||| |||||||||||||
Sbjct: 197 tccttcgcctcttcttccatgattgcttcgtcaatgtaatt 237

>dbj|AP004731.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC
clone:OSJNBa0016D02
Length = 157822

Score = 50.1 bits (25), Expect = 0.069
Identities = 37/41 (90%)
Strand = Plus / Minus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
||||||| | ||||||||| ||||||||| |||||||||||||
Sbjct: 82216 tccttcgcctcttcttccatgattgcttcgtcaatgtaatt 82176

>dbj|AB007645.1| Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K8K14
Length = 72698

Score = 50.1 bits (25), Expect = 0.069
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 760 ttcttccacgattgctttgtcaatgtaatt 788
||||||||||||||||| |||||||||||||
Sbjct: 46952 ttcttccacgattgcttcgtcaatgtaatt 46980

>emb|Y10465.1| S.oleracea mRNA for peroxidase, clone PC44
Length = 1176

Score = 50.1 bits (25), Expect = 0.069

Identities = 43/49 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 ||||| | ||||| ||||| |
Sbjct: 209 atgggtgcttccatacttcgttgttcttccacgactgctttgtaaatg 257

Score = 46.1 bits (23), Expect = 1.1
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 1481 ggaggccctacatggaatgttaaacttgaagaagagacgctagaac 1527
 ||||| ||||| || || |
Sbjct: 455 ggaggccccacatggaatgtaaaactaggtagaagagatgcaagaac 501

>gb|CP000102.1| Methanospaera stadtmanae DSM 3091, complete genome
 Length = 1767403

Score = 50.1 bits (25), Expect = 0.069
Identities = 25/25 (100%)
Strand = Plus / Plus

Query: 285 ttttcttttaatttcttaattaata 309
 ||||| ||||| |
Sbjct: 31679 ttttcttttaatttcttaattaata 31703

>emb|FP012230.5| Pig DNA sequence from clone CH242-162F1 on chromosome X, complete
 sequence
 Length = 116800

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 268 atttctataaaattatTTTTTcttttaa 295
 ||||| ||||| |
Sbjct: 24562 atttctataaaattatTTTTTcttttaa 24589

>gb|EZ275595.1| TSA: Artemisia annua strain Madagascar Contig1982, mRNA sequence
 Length = 688

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 69 cacacaattggacaagcaagatgcacaa 96

>gb|EZ286664.1| TSA: Artemisia annua strain Madagascar Contig13051, mRNA sequence
 Length = 813

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaaga 1513
 |||||
Sbjct: 789 cttggaggacctacatggaatgtgaaactgggaaga 754

Score = 46.1 bits (23), Expect = 1.1
Identities = 38/43 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
 |||||
Sbjct: 501 tcaggggacaacaatttggcaccactagactccaaactccaa 459

>gb|EZ342046.1| TSA: Artemisia annua strain Uganda Contig9262, mRNA sequence
 Length = 588

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 493 cacacaattggacaagcaagatgcacaa 466

>gb|EZ321242.1| TSA: Artemisia annua strain Madagascar Contig7788, mRNA sequence

Length = 1218

Score = 48.1 bits (24), Expect = 0.27

Identities = 27/28 (96%)

Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822

|||||

Sbjct: 599 cacacaattggacaagcaagatgcacaa 626

>gb|EZ318330.1| TSA: Artemisia annua strain Madagascar Contig4876, mRNA sequence

Length = 457

Score = 48.1 bits (24), Expect = 0.27

Identities = 33/36 (91%)

Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaaga 1513

|||||

Sbjct: 236 cttggaggacctacatggaatgtgaaactgggaaga 201

>gb|EZ247069.1| TSA: Artemisia annua strain Artemis Contig13739, mRNA sequence

Length = 438

Score = 48.1 bits (24), Expect = 0.27

Identities = 27/28 (96%)

Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822

|||||

Sbjct: 104 cacacaattggacaagcaagatgcacaa 131

>gb|EZ258457.1| TSA: Artemisia annua strain Madagascar Contig1560, mRNA sequence

Length = 246

Score = 48.1 bits (24), Expect = 0.27

Identities = 27/28 (96%)

Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822

|||||

Sbjct: 68 cacacaattggacaagcaagatgcacaa 95

>gb|EZ396283.1| TSA: Artemisia annua strain Uganda Contig12778, mRNA sequence
Length = 352

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||||
Sbjct: 119 cacacaattggacaagcaagatgcacaa 146

>gb|EZ220993.1| TSA: Artemisia annua Contig18004
Length = 707

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||||
Sbjct: 649 cacacaattggacaagcaagatgcacaa 622

>gb|EZ366681.1| TSA: Artemisia annua strain Uganda Contig132, mRNA sequence
Length = 790

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||||
Sbjct: 723 cacacaattggacaagcaagatgcacaa 696

>gb|EZ196247.1| TSA: Artemisia annua strain Artemis Contig9804, mRNA sequence
Length = 252

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaaga 1513
||||||| ||||||||||||| ||||| |||||
Sbjct: 223 cttggaggacctacatggaatgtgaaactgggaaga 188

>gb|EZ355157.1| TSA: Artemisia annua strain Uganda Contig2318, mRNA sequence
Length = 246

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
||||||||||||||||| |||||
Sbjct: 67 cacacaattggacaagcaagatgcacaa 94

>gb|EZ173232.1| TSA: Artemisia annua strain Artemis Contig32638, mRNA sequence
Length = 709

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
||||||||||||||||| |||||
Sbjct: 622 cacacaattggacaagcaagatgcacaa 595

>gb|BT102799.1| Picea glauca clone GQ02016_E21 mRNA sequence
Length = 953

Score = 48.1 bits (24), Expect = 0.27
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 2110 aagatgggagacattagtcctctcactggctccaatggagaaatcagg 2157
||||||| ||| ||||||| || ||||||| |||||||||
Sbjct: 768 aagatggggaacatcagtcctcttacaggctccaaggagaaatcagg 815

>gb|BT101612.1| Picea glauca clone GQ01308_P23 mRNA sequence
Length = 919

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)

Strand = Plus / Plus

Query: 1957 tttgacaactactacttcaagaac 1980

|||||

Sbjct: 605 tttgacaactactacttcaagaac 628

>gb|AC212861.3| Pongo abelii BAC clone CH276-236D6 from chromosome 1, complete sequence
Length = 192235

Score = 48.1 bits (24), Expect = 0.27

Identities = 24/24 (100%)

Strand = Plus / Plus

Query: 268 atttctataaaattatTTTTTctt 291

|||||

Sbjct: 126165 atttctataaaattatTTTTTctt 126188

>ref|XM_002451803.1| Sorghum bicolor hypothetical protein, mRNA
Length = 837

Score = 48.1 bits (24), Expect = 0.27

Identities = 53/60 (88%), Gaps = 2/60 (3%)

Strand = Plus / Plus

Query: 2059 tacagcaccaacccgggcac-cttctcctctgatttcgccgccgcatgatcaagatggg 2117

||||| ||||| ||| |||| ||| || ||||| ||||| |||||

Sbjct: 709 tacagctccaacccgg-cactcttcgcctcagacttcgccgccgcatgataaagatggg 767

>gb|AC235800.1| Solanum lycopersicum chromosome 3 clone C03HBa0137K15, complete
sequence
Length = 110892

Score = 48.1 bits (24), Expect = 0.27

Identities = 45/52 (86%)

Strand = Plus / Minus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787

||||| || ||||| ||||| | ||||| ||||| |||||

Sbjct: 31655 atgggagcgtctctcattcgcttcttcttccacgactgctttgtcgatgtaa 31604

>ref|XM_002285687.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257440

(LOC100257440), mRNA
Length = 1215

Score = 48.1 bits (24), Expect = 0.27
Identities = 48/56 (85%)
Strand = Plus / Plus

Query: 1156 gggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| || ||||| |||| | ||||| ||||| |||||
Sbjct: 307 gggatgtgatgcttctatattattggacgacactgcaagctttaccggagagaaga 362

>ref|XM_002269022.1| PREDICTED: Vitis vinifera hypothetical protein LOC100263220
(LOC100263220), mRNA
Length = 960

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcggttcagaagaagggtct 2000
||||||| ||| ||||| ||||| |||||
Sbjct: 748 tacttcaagaatctcattcagaagaagggtct 779

>dbj|AK323976.1| Solanum lycopersicum cDNA, clone: LEFL1068DD08, HTC in leaf
Length = 1123

Score = 48.1 bits (24), Expect = 0.27
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 2087 ctgattttcgccgccgcatgatcaagatgggagacattagtcctctcactgg 2138
|||||| | | ||||| || ||||| ||||| ||||| |||||
Sbjct: 924 ctgattttgctgcagccatgattaaatgggagatattagtcctctaactgg 975

>ref|XM_002320381.1| Populus trichocarpa predicted protein, mRNA
Length = 951

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatg 784

|||| |||||||||||||||| |||||||| ||||
Sbjct: 176 tctccgcttggttcttccacgactgctttgtgaatg 211

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1298 gtttcctgcgagatataccttgc 1320
||||||||||||||||||
Sbjct: 352 gtttcctgcgagatataccttgc 374

>gb|CP001098.1| Halothermothrix orenii H 168, complete genome
Length = 2578146

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 188 aaactaattaagaaattaataaaaaat 215
||||||||||| |||||||||
Sbjct: 1223172 aaactaattaagagattaataaaaaat 1223199

>gb|EF677600.1| Picea sitchensis clone WS02771_I11 unknown mRNA
Length = 1895

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1999 ctctccactctgatcagcaactgttcaacgg 2030
|||||||||||||||||| ||| |||||
Sbjct: 1536 ctctccactctgatcaggaactattcaacgg 1567

>gb|FJ050773.1| Pinus taeda isolate 4643 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 503 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 444

>gb|FJ050771.1| Pinus taeda isolate 4657 anonymous locus 0_13032_02 genomic sequence
Length = 597

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 460 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 401

>gb|FJ050770.1| Pinus taeda isolate 4649 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|FJ050769.1| Pinus taeda isolate 4648 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|FJ050768.1| Pinus taeda isolate 4659 anonymous locus 0_13032_02 genomic sequence
Length = 584

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)

Strand = Plus / Minus

```
Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
          ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 485 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 426
```

>gb|FJ050767.1| Pinus taeda isolate 4658 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

```
Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
          ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443
```

>gb|FJ050766.1| Pinus taeda isolate 4644 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

```
Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
          ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 503 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 444
```

>gb|FJ050765.1| Pinus taeda isolate 4645 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

```
Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
          ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443
```

>gb|FJ050763.1| Pinus taeda isolate 4660 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|FJ050762.1| Pinus taeda isolate 4647 anonymous locus 0_13032_02 genomic sequence
Length = 623

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 486 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 427

>gb|FJ050761.1| Pinus taeda isolate 4654 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|FJ050760.1| Pinus taeda isolate 4646 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|FJ050759.1| Pinus taeda isolate 4656 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 503 attaggtgcgcacaccatagccaagcgcggtgcacaagcttcagggcccgcatctacaa 444

>gb|FJ050756.1| Pinus taeda isolate 4652 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.27
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccatagccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|EF083074.1| Picea sitchensis clone WS02728_C07 unknown mRNA
Length = 690

Score = 48.1 bits (24), Expect = 0.27
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 2110 aagatgggagacattagtcctctcactggctccaatggagaaatcagg 2157
||||||| |||| |||||||| || |||||||| |||||||||
Sbjct: 269 aagatggggaacatcagtcctcttacaggctccaaggagaaatcagg 316

>gb|EU024896.1| Uncultured bacterium clone tgutfos2_Contig107 genomic sequence
Length = 33609

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 276 aaaattatTTTTCTTTAATTCTTAATTAATATC 311

|||||
Sbjct: 2185 aaaattattttttttataattacttaattaatatc 2220

>emb|BX548174.1| Prochlorococcus marinus MED4 complete genome
Length = 1657990

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 279 attattttttcttttaatttctta 302
|||||
Sbjct: 602985 attattttttcttttaatttctta 602962

>gb|CP000647.1| Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence
Length = 5315120

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 881 gaaacaacacttggttccttttatt 904
|||||
Sbjct: 3390746 gaaacaacacttggttccttttatt 3390723

>emb|AM454579.2| Vitis vinifera contig VV78X062755.15, whole genome shotgun sequence
Length = 6610

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Minus

Query: 192 taattaagaaattaaataaaaaatatttatca 223
|||||
Sbjct: 2152 taattaagaaattaaataaaaaatatttatca 2121

>emb|AM428729.2| Vitis vinifera contig VV78X273545.5, whole genome shotgun sequence
Length = 39883

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 284 tttttcttttaatttcttaattaa 307
|||||||
Sbjct: 39856 tttttcttttaatttcttaattaa 39879

>emb|AM462968.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X116164.8,
clone ENTAV 115
Length = 13500

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcggttcagaagaagggtct 2000
||||||| ||| |||||
Sbjct: 6764 tacttcaagaatctcattcagaagaagggtct 6795

>emb|AM453059.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X216487.15,
clone ENTAV 115
Length = 18125

Score = 48.1 bits (24), Expect = 0.27
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcggttcagaagaagggtct 2000
||||||| ||| |||||
Sbjct: 4424 tacttcaagaatctcattcagaagaagggtct 4455

>emb|AM481723.1| Vitis vinifera contig VV78X090480.3, whole genome shotgun sequence
Length = 13986

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1747 ttttggtgaggaatattgcatggt 1770
|||||||
Sbjct: 3837 ttttggtgaggaatattgcatggt 3860

>dbj|AP006865.1| Lotus japonicus genomic DNA, chromosome 2, clone: LjT37H21, TM1032,

complete sequence
Length = 95067

Score = 48.1 bits (24), Expect = 0.27
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattctattggatgacaca 1189
|||||||
Sbjct: 32185 cagggatgtgatgcatcaatactattggatgacaca 32220

>dbj|AB049589.1| Avicennia marina PER mRNA for secretory peroxidase, complete cds
Length = 1345

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1292 ggagttgtttcctgcgagatattccttg 1319
|||||||
Sbjct: 412 ggagttgtttcctgcgagatattccttg 439

>emb|BX828399.1| Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH84ZE10 of Hormone Treated Callus of strain col-0
of Arabidopsis thaliana (thale cress)
Length = 1002

Score = 48.1 bits (24), Expect = 0.27
Identities = 39/44 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatattccttgccatcgctgc 1329
|||||||
Sbjct: 380 tgtccaggagttgtatcatgcgagatattgcatggctgc 423

>emb|BX832751.1| Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH95ZG01 of Hormone Treated Callus of strain col-0
of Arabidopsis thaliana (thale cress)
Length = 1192

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1956 ctttgacaactactacttcaagaacctc 1983
|||||
Sbjct: 820 ctttcacaactactacttcaagaacctc 847

>dbj|AB010692.1| Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18I23
Length = 72691

Score = 48.1 bits (24), Expect = 0.27
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 760 ttcttccacgattgctttgtcaatgtaa 787
|||||
Sbjct: 31924 ttcttccacgattgctttgtcaacgtaa 31897

>emb|Y10467.1| S.oleracea mRNA for peroxidase, clone PC23
Length = 1091

Score = 48.1 bits (24), Expect = 0.27
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 127 cgcatgggcgcttcaatacttcgcttgttcttcatgactgctttgtcaatg 178

>ref|XM_670091.1| Plasmodium berghei strain ANKA hypothetical protein (PB301568.00.0)
partial mRNA
Length = 2721

Score = 48.1 bits (24), Expect = 0.27
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 275 taaaattatttttcttttaattt 298
|||||
Sbjct: 2667 taaaattatttttcttttaattt 2644

>gb|AF109124.1|AF109124 Ipomoea batatas anionic peroxidase swpa2 (swpa2) mRNA, complete cds
Length = 1291

Score = 48.1 bits (24), Expect = 0.27
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtc 780
 ||||||| ||||| ||| |||| | |||||||||||||||||
Sbjct: 322 cgcatggggcttcctcattcgtctcttcttccacgattgctttgtc 369

>gb|EZ295716.1| TSA: Artemisia annua strain Madagascar Contig1601, mRNA sequence
Length = 540

Score = 46.1 bits (23), Expect = 1.1
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1796 acacaattggacaagcaaggtgcacaa 1822
 ||||||||||||||||| |||||
Sbjct: 72 acacaattggacaagcaagatgcacaa 98

>gb|EZ256521.1| TSA: Artemisia annua strain Artemis Contig23191, mRNA sequence
Length = 253

Score = 46.1 bits (23), Expect = 1.1
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactgg 2138
 ||||||| || ||||||||||||||| || ||||||| || |||||
Sbjct: 165 gatttcgggctgccatgatcaagatggntgatattagtcgcttactgg 214

>gb|EZ360402.1| TSA: Artemisia annua strain Uganda Contig7563, mRNA sequence
Length = 276

Score = 46.1 bits (23), Expect = 1.1
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
 ||||||||||||||| ||||||||| || | |||||||||
Sbjct: 208 tcaggggacaacaatttggcaccactagacgtccaaactccaa 250

>gb|EZ150610.1| TSA: Artemisia annua strain Artemis Contig10016, mRNA sequence
Length = 265

Score = 46.1 bits (23), Expect = 1.1
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
|||||||
Sbjct: 176 tcaggggacaacaatttggcaccactagacgtccaaactccaa 218

>gb|AC239433.3| Solanum lycopersicum strain Heinz 1706 chromosome 1 clone hba-208m24
map 1, complete sequence
Length = 154446

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 274 ataaaattatTTTTCTTTaat 296
|||||||
Sbjct: 83633 ataaaattatTTTTCTTTaat 83655

>ref|NW_003037936.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000150
Length = 760080

Score = 46.1 bits (23), Expect = 1.1
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 172 aatcagtatctttgaaaactaattaagaaattaa 206
|||||||
Sbjct: 116245 aatcagtatctttgaaaattaattatgaaattaa 116279

>gb|BT095984.1| Soybean clone JCVI-FLGm-20M19 unknown mRNA
Length = 1268

Score = 46.1 bits (23), Expect = 1.1
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1810 gcaaggtgcacaaacttcagagcccgcatctacaacgagacca 1852
||||||| | ||||| | ||||| |||||
Sbjct: 643 gcaaggtgcactaccttcagggaccgcatctacaacgacacca 685

>gb|BT093602.1| Soybean clone JCVI-FLGm-17D17 unknown mRNA
Length = 1079

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattct 1176
||||||| |||||
Sbjct: 850 cagggatgtgatggttcaattct 828

>gb|AC237089.1| Oryza granulata clone OG_ABa0096023, complete sequence
Length = 145921

Score = 46.1 bits (23), Expect = 1.1
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 762 cttccacgattgctttgtcaatgtaat 788
||||||| |||||
Sbjct: 78176 cttccacgattgctttgttaaataatgtaat 78150

>ref|XM_002448761.1| Sorghum bicolor hypothetical protein, mRNA
Length = 2469

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
||||||| |||||
Sbjct: 1616 gttttgcttttgcttctaaatta 1594

>emb|FN357570.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000279
Length = 107846

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)

Strand = Plus / Plus

Query: 2232 attgtgtttaataagttgttaaa 2254
|||||
Sbjct: 30598 attgtgtttaataagttgttaaa 30620

>emb|FN357441.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000150
Length = 760080

Score = 46.1 bits (23), Expect = 1.1
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 172 aatcagtatctttagaaaactaattaagaaattaa 206
|||||
Sbjct: 116245 aatcagtatctttgaaaattaattatgaaattaa 116279

>gb|BT086529.1| Zea mays full-length cDNA clone ZM_BFc0177005 mRNA, complete cds
Length = 2218

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
|||||
Sbjct: 1467 gttttgcttttgcttctaaatta 1445

>gb|EZ053600.1| TSA: Zea mays contig54722, mRNA sequence
Length = 1441

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
|||||
Sbjct: 688 gttttgcttttgcttctaaatta 666

>emb|AL844509.2| Plasmodium falciparum 3D7 chromosome 13
Length = 2895605

Score = 46.1 bits (23), Expect = 1.1
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 193 aattaagaaattaaataaaaaaatattt 219
 ||||| ||||| ||||| |||||
Sbjct: 2326925 aattaagaaataaaataaaaaaatattt 2326951

>gb|AC235371.1| Glycine max strain Williams 82 clone GM_WBb0104B04, complete sequence
Length = 191941

Score = 46.1 bits (23), Expect = 1.1
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 269 tttctataaaattatTTTTCTTTtaatttcttaattaatcctaa 315
 ||| ||||| ||||| ||| ||||| ||||| ||||| |||||
Sbjct: 155381 tttcaataaaaaatTTTTattttaatttttaattaatcctaa 155427

>gb|AC235196.1| Glycine max strain Williams 82 clone GM_WBb0014G10, complete sequence
Length = 114082

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattct 1176
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 65728 cagggatgtgatggttcaattct 65750

>gb|AC235187.1| Glycine max strain Williams 82 clone GM_WBb0010C08, complete sequence
Length = 184070

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 281 tattttttcttttaatttcttaa 303
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 7796 tattttttcttttaatttcttaa 7774

>gb|AC235182.1| Glycine max strain Williams 82 clone GM_WBb0008C11, complete sequence
Length = 100806

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 293 taatttcttaattaataatcctaa 315
|||||||
Sbjct: 22206 taatttcttaattaataatcctaa 22184

>ref|XM_002319931.1| Populus trichocarpa predicted protein, mRNA
Length = 939

Score = 46.1 bits (23), Expect = 1.1
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaa 782
||||||| ||| ||||| || ||||| |||||
Sbjct: 148 atgggtgcttctcttgttcggttcttcttcattgattgtttgtcaa 194

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1993 aagggtctcctccactctgatca 2015
|||||||
Sbjct: 751 aagggtctcctccactctgatca 773

>ref|NM_001158468.1| Zea mays peroxidase 52 (LOC100285577), mRNA
>gi|195651250|gb|EU972975.1| Zea mays clone 391021
peroxidase 52 precursor, mRNA, complete cds
Length = 1358

Score = 46.1 bits (23), Expect = 1.1
Identities = 53/63 (84%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853

Sbjct: 670 t c a c a c c a t c g g c c a a g c a c g c t g c a c c a a c t t c a g a g c c c a c g t g t a c a a c g a c a c c a a 729

Query: 1854 cat 1856

Sbjct: 730 ||| cat 732

```
>gb|EU954765.1| Zea mays clone 1482328 mRNA sequence
      Length = 1445
```

Score = 46.1 bits (23), Expect = 1.1
Identities = 47/55 (85%)
Strand = Plus / Plus

Identities = 47/55 (85%)

Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787

[illegible]

>gb|EU951047.1| Zea mays clone 687198 mRNA sequence
Length = 845

Score = 46.1 bits (23), Expect = 1.1
Identities = 23/23 (100%)
Strand = Plus / Minus

Identities = 23/23 (100%)

Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483

Sbjct: 231 gttttgcttttgcttctaaatta 209

>gb|FJ088527.1| Pinus taeda isolate 6658 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Identities = 50/59 (84%)

Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggaagaattaggaagaa 318

```
>gb|FJ088526.1| Pinus taeda isolate 6661 anonymous locus 2 10243 02 genomic sequence
```

Length = 450

Score = 46.1 bits (23), Expect = 1.1

Identities = 50/59 (84%)

Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

||||| ||||||| || | ||||||||||||| || | ||||||| |||||||

Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088525.1| Pinus taeda isolate 6650 anonymous locus 2_10243_02 genomic sequence

Length = 450

Score = 46.1 bits (23), Expect = 1.1

Identities = 50/59 (84%)

Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

||||| ||||||| || | ||||||||||||| || | ||||||| |||||||

Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088524.1| Pinus taeda isolate 6653 anonymous locus 2_10243_02 genomic sequence

Length = 450

Score = 46.1 bits (23), Expect = 1.1

Identities = 50/59 (84%)

Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

||||| ||||||| || | ||||||||||||| || | ||||||| |||||||

Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088523.1| Pinus taeda isolate 6663 anonymous locus 2_10243_02 genomic sequence

Length = 450

Score = 46.1 bits (23), Expect = 1.1

Identities = 50/59 (84%)

Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

||||| ||||||| || | ||||||||||||| || | ||||||| |||||||

Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088522.1| Pinus taeda isolate 6662 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| ||| | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088521.1| Pinus taeda isolate 6654 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| ||| | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088520.1| Pinus taeda isolate 6655 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| ||| | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088519.1| Pinus taeda isolate 6657 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088518.1| Pinus taeda isolate 6664 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088517.1| Pinus taeda isolate 6651 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088516.1| Pinus taeda isolate 6649 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088515.1| Pinus taeda isolate 6666 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)

Strand = Plus / Minus

```
Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
          ||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318
```

>gb|FJ088514.1| Pinus taeda isolate 6660 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

```
Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
          ||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318
```

>gb|FJ088513.1| Pinus taeda isolate 6665 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

```
Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
          ||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318
```

>gb|FJ088512.1| Pinus taeda isolate 6656 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

```
Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
          ||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318
```

>gb|FJ088511.1| Pinus taeda isolate 4039 anonymous locus 2_10243_01 genomic sequence
Length = 579

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 2

>gb|FJ088510.1| Pinus taeda isolate 4033 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 2

>gb|FJ088509.1| Pinus taeda isolate 4024 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 2

>gb|FJ088508.1| Pinus taeda isolate 4026 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 2

>gb|FJ088507.1| Pinus taeda isolate 4025 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 2

>gb|FJ088506.1| Pinus taeda isolate 4031 anonymous locus 2_10243_01 genomic sequence
Length = 580

Score = 46.1 bits (23), Expect = 1.1
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 60 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 2

Database: /usr/local/blast/db/blastlibs/nt
Posted date: Feb 13, 2010 7:27 AM
Number of letters in database: 30,212,464,392
Number of sequences in database: 10,930,266

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 10930266
Number of Hits to DB: 956,652,574
Number of extensions: 59923270
Number of successful extensions: 1533110
Number of sequences better than 10.0: 507
Number of HSP's gapped: 1533086
Number of HSP's successfully gapped: 615

Length of query: 2730
Length of database: 30,212,464,392
Length adjustment: 24
Effective length of query: 2706
Effective length of database: 29,950,138,008
Effective search space: 81045073449648
Effective search space used: 81045073449648
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 14 (28.2 bits)
S2: 22 (44.1 bits)

BLASTn Output of the 5' Border Sequence Flanking the Insert in Soybean Event DAS-68416-4 against GenBank No_human and No_mouse ESTs (est_others)

BLASTN 2.2.21 [Jun-14-2009]

+

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 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.

Query= 68416_5_border
(2730 letters)

Database: /usr/local/blast/db/blastlibs/est_others
51,680,690 sequences; 29,218,461,503 total letters

Searching.....done

Sequences producing significant alignments:				Score	E
				(bits)	Value
gb CX703225.1	gmrtDrNS01_14-B_M13R_D10_074.s2	Water stressed 5h...		1070	0.0
gb CX709633.1	gmrtDrNS01_10-D_M13R_A04_032.s2	Water stressed 5h...		1063	0.0
gb CF807990.1	psHB031xA07f	USDA-IFAFS:Expression of Phytophthor...		1059	0.0
gb BG509781.1	sad25h05.y1	Gm-c1074 Glycine max cDNA clone GENOM...		924	0.0
gb BM731124.1	sal68a04.y1	Gm-c1061 Glycine max cDNA clone SOYBE...		894	0.0
gb BG882707.1	sae51e08.y2	Gm-c1051 Glycine max cDNA clone GENOM...		880	0.0
gb EV267121.1	GLLBF04TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...		731	0.0
gb CF806428.1	psHB011xIO5f	USDA-IFAFS:Expression of Phytophthor...		646	0.0
gb AW349107.1	GM210004A21E9	Gm-r1021 Glycine max cDNA clone Gm-...		626	e-175
gb BG156628.1	sab31a07.y1	Gm-c1026 Glycine max cDNA clone GENOM...		618	e-173
gb FK018609.1	GLND133TF	JCVI-SOY3 Glycine max cDNA 5', mRNA seq...		557	e-154
gb BU577048.1	sar71e12.y1	Gm-c1074 Glycine max cDNA clone SOYBE...		545	e-151
gb BM093025.1	saj04a09.y1	Gm-c1065 Glycine max cDNA clone GENOM...		527	e-145
gb BE210375.1	so42h10.y1	Gm-c1039 Glycine max cDNA clone GENOME...		527	e-145
gb EV263181.1	GLLA357TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...		525	e-145
gb CF806168.1	psHB004x020f	USDA-IFAFS:Expression of Phytophthor...		523	e-144
gb BI972311.1	sag89h02.y1	Gm-c1084 Glycine max cDNA clone GENOM...		502	e-138
gb BE209964.1	so37a08.y1	Gm-c1039 Glycine max cDNA clone GENOME...		490	e-134
gb BG725689.1	sae39d12.y1	Gm-c1051 Glycine max cDNA clone GENOM...		464	e-126
gb FG889629.1	UCRVU08_CCNS10828_g1	Cowpea IT97K-461-4 Mixed Tis...		444	e-120
gb BE022389.1	sm85b11.y1	Gm-c1015 Glycine max cDNA clone GENOME...		438	e-119
gb BG359695.1	sac27d09.y1	Gm-c1051 Glycine max cDNA clone GENOM...		436	e-118
gb EV265313.1	GLLAS95TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...		412	e-111
gb AW132280.1	se02a03.y1	Gm-c1013 Glycine max cDNA clone GENOME...		381	e-101
gb CF809087.1	psHB042xH14f	USDA-IFAFS:Expression of Phytophthor...		373	3e-99

gb BU577870.1	sar93g05.y1 Gm-c1074 Glycine max cDNA clone SOYBE...	373	3e-99
gb AW432575.1	sh76b11.y1 Gm-c1015 Glycine max cDNA clone GENOME...	361	1e-95
gb FG825601.1	UCRVU04_CCNI8859_g1 Cowpea 524B Mixed Tissue and ...	343	3e-90
gb FF387035.1	MO0BI56TF MOO Vigna unguiculata cDNA 5', mRNA seq...	335	8e-88
gb BE807926.1	ss31h12.y1 Gm-c1061 Glycine max cDNA clone GENOME...	331	1e-86
gb FF386168.1	MO0BI56TRB MOO Vigna unguiculata cDNA, mRNA sequence	321	1e-83
gb AI441922.1	sa51f09.y1 Gm-c1004 Glycine max cDNA clone GENOME...	291	1e-74
gb G0029196.1	LJMAW92T0 JCVI-LJ2 Lotus japonicus cDNA 3', mRNA ...	289	4e-74
dbj BP048143.1	BP048143 Lotus corniculatus var. japonicus pods ...	289	4e-74
dbj BP048038.1	BP048038 Lotus corniculatus var. japonicus pods ...	289	4e-74
dbj AV768169.1	AV768169 Lotus japonicus Young plants (two-weeks...	289	4e-74
dbj BP048158.1	BP048158 Lotus corniculatus var. japonicus pods ...	274	2e-69
gb G0017605.1	LJGBF85T0 JCVI-LJ1 Lotus japonicus cDNA 3', mRNA ...	266	6e-67
gb G0023584.1	LJMCD71TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA ...	262	9e-66
gb FG825600.1	UCRVU04_CCNI8859_b1 Cowpea 524B Mixed Tissue and ...	246	5e-61
gb FF394030.1	MO0DS81TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	5e-61
gb FF387818.1	MO0C268TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	5e-61
gb FF383796.1	MO0B233TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	5e-61
dbj FS240762.1	FS240762 RPSC Glycyrrhiza uralensis cDNA clone K...	244	2e-60
gb FG889628.1	UCRVU08_CCNS10828_b1 Cowpea IT97K-461-4 Mixed Tis...	238	1e-58
gb FF403045.1	MO0F734TF MOO Vigna unguiculata cDNA 5', mRNA seq...	238	1e-58
gb FF392448.1	MO0CV65TF MOO Vigna unguiculata cDNA 5', mRNA seq...	238	1e-58
gb FF399144.1	MO0EV84TF MOO Vigna unguiculata cDNA 5', mRNA seq...	234	2e-57
gb G0019707.1	LJMAW92TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA ...	208	1e-49
dbj AV412875.1	AV412875 Lotus japonicus young plants (two-week ...	208	1e-49
dbj AV771838.1	AV771838 Lotus japonicus Pods (20-30 mm in lengt...	202	7e-48
dbj BW620524.1	BW620524 Lotus japonicus protoplasts from suspen...	196	4e-46
dbj BW630489.1	BW630489 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj BW629863.1	BW629863 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj BW628107.1	BW628107 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj BW627140.1	BW627140 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj BW624354.1	BW624354 Lotus japonicus salicylic acid and meth...	196	4e-46
dbj BW595840.1	BW595840 Lotus japonicus suspension-cultured cel...	196	4e-46
gb EY976963.1	EST 83 Alfalfa aluminum suppression subtractive l...	190	3e-44
gb EH613355.1	EST 02 Alfalfa aluminum suppression subtractive l...	190	3e-44
dbj BB913062.1	BB913062 Trifolium pratense three week-old plant...	190	3e-44
gb BI969832.1	GM830009A23A12 Gm-r1083 Glycine max cDNA clone Gm...	180	3e-41
gb BI700509.1	sag61f05.y1 Gm-c1082 Glycine max cDNA clone GENOM...	180	3e-41
gb BU578183.1	sar49a02.y1 Gm-c1074 Glycine max cDNA clone SOYBE...	176	4e-40
gb G0258927.1	VBL1_16_M09_E001.g1 Normalized cDNA library from ...	174	2e-39
gb CA852976.1	E14E06_J06_09.ab1 cDNA Peking library 6, 8 day SC...	174	2e-39
gb CA852554.1	E09B05_C17_03.ab1 cDNA Peking library 6, 8 day SC...	174	2e-39
gb AW350788.1	GM210009A20D5 Gm-r1021 Glycine max cDNA clone Gm...	174	2e-39
gb FF401698.1	MO0E192TF MOO Vigna unguiculata cDNA 5', mRNA seq...	168	1e-37
gb EY476317.1	METAQ01TF JCVI-MT3 Medicago truncatula cDNA 5', m...	167	4e-37
gb EX530374.1	MTGland_A066_2007-06-28/MTGlandA066_C04_014_1 Med...	167	4e-37
gb CX528854.1	s13dNF01B01MJ009_243775 Methyl Jasmonate-Elicited...	167	4e-37
gb CF068375.1	EST669096 MTUS Medicago truncatula cDNA clone MTU...	167	4e-37
gb AW268020.1	EST306242 DSIR Medicago truncatula cDNA clone pDS...	167	4e-37

gb	BI969294.1	GM830007B20G07 Gm-r1083 Glycine max cDNA clone Gm...	165	2e-36
gb	FG998035.1	GLPA295TF JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	163	6e-36
gb	EY477044.1	METAY48TF JCVI-MT3 Medicago truncatula cDNA 5', m...	163	6e-36
gb	BG448404.1	NF024B09EC1F1074 Elicited cell culture Medicago t...	155	2e-33
gb	BF644619.1	NF017G06EC1F1051 Elicited cell culture Medicago t...	155	2e-33
gb	CA919059.1	EST636777 MTUS Medicago truncatula cDNA clone MTU...	151	2e-32
gb	AW830120.1	sm23a02.y1 Gm-c1028 Glycine max cDNA clone GENOME...	151	2e-32
gb	C0513054.1	s13dSG89B0900073_122034 Glandular trichomes Medic...	149	9e-32
gb	FG998036.1	GLPA295TR JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	147	4e-31
gb	C0516034.1	s13dSG64B1200101_445396 Glandular trichomes Medic...	147	4e-31
gb	C0514259.1	s13dSG76D0500042_157180 Glandular trichomes Medic...	147	4e-31
gb	AW686470.2	NF041G08NR1F1000 Nodulated root Medicago truncatu...	145	1e-30
gb	BF639633.1	NF015A12IN1F1097 Insect herbivory Medicago trunca...	145	1e-30
gb	CX530413.1	s13dNF99F02MJ016_246858 Methyl Jasmonate-Elicited...	141	2e-29
gb	CX529528.1	s13dNF97C05MJ034_245107 Methyl Jasmonate-Elicited...	141	2e-29
gb	BF647501.1	NF068D03EC1F1029 Elicited cell culture Medicago t...	141	2e-29
gb	BF645317.1	NF030B11EC1F1092 Elicited cell culture Medicago t...	141	2e-29
gb	C0515766.1	s13dSG77F0400043_419681 Glandular trichomes Medic...	139	9e-29
gb	AW830346.1	sm33e02.y1 Gm-c1028 Glycine max cDNA clone GENOME...	139	9e-29
gb	AW703873.1	sk25b09.y1 Gm-c1028 Glycine max cDNA clone GENOME...	139	9e-29
gb	AI495213.1	sb02b01.y1 Gm-c1004 Glycine max cDNA clone GENOME...	139	9e-29
gb	AW830098.1	sm22c01.y1 Gm-c1028 Glycine max cDNA clone GENOME...	137	4e-28
gb	AW704238.1	sk18d12.y1 Gm-c1028 Glycine max cDNA clone GENOME...	135	1e-27
emb	CU524253.1	CU524253 STSSH2Sb_KZOACB Theobroma cacao cDNA ...	133	6e-27
dbj	AV771209.1	AV771209 Lotus japonicus Pods (20-30 mm in lengt...	133	6e-27
gb	C0516246.1	s13dSG69B0900075_445820 Glandular trichomes Medic...	131	2e-26
gb	BF071209.1	st04h08.y1 Gm-c1065 Glycine max cDNA clone GENOME...	131	2e-26
gb	EX660929.1	JS1BF51JG Salt stressed Fragaria vesca (strain Ha...	129	9e-26
gb	DN950706.1	Ost2T_331 Oak tissue culture growing 2 days in hy...	129	9e-26
gb	C0511866.1	s13dSG02H0700064_103632 Glandular trichomes Medic...	129	9e-26
gb	BF650349.1	NF096E02EC1F1017 Elicited cell culture Medicago t...	129	9e-26
gb	BE022178.1	sm68f01.y1 Gm-c1028 Glycine max cDNA clone GENOME...	129	9e-26
gb	AW666186.1	sk33d05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	125	1e-24
gb	AW685593.1	NF029D05NR1F1000 Nodulated root Medicago truncatu...	117	3e-22
dbj	FS263447.1	FS263447 RPSC Glycyrrhiza uralensis cDNA clone S...	113	5e-21
gb	BF650698.1	NF099E07EC1F1053 Elicited cell culture Medicago t...	113	5e-21
gb	EV262518.1	MTYEW71TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	2e-20
gb	EV260463.1	MTYE803TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	2e-20
gb	EV258111.1	MTYDG59TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	2e-20
gb	DW017370.1	EST1226331 MTY Medicago truncatula cDNA clone MTY...	111	2e-20
gb	DW015340.1	EST1224301 MTY Medicago truncatula cDNA clone MTY...	111	2e-20
gb	C0513179.1	s13dSG23G0900068_129522 Glandular trichomes Medic...	111	2e-20
gb	C0512465.1	s13dSG100C120008_114444 Glandular trichomes Medic...	111	2e-20
gb	BG456493.1	NF082E02PL1F1017 Phosphate starved leaf Medicago ...	111	2e-20
gb	BG456057.1	NF073F02PL1F1025 Phosphate starved leaf Medicago ...	111	2e-20
gb	DW481567.1	GH_RMIRS_031_E08_R Cotton Normalized Library rand...	109	8e-20
gb	DW481566.1	GH_RMIRS_031_E08_056_F Cotton Normalized Library ...	109	8e-20
gb	DV443257.1	CV01009B1D06.f1 CV01-normalized library Manihot e...	107	3e-19
gb	DY633234.1	Medicago--03-I06.g1 Subtracted medicago cDNA libr...	105	1e-18

gb DY633115.1	Medicago--03-I06.b1 Subtracted medicago cDNA libr...	105	1e-18
gb BG359643.1	sac26g07.y1 Gm-c1051 Glycine max cDNA clone GENOM...	105	1e-18
gb GT138697.1	METCC85TF JCVI-MT3 Medicago truncatula cDNA 5', m...	103	5e-18
gb AW235016.1	sf21h05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	103	5e-18
emb CU485516.1	CU485516 CUSHIONC_KZOACAC Theobroma cacao cDNA c...	101	2e-17
gb BG454205.1	NF108A01LF1F1001 Developing leaf Medicago truncat...	101	2e-17
gb BE943474.1	EST423053 MGHG Medicago truncatula cDNA clone pMG...	101	2e-17
gb ES840062.1	UFL_061_05 Cotton fiber 0-10 day post anthesis Go...	100	8e-17
gb BI262826.1	NF091E03EC1F1023 Elicited cell culture Medicago t...	100	8e-17
gb AW666202.1	sk33f05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	100	8e-17
gb G0006531.1	LJGBF85TF JCVI-LJ1 Lotus japonicus cDNA 5', mRNA ...	98	3e-16
gb C0511819.1	s13dSG02D0500046_103538 Glandular trichomes Medic...	98	3e-16
gb BF648119.1	NF027G10EC1F1083 Elicited cell culture Medicago t...	98	3e-16
gb AW309606.1	sf21h05.x1 Gm-c1028 Glycine max cDNA clone GENOME...	98	3e-16
gb C0513848.1	s13dSG73C1100082_156358 Glandular trichomes Medic...	96	1e-15
gb AW691930.2	NF050G04ST1F1000 Developing stem Medicago truncat...	96	1e-15
emb AJ548283.1	AJ548283 MTAPHEU Medicago truncatula cDNA clone ...	88	3e-13
gb BF520761.1	EST458234 DSIL Medicago truncatula cDNA clone pDS...	88	3e-13
emb FN039861.1	FN039861 Petunia axillaris subsp. axillaris pool...	86	1e-12
emb FN039860.1	FN039860 Petunia axillaris subsp. axillaris pool...	86	1e-12
gb EG559283.1	CR03032H04 Root CR03 cDNA library Catharanthus ro...	86	1e-12
gb DW500373.1	GH_TMIRS_045_H05_F Cotton Normalized Library dT p...	86	1e-12
dbj CI189311.1	CI189311 Oryza sativa (japonica cultivar-group) ...	86	1e-12
dbj CI256090.1	CI256090 Oryza sativa (japonica cultivar-group) ...	86	1e-12
gb C0498078.1	G.h.fbr-sw07468 G.h.fbr-sw Gossypium hirsutum cDN...	86	1e-12
gb EY707107.1	CS00-C3-701-064-H11-CT.F Sweet orange fruit, deve...	84	5e-12
gb FD423297.1	RT00024R_T3_024_F11_31MAY2004_085_ab1 CrUniGene r...	84	5e-12
gb FD422675.1	RT00017R_T3_017_E10_31MAY2004_072_ab1 CrUniGene r...	84	5e-12
gb FD422951.1	RT00020R_T3_020_G01_31MAY2004_003_ab1 CrUniGene r...	84	5e-12
gb FD420140.1	1_SM-JB_R10-G12_T3_G12_3100394_14_ab1 CrUniGene ...	84	5e-12
gb DW508346.1	GH_TMIRS_123_D07_F Cotton Normalized Library dT p...	82	2e-11
gb GT143205.1	METCC85TR JCVI-MT3 Medicago truncatula cDNA 3', m...	80	7e-11
gb DR280730.1	157654 CERES-148 Arabidopsis thaliana cDNA clone ...	80	7e-11
gb CN910539.1	030128ABLC005555HT (ABLC) Braeburn cell culture t...	80	7e-11
gb CN908859.1	030122ABLC003031HT (ABLC) Braeburn cell culture t...	80	7e-11
gb CN908310.1	030109ABLC001919HT (ABLC) Braeburn cell culture t...	80	7e-11
dbj AU238571.1	AU238571 RAFL17 Arabidopsis thaliana cDNA clone ...	80	7e-11
emb FN019009.1	FN019009 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN019008.1	FN019008 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN021689.1	FN021689 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN021688.1	FN021688 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN034858.1	FN034858 Petunia axillaris subsp. axillaris pool...	78	3e-10
emb FN019751.1	FN019751 Petunia axillaris subsp. axillaris pool...	78	3e-10
gb FC869557.1	C31102G05EF AbioticR1 Citrus reshni cDNA clone C3...	78	3e-10
gb FC870159.1	C31109C09EF AbioticR1 Citrus reshni cDNA clone C3...	78	3e-10
gb FC924498.1	C31806G11EF StrCleopN Citrus reshni cDNA clone C3...	78	3e-10
gb FC875256.1	C31505H10EF CEVdCidro1 Citrus medica cDNA clone C...	78	3e-10
gb FC921479.1	C32105D10EF RVDevelopN Citrus clementina cDNA clo...	78	3e-10
gb FC875071.1	C31503H10EF CEVdCidro1 Citrus medica cDNA clone C...	78	3e-10

gb EY867689.1	CL06-C4-500-007-B02-CT.F Rangpur lime root, green...	78	3e-10
gb FC325468.1	P00462_C7-H9_M13-F_A09_079.ab1 Onu-Ua-pathc Ulmus...	78	3e-10
gb EG985866.1	GLE049_D04_013 Cyamopsis tetragonoloba (L.) Taub ...	78	3e-10
gb EG356679.1	P00462_C7-H9_M13-F_A09_079 Onu-Ua-pathc Ulmus ame...	78	3e-10
emb FN034857.1	FN034857 Petunia axillaris subsp. axillaris pool...	76	1e-09
emb FN045147.1	FN045147 Petunia axillaris subsp. axillaris pool...	76	1e-09
emb FN019752.1	FN019752 Petunia axillaris subsp. axillaris pool...	76	1e-09
gb G0517646.1	Mdfbg8014P16.g1 Apple_EST_Mdfbg Malus hybrid root...	76	1e-09
gb EV227910.1	VV_PEA016c06.b1 Vitis vinifera cv. perlette LibA ...	76	1e-09
gb EH047301.1	AS2RM4P1E10.ab1 Roots inoculated with Meloidogyne...	76	1e-09
gb EC991497.1	WIN1142.C21_L14 Muscat Hamburg pre-veraison berry...	76	1e-09
gb EC987303.1	WIN1130.C21_E15 Muscat Hamburg pre-veraison berry...	76	1e-09
gb EC985323.1	WIN1124.C21_I01 Muscat Hamburg pre-veraison berry...	76	1e-09
gb CV861937.1	gonad_EST09518 Embryonic gonad cDNA Library Gallu...	76	1e-09
gb CX309187.1	C18022D10Rv Drought2 Citrus reshni cDNA clone C18...	76	1e-09
gb CA105303.1	SCJFHR1C05E10.g HR1 Saccharum officinarum cDNA cl...	76	1e-09
gb CA102350.1	SCBGHR1058E08.g HR1 Saccharum officinarum cDNA cl...	76	1e-09
gb CF205258.1	RR890915I0004_IVa_Ra_B09 Vitis sp. RR890915I Viti...	76	1e-09
dbj FS421608.1	FS421608 normalized full-length tobacco cDNA lib...	74	4e-09
dbj FS420315.1	FS420315 normalized full-length tobacco cDNA lib...	74	4e-09
gb ES441310.1	TSH_EST01528 Theobroma cacao-Moniliophthora perni...	74	4e-09
emb CU488677.1	CU488677 DROUGHTLS_KZOACAF Theobroma cacao cDNA ...	74	4e-09
gb FG154278.1	AGN_RNC104xj04f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	4e-09
gb FG173223.1	AGN_RNC126xi04f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	4e-09
gb FG156951.1	AGN_RNC026xe21f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	4e-09
gb FG157638.1	AGN_RNC025xk16f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	4e-09
dbj DB920515.1	DB920515 full-length enriched cassava cDNA libra...	74	4e-09
gb EB450877.1	KT7C.108P16F.051219T7 KT7 Nicotiana tabacum cDNA ...	74	4e-09
gb DY356036.1	ZO_Ec0009K09.f ZO_Ec Zingiber officinale cDNA c...	74	4e-09
gb CV005110.1	atr02-9ms3-h07 Atr02 Amborella trichopoda cDNA cl...	74	4e-09
gb CN782128.1	EST00224 cqseed Chenopodium quinoa cDNA clone S02...	74	4e-09
gb FC869818.1	C31105F02EF AbioticR1 Citrus reshni cDNA clone C3...	72	2e-08
gb FC874065.1	C31202A05EF BiotPhyR1 Citrus aurantium cDNA clone...	72	2e-08
gb GD471713.1	454PCS0099417 Scarlet Runner Bean globular-stage ...	72	2e-08
gb GD391465.1	454PCS0019156 Scarlet Runner Bean globular-stage ...	72	2e-08
gb FG480776.1	020324KANA001021HT (KANA) Actinidia setosa stem A...	72	2e-08
gb EY845171.1	CA26-C1-002-040-C02-CT.F Sour orange leaf, field ...	72	2e-08
gb EY794850.1	CR05-C3-701-027-F03-CT.F Mandarin fruit, developm...	72	2e-08
gb EY776217.1	CR05-C1-103-015-D05-CT.F Mandarin leaf, infected ...	72	2e-08
gb EY725128.1	CS00-C3-703-086-B09-CT.F Sweet orange fruit, deve...	72	2e-08
gb C0500329.1	KH01008A04 KH01 Ipomoea batatas cDNA, mRNA sequence	72	2e-08
gb DW500299.1	GH_TMIRS_045_B08_F Cotton Normalized Library dT p...	72	2e-08
gb CX670039.1	UCRCP01_048_E06_T7 Swingle citrumelo nematode-cha...	72	2e-08
gb CX050341.1	UCRCS09_31H06_b Ruby Orange Developing Seed cDNA ...	72	2e-08
gb CV717574.1	UCRCS08_0009D08_f Parent Washington Navel Orange ...	72	2e-08
gb CV093292.1	FAMU_USDA_FP_1315 Vitis shuttleworthii L., grape ...	72	2e-08
gb C0866271.1	Mdfrt3046b02.y1 Mdfrt Malus x domestica cDNA clon...	72	2e-08
gb C0417575.1	Mdfrt3031k23.y1 Mdfrt Malus x domestica cDNA clon...	72	2e-08
gb C0070833.1	GR_Ea28B05.r GR_Ea Gossypium raimondii cDNA clo...	72	2e-08

gb	G0566201.1	Mddb5025B21_e2932.g1 Mddb Malus x domestica cDNA ...	70	7e-08
emb	CU537036.1	CU537036 TISCIVS_KZ0AAQ Theobroma cacao cDNA clo...	70	7e-08
emb	CU505430.1	CU505430 PODMEUPA_KZOACAB Theobroma cacao cDNA c...	70	7e-08
emb	CU478688.1	CU478688 COPHAS_KZ0AAL Theobroma cacao cDNA clon...	70	7e-08
emb	CU478933.1	CU478933 COPHAS_KZ0AAL Theobroma cacao cDNA clon...	70	7e-08
emb	CU480774.1	CU480774 CORTEXS_KZ0AAT Theobroma cacao cDNA clo...	70	7e-08
dbj	DC895850.1	DC895850 PCC Citrus unshiu cDNA clone PCC0206 5'...	70	7e-08
gb	EX266960.1	1447232_5_A14_063 PY06 Carica papaya cDNA, mRNA s...	70	7e-08
gb	EX289762.1	1577761_5_L07_022 PY06 Carica papaya cDNA, mRNA s...	70	7e-08
gb	EX272151.1	1452845_5_K11_038 PY06 Carica papaya cDNA, mRNA s...	70	7e-08
gb	EB110403.1	000430AFBC008068HT (AFBC) Royal Gala pre-opened f...	70	7e-08
gb	DW157696.1	CLVX9795.b1_E02.ab1 CLV(XYZ) lettuce virosa Lactu...	70	7e-08
gb	DW145800.1	CLVX10900.b1_H13.ab1 CLV(XYZ) lettuce virosa Lact...	70	7e-08
gb	C0900249.1	Mddb5025b21.y1 Mddb Malus x domestica cDNA clone ...	70	7e-08
gb	C0051719.1	Mdfw2055d05.y1 Mdfw Malus x domestica cDNA clone ...	70	7e-08
gb	CN880015.1	010418AASA009843HT (AASA) Royal Gala 10 DAFB frui...	70	7e-08
gb	GR871114.1	Pq_F_00457 American ginseng Flower cDNA Library P...	68	3e-07
gb	GR875194.1	Pq_R_02677 American ginseng Root cDNA Library Pan...	68	3e-07
gb	GR873483.1	Pq_R_00966 American ginseng Root cDNA Library Pan...	68	3e-07
gb	GR873276.1	Pq_R_00759 American ginseng Root cDNA Library Pan...	68	3e-07
gb	GR871777.1	Pq_F_01120 American ginseng Flower cDNA Library P...	68	3e-07
gb	GR874357.1	Pq_R_01840 American ginseng Root cDNA Library Pan...	68	3e-07
gb	GR874227.1	Pq_R_01710 American ginseng Root cDNA Library Pan...	68	3e-07
emb	CU507988.1	CU507988 PODSSHWB1Sb_KZOACD Theobroma cacao cDNA...	68	3e-07
gb	EY664481.1	CS00-C1-101-067-A09-CT.F Sweet orange leaf, infec...	68	3e-07
gb	EW712042.1	Ginseng-Feq Contig4 Ginseng F. equiseti subtracti...	68	3e-07
gb	EL366609.1	CCES2712.b1_005.ab1 CCE(LMS) endive Cichorium end...	68	3e-07
gb	EH664510.1	11.2E05 Transformed tobacco Lambda Zap II library...	68	3e-07
gb	EC600006.1	PNSSH3G-1469 panax notoginseng subtracted cDNA li...	68	3e-07
dbj	CI205074.1	CI205074 Oryza sativa (japonica cultivar-group) ...	68	3e-07
gb	C0898341.1	Mdfrt3034e04.y3 Mdfrt Malus x domestica cDNA clon...	68	3e-07
gb	CN848323.1	PG07017B01 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN847185.1	PG07026G09 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN846818.1	PG07018H01 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN846698.1	PG07019B09 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN846059.1	PG07005D12 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CN845966.1	PG07006B07 Ginseng cDNA library from MeJA treated...	68	3e-07
gb	CK265901.1	EST711979 potato abiotic stress cDNA library Sola...	68	3e-07
gb	CK259240.1	EST742877 potato callus cDNA library, normalized ...	68	3e-07
gb	CK257963.1	EST741600 potato callus cDNA library, normalized ...	68	3e-07
gb	CK257684.1	EST741321 potato callus cDNA library, normalized ...	68	3e-07
gb	CK256437.1	EST740074 potato callus cDNA library, normalized ...	68	3e-07
gb	CK256141.1	EST739778 potato callus cDNA library, normalized ...	68	3e-07
gb	CK254968.1	EST738605 potato callus cDNA library, normalized ...	68	3e-07
gb	CK254173.1	EST737810 potato callus cDNA library, normalized ...	68	3e-07
gb	CK253943.1	EST737580 potato callus cDNA library, normalized ...	68	3e-07
gb	CK252132.1	EST735769 potato callus cDNA library, normalized ...	68	3e-07
gb	CK250936.1	EST734573 potato callus cDNA library, normalized ...	68	3e-07
gb	CK250929.1	EST734566 potato callus cDNA library, normalized ...	68	3e-07

gb	CK249912.1	EST733549 potato callus cDNA library, normalized ...	68	3e-07
gb	CK249875.1	EST733512 potato callus cDNA library, normalized ...	68	3e-07
gb	CK249724.1	EST733361 potato callus cDNA library, normalized ...	68	3e-07
gb	CK249638.1	EST733275 potato callus cDNA library, normalized ...	68	3e-07
gb	CK248882.1	EST732519 potato callus cDNA library, normalized ...	68	3e-07
gb	CK248392.1	EST732029 potato callus cDNA library, normalized ...	68	3e-07
gb	CK247774.1	EST731411 potato callus cDNA library, normalized ...	68	3e-07
gb	CK247097.1	EST730734 potato callus cDNA library, normalized ...	68	3e-07
gb	CK246328.1	EST729965 potato callus cDNA library, normalized ...	68	3e-07
gb	CK246259.1	EST729896 potato callus cDNA library, normalized ...	68	3e-07
gb	CK246252.1	EST729889 potato callus cDNA library, normalized ...	68	3e-07
gb	CK245537.1	EST729174 potato callus cDNA library, normalized ...	68	3e-07
gb	CK245042.1	EST728679 potato callus cDNA library, normalized ...	68	3e-07
gb	CK243469.1	EST727106 potato callus cDNA library, normalized ...	68	3e-07
gb	CK243468.1	EST727105 potato callus cDNA library, normalized ...	68	3e-07
dbj	AU229763.1	AU229763 RAFL17 Arabidopsis thaliana cDNA clone ...	68	3e-07
gb	BF273768.1	GA_Eb0018024f Gossypium arboreum 7-10 dpa fiber ...	68	3e-07
dbj	FS194878.1	FS194878 Solanum lycopersicum cv Micro-Tom root ...	66	1e-06
dbj	FS205634.1	FS205634 Solanum lycopersicum cv Micro-Tom root ...	66	1e-06
dbj	FS197980.1	FS197980 Solanum lycopersicum cv Micro-Tom root ...	66	1e-06
gb	GE650850.1	EST1177 Tender roots cDNA library of tea plant Ca...	66	1e-06
gb	EY412917.1	pOP-E008268_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	66	1e-06
gb	FG526917.1	030704KAYC002574HT (KAYC) Actinidia chinensis you...	66	1e-06
gb	FG525755.1	030628KAYC001240HT (KAYC) Actinidia chinensis you...	66	1e-06
gb	FE966530.1	PLATE_T3_028_D07_01DEC2004_057 Opium poppy elicit...	66	1e-06
gb	FE968334.1	PLATE_T3_047_H06_03DEC2004_034 Opium poppy elicit...	66	1e-06
gb	FE966485.1	PLATE_T3_027_H10_01DEC2004_066 Opium poppy elicit...	66	1e-06
gb	FE967467.1	PLATE_T3_038_E11_01DEC2004_087 Opium poppy elicit...	66	1e-06
gb	FE966062.1	PLATE_T3_023_D04_02DEC2004_026 Opium poppy elicit...	66	1e-06
gb	EX165442.1	A05_P-14_034 Cotton 1-14 day post anthesis Lambda...	66	1e-06
gb	EH665793.1	26.2D06 Transformed tobacco Lambda Zap II library...	66	1e-06
dbj	DB685271.1	DB685271 Solanum lycopersicum cv. Micro-Tom leaf...	66	1e-06
dbj	DB689063.1	DB689063 Solanum lycopersicum cv. Micro-Tom leaf...	66	1e-06
dbj	DB699350.1	DB699350 Solanum lycopersicum cv. Micro-Tom leaf...	66	1e-06
dbj	DB692736.1	DB692736 Solanum lycopersicum cv. Micro-Tom leaf...	66	1e-06
gb	DW080731.1	CLPX3640.b1_P21.ab1 CLP(XYZ) lettuce perennis Lac...	66	1e-06
gb	DT523193.1	WS02039.B21_A17 PTxN-IB-N-A-11 Populus trichocarp...	66	1e-06
gb	DT517809.1	WS02435.B21_F23 PTxD-ICC-N-A-14 Populus trichocar...	66	1e-06
gb	DT516973.1	WS02432.B21_P02 PTxD-ICC-N-A-14 Populus trichocar...	66	1e-06
gb	DT515726.1	WS02429.B21.1_F18 PTxD-ICC-N-A-14 Populus trichoc...	66	1e-06
gb	DT511026.1	WS02429.BR_F18 PTxD-ICC-N-A-14 Populus trichocarp...	66	1e-06
gb	DT507952.1	WS02419.BR_K15 PTxD-ICC-N-A-14 Populus trichocarp...	66	1e-06
gb	DN586754.1	46565.1 Late Blight-Challenged Tubers Solanum tub...	66	1e-06
gb	DN485372.1	M129C08.3pR Populus female catkins cDNA library P...	66	1e-06
gb	CV475162.1	23658.1 Developing Tubers Solanum tuberosum cDNA ...	66	1e-06
gb	CV269494.1	WS0208.B21_G14 PTxN-IB-N-A-11 Populus trichocarpa...	66	1e-06
gb	CV269008.1	WS0207.B21_B07 PTxN-IB-N-A-11 Populus trichocarpa...	66	1e-06
gb	CV256197.1	WS0243.B21_D05 PTxD-ICC-N-A-14 Populus trichocarp...	66	1e-06
gb	CK298355.1	EST761069 Nicotiana benthamiana mixed tissue cDNA...	66	1e-06

gb	CK296485.1	EST759199 <i>Nicotiana benthamiana</i> mixed tissue cDNA...	66	1e-06
gb	CK295751.1	EST758465 <i>Nicotiana benthamiana</i> mixed tissue cDNA...	66	1e-06
gb	CK293902.1	EST756616 <i>Nicotiana benthamiana</i> mixed tissue cDNA...	66	1e-06
gb	CK283472.1	EST746194 <i>Nicotiana benthamiana</i> mixed tissue cDNA...	66	1e-06
gb	CK277562.1	EST723640 potato abiotic stress cDNA library Sola...	66	1e-06
gb	CK268372.1	EST714450 potato abiotic stress cDNA library Sola...	66	1e-06
gb	CK260187.1	EST706265 potato abiotic stress cDNA library Sola...	66	1e-06
gb	CK245041.1	EST728678 potato callus cDNA library, normalized ...	66	1e-06
gb	CA927256.1	MTU6CR.P6.H02 Aspen root cDNA Library <i>Populus tre...</i>	66	1e-06
gb	BG597610.1	EST496288 cSTS <i>Solanum tuberosum</i> cDNA clone cSTS1...	66	1e-06
gb	BG594826.1	EST493516 cSTS <i>Solanum tuberosum</i> cDNA clone cSTS8...	66	1e-06
gb	AW429264.1	EST306720 tomato flower buds 0-3 mm, Cornell Univ...	66	1e-06
gb	AW035301.1	EST280664 tomato callus, TAMU <i>Solanum lycopersicu...</i>	66	1e-06
gb	G0345282.1	CS01010G03 Hotpepper under oxidative stress <i>Capsi...</i>	64	4e-06
dbj	FS200575.1	FS200575 <i>Solanum lycopersicum</i> cv Micro-Tom root ...	64	4e-06
gb	GD103440.1	KS21047N18 KS21 <i>Capsicum annuum</i> cDNA, mRNA sequence	64	4e-06
gb	FG173286.1	AGN_RNC126xi04r1.ab1 AGN_RNC <i>Nicotiana tabacum</i> cD...	64	4e-06
gb	FG157705.1	AGN_RNC025xk16r1.ab1 AGN_RNC <i>Nicotiana tabacum</i> cD...	64	4e-06
gb	FG157012.1	AGN_RNC026xe21r1.ab1 AGN_RNC <i>Nicotiana tabacum</i> cD...	64	4e-06
gb	EY868947.1	CL06-C4-500-024-E11-CT.F Rangpur lime root, green...	64	4e-06
gb	FE964503.1	PLATE_T3_006_A01_18NOV2004_015 Opium poppy elicit...	64	4e-06
gb	EL689149.1	OPSC00922 <i>Elaeis guineensis</i> Suspension cell cultu...	64	4e-06
gb	EL688532.1	OPSC00287 <i>Elaeis guineensis</i> Suspension cell cultu...	64	4e-06
gb	EL689060.1	OPSC00829 <i>Elaeis guineensis</i> Suspension cell cultu...	64	4e-06
gb	EW741112.1	10 <i>Capsicum annuum</i> with binucleate <i>Rhizoctonia Li...</i>	64	4e-06
emb	AM806126.1	AM806126 seedling library, SL <i>Nicotiana tabacum</i> ...	64	4e-06
gb	EV281455.1	GLNB506TF JCVI-SOY3 <i>Glycine max</i> cDNA 5', mRNA seq...	64	4e-06
gb	EB125073.1	010417AASA002377HT (AASA) Royal Gala 10 DAFB frui...	64	4e-06
gb	DY357012.1	ZO_Ed0001B05.r ZO_Ed <i>Zingiber officinale</i> cDNA c...	64	4e-06
gb	CN910664.1	030221ABLC006597HT (ABLC) Braeburn cell culture t...	64	4e-06
gb	CN909288.1	030123ABLC003427HT (ABLC) Braeburn cell culture t...	64	4e-06
gb	CN908413.1	030121ABLC002155HT (ABLC) Braeburn cell culture t...	64	4e-06
gb	CN908053.1	030109ABLC001478HT (ABLC) Braeburn cell culture t...	64	4e-06
gb	CF446769.1	EST683114 normalized cDNA library of onion <i>Allium...</i>	64	4e-06
gb	CF445486.1	EST681831 normalized cDNA library of onion <i>Allium...</i>	64	4e-06
gb	CF437063.1	EST673408 normalized cDNA library of onion <i>Allium...</i>	64	4e-06
gb	BM878736.1	P12-A07 Sweetpotato <i>Ipomoea batatas</i> cDNA similar ...	64	4e-06
dbj	FS124984.1	FS124984 library TVR <i>Solanum torvum</i> cDNA clone T...	62	2e-05
dbj	FS024422.1	FS024422 library MLF <i>Solanum melongena</i> cDNA clon...	62	2e-05
dbj	FS121328.1	FS121328 library TVR <i>Solanum torvum</i> cDNA clone T...	62	2e-05
dbj	FS117052.1	FS117052 library TVR <i>Solanum torvum</i> cDNA clone T...	62	2e-05
dbj	FS105158.1	FS105158 library TVR <i>Solanum torvum</i> cDNA clone T...	62	2e-05
dbj	FS107745.1	FS107745 library TVR <i>Solanum torvum</i> cDNA clone T...	62	2e-05
dbj	FS109925.1	FS109925 library TVR <i>Solanum torvum</i> cDNA clone T...	62	2e-05
dbj	FS110172.1	FS110172 library TVR <i>Solanum torvum</i> cDNA clone T...	62	2e-05
dbj	FS119211.1	FS119211 library TVR <i>Solanum torvum</i> cDNA clone T...	62	2e-05
dbj	FS049153.1	FS049153 library PST <i>Solanum melongena</i> cDNA clon...	62	2e-05
dbj	FS021644.1	FS021644 library LS5 <i>Solanum melongena</i> cDNA clon...	62	2e-05
dbj	FS020310.1	FS020310 library LS5 <i>Solanum melongena</i> cDNA clon...	62	2e-05

gb	GR347634.1	CCOX3299.g1 CCOX Avena barbata root, pooled from ...	62	2e-05
gb	GE299450.1	P006002D02 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299223.1	P005007B06 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299125.1	P005005G03 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299103.1	P005005D09 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299068.1	P005004H11 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299038.1	P005004D05 Subtractive cDNA library from laminari...	62	2e-05
gb	EY410241.1	pOP-E007772_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	EY410393.1	pOP-E004088_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	EY412233.1	pOP-E002255_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	DW248736.1	pOP-EON01090_EST_C_1_pSK_SK EON (Oil Palm Embryoi...	62	2e-05
gb	EY032292.1	CAIT669.fwd CAIT Artemisia annua leaf Artemisia a...	62	2e-05
gb	DY980921.1	CLSS2910.b1_K08.ab1 CLS(LMS) lettuce sativa Lactu...	62	2e-05
gb	DY963072.1	CLSM13334.b1_K22.ab1 CLS(LMS) lettuce sativa Lactu...	62	2e-05
gb	DW141853.1	CLSY9921.b1_B10.ab1 CLS(XYZ) lettuce sativa Lactu...	62	2e-05
gb	DW118586.1	CLRY7219.b1_F06.ab1 CLR(XYZ) lettuce serriola Lac...	62	2e-05
gb	DN494839.1	M129C08.5pR Populus female catkins cDNA library P...	62	2e-05
gb	CX658639.1	P001020D11 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CX658354.1	P001034B06 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CX656775.1	P002024B08 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	C0754834.1	Mdfrt3051n10.y1 Mdfrt Malus x domestica cDNA clon...	62	2e-05
gb	GR182521.1	CBPG8855.g1 CBPG Mimulus guttatus IM62 roots, see...	60	7e-05
gb	GR182520.1	CBPG8855.b1 CBPG Mimulus guttatus IM62 roots, see...	60	7e-05
gb	GR101494.1	CCIF25878.b1 CCIF Mimulus guttatus IM62 leaves (H...	60	7e-05
gb	GR030153.1	CCIC14356.g1 CCIC Mimulus guttatus IM62 roots (H)...	60	7e-05
gb	GR010964.1	CCIC3934.g1 CCIC Mimulus guttatus IM62 roots (H) ...	60	7e-05
gb	GR010963.1	CCIC3934.b1 CCIC Mimulus guttatus IM62 roots (H) ...	60	7e-05
gb	GE591881.1	CCPW15817.b1_A19.ab1 CCP(UWX) Globe Artichoke Cyn...	60	7e-05
gb	GE347117.1	MEUB360TF JCVI-MT2 Medicago truncatula cDNA 5', m...	60	7e-05
gb	GE299609.1	P006004H07 Subtractive cDNA library from laminari...	60	7e-05
dbj	BY912248.1	BY912248 Cryptomeria japonica male strobilus Cry...	60	7e-05
gb	FG610783.1	stem_S064_F03.SEQ Opium poppy stem cDNA library P...	60	7e-05
gb	FG230888.1	pvreacc010002_J13_M13rev_phred13_vc root hairs of...	60	7e-05
gb	FD792211.1	08VNAA8_T7_003_G04_17FEB2006_020 08VNAA8 Phaseolu...	60	7e-05
gb	FD793984.1	08VNAA8_T7_031_G10_16MAR2006_068 08VNAA8 Phaseolu...	60	7e-05
gb	EX135466.1	BR119296 root cDNA library KHRT Brassica rapa sub...	60	7e-05
gb	EX114527.1	BR100817 whole plant cDNA library KFYP Brassica r...	60	7e-05
gb	EX032022.1	BR016666 callus cDNA library KBCG Brassica rapa s...	60	7e-05
gb	EL424106.1	CHCM3704.b1_014.ab1 CHC(LMS) Texas blueweed Helia...	60	7e-05
gb	EL362738.1	CCEM7256.b1_P14.ab1 CCE(LMS) endive Cichorium end...	60	7e-05
gb	EL022129.1	EBENXNS02I7QWK 8-day Arabidopsis seedlings, aeria...	60	7e-05
gb	EH665640.1	24E09 Transformed tobacco Lambda Zap II library N...	60	7e-05
gb	EC927161.1	WIN0214.TB24_N12 Cab Sauv flower, leaf and root n...	60	7e-05
gb	DW520518.1	GH_TMIRS_241_D04_F Cotton Normalized Library dT p...	60	7e-05
dbj	BW994485.1	BW994485 Cryptomeria japonica male cone Cryptome...	60	7e-05
dbj	BW990328.1	BW990328 Chamaecyparis obtusa cambium and surrou...	60	7e-05
gb	DV857611.1	col4871 Colonial bentgrass EST Agrostis capillari...	60	7e-05
gb	DV127237.1	CV03047B1C06.f1 CV03-normalized library Euphorbia...	60	7e-05
gb	DV126025.1	CV03044A1B02.f1 CV03-normalized library Euphorbia...	60	7e-05

gb	DT512242.1	WS02418.B21_L24 PTxD-ICC-N-A-14 Populus trichocar...	60	7e-05
gb	DT507614.1	WS02418.BR_L24 PTxD-ICC-N-A-14 Populus trichocarp...	60	7e-05
gb	DT492311.1	WS02550.C21_F01 PT-MB-N-A-15 Populus trichocarpa ...	60	7e-05
gb	DT487692.1	WS02534.B21_G10 PT-MB-N-A-15 Populus trichocarpa ...	60	7e-05
gb	DT487423.1	WS02533.B21_K13 PT-MB-N-A-15 Populus trichocarpa ...	60	7e-05
gb	DT483262.1	WS02522.B21_B19 PT-MB-N-A-15 Populus trichocarpa ...	60	7e-05
gb	DT482024.1	WS02533.BR_K13 PT-MB-N-A-15 Populus trichocarpa c...	60	7e-05
gb	DT478196.1	WS02522.BR_B19 PT-MB-N-A-15 Populus trichocarpa c...	60	7e-05
gb	CX169952.1	B06_69-16_04.ab1 leaf inoculated with Marssonina p...	60	7e-05
gb	CV278268.1	WS0145.B21_O21 PTxD-IL-A-5 Populus trichocarpa x ...	60	7e-05
gb	CV277650.1	WS0144.B21_C22 PTxD-IL-A-5 Populus trichocarpa x ...	60	7e-05
gb	CV131018.1	L1P03d05 Populus stem seasonal library Populus de...	60	7e-05
gb	CN848150.1	PG07006D08 Ginseng cDNA library from MeJA treated...	60	7e-05
gb	CK288635.1	EST751357 Nicotiana benthamiana mixed tissue cDNA...	60	7e-05
gb	CK258594.1	EST742231 potato callus cDNA library, normalized ...	60	7e-05
gb	CK255769.1	EST739406 potato callus cDNA library, normalized ...	60	7e-05
gb	CK255201.1	EST738838 potato callus cDNA library, normalized ...	60	7e-05
gb	CK244542.1	EST728179 potato callus cDNA library, normalized ...	60	7e-05
gb	CK244541.1	EST728178 potato callus cDNA library, normalized ...	60	7e-05
gb	CA992234.1	HC0822 GIBCOBRL CAT. NO. 19643-014 Brassica rapa ...	60	7e-05
gb	CA296237.1	SCAGLV1043F09.g LV1 Saccharum officinarum cDNA cl...	60	7e-05
dbj	BP175580.1	BP175580 Cryptomeria japonica inner bark Cryptom...	60	7e-05
gb	AI054926.1	coau0002I16 Cotton Boll Abscission Zone cDNA Libr...	60	7e-05
dbj	FS184353.1	FS184353 Solanum lycopersicum cv Micro-Tom root ...	58	3e-04
dbj	FS185438.1	FS185438 Solanum lycopersicum cv Micro-Tom root ...	58	3e-04
gb	GD111776.1	KS23009A10 KS23 Capsicum annuum cDNA, mRNA sequence	58	3e-04
gb	GE508830.1	CCFT6761.b1_A12.ab1 CCF(STU) sunflower Helianthus...	58	3e-04
gb	GE507030.1	CCFT5541.g1_J17.ab1 CCF(STU) sunflower Helianthus...	58	3e-04
gb	GE507029.1	CCFT5541.b1_J17.ab1 CCF(STU) sunflower Helianthus...	58	3e-04
gb	ES294238.1	_08Y_C12 Bermudagrass Normalized cDNA Library Cyn...	58	3e-04
gb	GD594567.1	454PCS0222258 Scarlet Runner Bean globular-stage ...	58	3e-04
gb	FG509216.1	030312KAPC001477HT (KAPC) Actinidia eriantha peta...	58	3e-04
gb	FG486094.1	021104KAUB001004HT (KAUB) Actinidia chinensis CK5...	58	3e-04
gb	FG486083.1	021015KAUB999084HT (KAUB) Actinidia chinensis CK5...	58	3e-04
gb	ES595125.1	000001603252_M19.ab1 Eucalyptus globulus under lo...	58	3e-04
gb	EY948213.1	RS3DN57TF RS3(RT) Raphanus sativus cDNA 5', mRNA ...	58	3e-04
gb	EY063068.1	CATF7534.fwd CATF Artemisia annua, Tanzanian, fro...	58	3e-04
gb	EY063067.1	CATF7534.rev CATF Artemisia annua, Tanzanian, fro...	58	3e-04
gb	EY091175.1	CAZI19752.rev CAZI Artemisia annua normalized lea...	58	3e-04
gb	EX515663.1	Hops-Column-29R_2007-06-04/Hops-Column-29R_F02_00...	58	3e-04
gb	DN965021.1	218e04 longbai no.2 one month old leaves Brassica...	58	3e-04
gb	EL434417.1	CHTL1481.b2_B12.ab1 CHT (LMS) Jerusalem artichoke ...	58	3e-04
gb	EL425067.1	CHCM4607.b1_N24.ab1 CHC (LMS) Texas blueweed Helia...	58	3e-04
gb	EL424239.1	CHCM3838.b1_L24.ab1 CHC (LMS) Texas blueweed Helia...	58	3e-04
gb	DY012178.1	40JKME7D_UP_003_D09_25MAR2004_073 40JKME7D Brassi...	58	3e-04
gb	DT212598.1	E002_B10 Embryogenic SSH library Cichorium intybu...	58	3e-04
gb	DT014039.1	VVH007H01_739521 CabSau Flower Nectary Stage 25 (...)	58	3e-04
gb	DT010226.1	VVH055D09_748099 CabSau Flower Nectary Stage 25 (...)	58	3e-04
gb	DR929061.1	EST1120600 Aquilegia cDNA library Aquilegia formo...	58	3e-04

gb DR742871.1	RTCU1_7_C01.g2_A029	Roots plus added copper Pinus...	58	3e-04
gb DR742794.1	RTCU1_7_C01.b2_A029	Roots plus added copper Pinus...	58	3e-04
gb DR094964.1	STRR1_17_H08.g1_A033	Stem Response Resistant Pinu...	58	3e-04
gb DR094953.1	STRR1_17_G08.g1_A033	Stem Response Resistant Pinu...	58	3e-04
gb DR094872.1	STRR1_17_G08.b1_A033	Stem Response Resistant Pinu...	58	3e-04
gb DR090538.1	RTAL1_15_F06.g1_A029	Roots plus added aluminum Pi...	58	3e-04
gb DR090469.1	RTAL1_15_F06.b1_A029	Roots plus added aluminum Pi...	58	3e-04
gb DR089595.1	RTAL1_9_E05.g1_A029	Roots plus added aluminum Pin...	58	3e-04
gb DR088958.1	RTAL1_5_E09.g1_A029	Roots plus added aluminum Pin...	58	3e-04
gb DR023270.1	STRS1_56_B11.g1_A034	Shoot tip pitch canker susce...	58	3e-04
gb DR021354.1	STRS1_44_C09.b1_A034	Shoot tip pitch canker susce...	58	3e-04
gb CX658976.1	P001024H07	Poplar SC cDNA library Populus alba x ...	58	3e-04
gb C0499512.1	G.h.fbr-sw08902	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0498821.1	G.h.fbr-sw08211	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0498720.1	G.h.fbr-sw08110	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0496527.1	G.h.fbr-sw05917	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0494300.1	G.h.fbr-sw03690	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb C0491848.1	G.h.fbr-sw01238	G.h.fbr-sw Gossypium hirsutum cDN...	58	3e-04
gb CV094175.1	FAMU_USDA_FP_2198	Vitis shuttleworthii L., grape ...	58	3e-04
emb AJ805072.1	AJ805072	Antirrhinum majus whole plant Antirrhin...	58	3e-04
emb AJ795563.1	AJ795563	Antirrhinum majus whole plant Antirrhin...	58	3e-04
emb AJ795101.1	AJ795101	Antirrhinum majus whole plant Antirrhin...	58	3e-04
emb AJ793569.1	AJ793569	Antirrhinum majus whole plant Antirrhin...	58	3e-04
gb C0200887.1	RTCNT2_2_F01.b1_A029	Root control 2 (late) Pinus ...	58	3e-04
gb CN604982.1	USDA_FP_132082	Vitis shuttleworthii L., grape Vit...	58	3e-04
gb CN604205.1	USDA_FP_131305	Vitis shuttleworthii L., grape Vit...	58	3e-04
gb CF476953.1	RTWW3_4_G10.g1_A022	Well-watered loblolly pine ro...	58	3e-04
gb CF401192.1	RTWW1_10_H07.g1_A015	Well-watered loblolly pine r...	58	3e-04
gb CF401118.1	RTWW1_10_H07.b1_A015	Well-watered loblolly pine r...	58	3e-04
gb CF400173.1	RTWW1_3_F07.g1_A015	Well-watered loblolly pine ro...	58	3e-04
gb CF400086.1	RTWW1_3_F07.b1_A015	Well-watered loblolly pine ro...	58	3e-04
gb CF387460.1	RTDR1_20_H12.b1_A015	Loblolly pine roots recoveri...	58	3e-04
gb CF387171.1	RTDR1_11_H09.b1_A015	Loblolly pine roots recoveri...	58	3e-04
gb CF387078.1	RTDR1_10_H09.g1_A015	Loblolly pine roots recoveri...	58	3e-04

>gb|CX703225.1| gmrtDrNS01_14-B_M13R_D10_074.s2 Water stressed 5h segment 2
gmrtDrNS01 Glycine max cDNA 3', mRNA sequence
Length = 743

Score = 1070 bits (540), Expect = 0.0
Identities = 543/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 640 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 581

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagAACATcaggg 1908
|||||
Sbjct: 580 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagAACATcaggg 521

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 520 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 461

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 460 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 401

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 2088
|||||
Sbjct: 400 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 341

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 340 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 281

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 280 gaaatcaggaagaattgtagaaggattaactaatttaattcagtccttgaatattaagggt 221

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 2268
|||||
Sbjct: 220 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 161

Query: 2269 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 2328
|||||
Sbjct: 160 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 101

Query: 2329 tccc 2332
||||
Sbjct: 100 tccc 97

Score = 210 bits (106), Expect = 3e-50
Identities = 106/106 (100%)
Strand = Plus / Minus

Query: 1540 tgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatt 1599
|||||
Sbjct: 743 tgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatt 684

Query: 1600 tagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645
|||||
Sbjct: 683 tagcgctcttggactttccaccaaggacttggtcgccttgtccggt 638

Score = 79.8 bits (40), Expect = 7e-11
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 40 tcctttatcaagcatttatcaagaacggagtttgcttttt 1

>gb|CX709633.1| gmrtDrNS01_10-D_M13R_A04_032.s2 Water stressed 5h segment 2
gmrtDrNS01 Glycine max cDNA 3', mRNA sequence
Length = 791

Score = 1063 bits (536), Expect = 0.0
Identities = 542/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 640 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 581

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 580 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 521

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 520 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 461

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 460 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 401

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 400 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttttcctct 341

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||

Sbjct: 340 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 281

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||

Sbjct: 280 gaaatcaggaagaattgtagaaggattaactaatttaattcagtccttgaatattaagggt 221

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 2268
|||||

Sbjct: 220 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 161

Query: 2269 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 2328
|||||

Sbjct: 160 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 101

Query: 2329 tccc 2332
||||

Sbjct: 100 tccc 97

Score = 297 bits (150), Expect = 2e-76

Identities = 153/154 (99%)

Strand = Plus / Minus

Query: 1492 atggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaaca 1551
|||||

Sbjct: 791 atggaatgttaaacttggaagaagagacgctagaattgctagccaatctgctgctaaca 732

Query: 1552 tggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgg 1611
|||||

Sbjct: 731 tggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgg 672

Query: 1612 actttccaccaaggacttggtcgcttgtccggt 1645
|||||
Sbjct: 671 actttccaccaaggacttggtcgcttgtccggt 638

Score = 79.8 bits (40), Expect = 7e-11
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 40 tcctttatcaagcatttatcaagaacggagtttgcttttt 1

>gb|CF807990.1| psHB031xA07f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB031A07 5, mRNA sequence
Length = 708

Score = 1059 bits (534), Expect = 0.0
Identities = 543/545 (99%), Gaps = 1/545 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 149 ggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacgag 208

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 209 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 268

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 269 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 328

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 329 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 388

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 389 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 448

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 449 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 508

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 509 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 568

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaaacat-gttttggtt 2267
|||||
Sbjct: 569 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaaacatggttttggtt 628

Query: 2268 gtattttgattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctac 2327
|||||
Sbjct: 629 gtattttgattcctagtgtagnttcggtgatcaatgccgtctactttagtgtgttctac 688

Query: 2328 ttccc 2332
|||||
Sbjct: 689 ttccc 693

Score = 299 bits (151), Expect = 4e-77
Identities = 151/151 (100%)
Strand = Plus / Plus

Query: 1495 gaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatgg 1554
|||||
Sbjct: 1 gaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatgg 60

Query: 1555 catccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgact 1614
|||||
Sbjct: 61 catccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgact 120

Query: 1615 ttccaccaaggacttggctgccttgtccggt 1645
|||||
Sbjct: 121 ttccaccaaggacttggctgccttgtccggt 151

>gb|BG509781.1| sad25h05.y1 Gm-c1074 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1074-1498 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 493

Score = 924 bits (466), Expect = 0.0
Identities = 472/474 (99%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 20 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 79

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 80 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagatcatcaggg 139

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 140 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 199

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 200 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 259

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 2088
|||||
Sbjct: 260 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 319

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||
Sbjct: 320 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 379

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 380 gaaatcaggaagaattgtagaaggattaactaatttaattcagtccttgaatattaagggt 439

Query: 2209 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgttt 2262
|||||
Sbjct: 440 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgttt 493

Score = 44.1 bits (22), Expect = 4.0
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1624 ggacttggtcgccttgtccggt 1645
 |||||
Sbjct: 1 ggacttggtcgccttgtccggt 22

>gb|BM731124.1| sal68a04.y1 Gm-cl061 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-cl061-4231 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
 ;, mRNA sequence
 Length = 506

Score = 894 bits (451), Expect = 0.0
Identities = 454/455 (99%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
 |||||
Sbjct: 52 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 111

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
 |||||
Sbjct: 112 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 171

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
 |||||
Sbjct: 172 tcagaggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 231

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
 |||||
Sbjct: 232 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 291

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 2088
 |||||
Sbjct: 292 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 351

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
 |||||
Sbjct: 352 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 411

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 412 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 471

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaat 2243
|||||
Sbjct: 472 cctacacatacgcaagcaatttaattgtgtttaat 506

Score = 107 bits (54), Expect = 3e-19
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1592 tcaagatttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 1 tcaagatttagcgctcttggactttccaccaaggacttggcgccttgtccggt 54

>gb|BG882707.1| sae51e08.y2 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl051-8679 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 483

Score = 880 bits (444), Expect = 0.0
Identities = 444/444 (100%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948
|||||
Sbjct: 1 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 60

Query: 1949 caaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctcctccact 2008
|||||
Sbjct: 61 caaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctcctccact 120

Query: 2009 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 2068
|||||
Sbjct: 121 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 180

Query: 2069 acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 2128

|||||
Sbjct: 181 acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 240

Query: 2129 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatttgatt 2188
|||||

Sbjct: 241 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatttgatt 300

Query: 2189 cagtcttgaatattaagggtcctacacatacgcaagcaatttaattgtgtttaataagtt 2248
|||||

Sbjct: 301 cagtcttgaatattaagggtcctacacatacgcaagcaatttaattgtgtttaataagtt 360

Query: 2249 gttaaaacatgttttggttgatcttggattcctagtgtagtttcggtgatcaatgccgt 2308
|||||

Sbjct: 361 gttaaaacatgttttggttgatcttggattcctagtgtagtttcggtgatcaatgccgt 420

Query: 2309 ctacttttagtgtgttctacttccc 2332
|||||

Sbjct: 421 ctacttttagtgtgttctacttccc 444

>gb|EV267121.1| GLLBF04TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 719

Score = 731 bits (369), Expect = 0.0
Identities = 467/498 (93%), Gaps = 5/498 (1%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||

Sbjct: 113 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 172

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
| |||||

Sbjct: 173 agcaacatagacaccgcatttgcaaggacaaggcaaaaagctgccaagaacatcaggg 232

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||

Sbjct: 233 tcaggggacaataatcttgcgacgcttgatcttcaaactccaaccgaattcgacaactac 292

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 293 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 352

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||||

Sbjct: 353 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgagctccttctcctct 412

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|| |||||

Sbjct: 413 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaacgga 472

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagtccttgaatattaagg 2206
|||||||

Sbjct: 473 gaaatcaggaagaattgtagaaggattaactaattactaattgagtcctcaatattaagg 532

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaacaatgtttt 2263
||| |||||

Sbjct: 533 gtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaacaatgtttt 592

Query: 2264 ggttgtattttggattcc 2281
|||||

Sbjct: 593 ggttgtgttttggattcc 610

Score = 210 bits (106), Expect = 3e-50

Identities = 112/114 (98%)

Strand = Plus / Plus

Query: 1532 agccaatctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatc 1591
|||||||

Sbjct: 2 agccaatctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatc 61

Query: 1592 tcaagatttagcgctcttggactttccaccaaggacttggtcgccttgtccgggt 1645
|||||||

Sbjct: 62 tcaagattcagcgctcttggactttccaccaaggacttggtcgccttgtccgggt 115

>gb|CF806428.1| psHB011xI05f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB011I05 5, mRNA sequence
Length = 606

Score = 646 bits (326), Expect = 0.0
Identities = 415/443 (93%), Gaps = 5/443 (1%)
Strand = Plus / Minus

Query: 1844 acgagaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacat 1903
||||| ||||||| ||||||||||||||| |||| ||||||||||| |||||||
Sbjct: 606 acgagagcaacatagacaccgcatttgcaaggacaaggcaacaaagctgccaagaacat 547

Query: 1904 cagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgaca 1963
|||||||||||||| |||| |||| ||||||||||||||||||| || |||||
Sbjct: 546 cagggtcaggggacaataatcttgaccgcttgatcttcaaactccaaccgaattcgaca 487

Query: 1964 actactacttcaagaacctcggtcagaagaagggtctcctccactctgatcagcaactgt 2023
|||||||||||||| | |||||||||||||||||||||||||||||||
Sbjct: 486 actactacttcaagaatcttggtcagaagaagggtctcctccactctgatcagcaactgt 427

Query: 2024 tcaacgggtgggtccaccgactccattgtgcgtgggtacagcaccaaccgggcaccttct 2083
|||| ||||||||||||||||||||||||||||||||||| || |||||||
Sbjct: 426 tcaatgggtgggtccaccgactccattgtgcgtgggtacagcaccaaccgagctccttct 367

Query: 2084 cctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtcca 2143
||||||| |||||||||||||||||||||||||||||||||||
Sbjct: 366 cctctgacttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtcca 307

Query: 2144 atggagaaatcaggaagaattgtagaaggattaactaatt--tgattcagtccttgaatat 2201
| ||||||||||||||||||||||||||||||| | ||| ||||| |||||||
Sbjct: 306 acggagaaatcaggaagaattgtagaaggattaactaattactaattgagtcctcgaatat 247

Query: 2202 taagggtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaaacat 2258
||||||| |||||||||||||||||||||||||||||||
Sbjct: 246 taagggtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaaacat 187

Query: 2259 gttttggttgatttttgattcc 2281
||||||||| |||||||
Sbjct: 186 gttttggttgatttttgattcc 164

Score = 63.9 bits (32), Expect = 4e-06
Identities = 38/40 (95%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
||||||| ||||||| |||||||
Sbjct: 41 tcctttatcaagaatttatcaagaacagagtttgcttttt 2

>gb|AW349107.1| GM210004A21E9 Gm-r1021 Glycine max cDNA clone Gm-r1021-1362 3', mRNA
sequence
Length = 609

Score = 626 bits (316), Expect = e-175
Identities = 449/498 (90%), Gaps = 5/498 (1%)
Strand = Plus / Minus

Query: 1789 ggtgggtcacacaattggacaaggaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||||||| ||||||| |||||||
Sbjct: 604 ggtgggtcacacaannnnacaaggaaggtgcacnannnnnngagcccgcanctacaacgag 545

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
| ||||||| ||||||| ||||||| |||||||
Sbjct: 544 agcaacatagannncgcatttgcaaggacaaggcaacaaagctgccaagaacatcaggg 485

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||| ||||| || | ||||||| ||||||| || ||| ||||
Sbjct: 484 tcaggggacaataatcttgcaacgcttgatcttcaaactccaaccgaattcgacnnctac 425

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||| || ||||| ||||||| ||||||| |||||||
Sbjct: 424 tacttcaagaatcttggttcaaaagaagggtctcctccactctgatcagcnctgttcaat 365

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
||||||| ||||||| ||||||| ||||||| || |||||||
Sbjct: 364 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgagctccttctcctct 305

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|| ||||||| ||||||| ||||||| |||||
Sbjct: 304 gacttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaacgga 245

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagtcttgaatattaagg 2206
||||||| ||||||| ||||||| ||||| |||||
Sbjct: 244 gaaatcaggaagaattgtagaaggattaactaattactaattgagtcctccaatattaagg 185

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaaacatgtttt 2263
||| ||||||||||||||||||||||||||||||||||||||||
Sbjct: 184 gtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaaacatgtttt 125

Query: 2264 ggttgtattttggattcc 2281
||||| |||||||||
Sbjct: 124 ggttgtgttttggattcc 107

>gb|BG156628.1| sab31a07.y1 Gm-c1026 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1026-3086 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 425

Score = 618 bits (312), Expect = e-173
Identities = 325/328 (99%), Gaps = 1/328 (0%)
Strand = Plus / Plus

Query: 2005 cactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagc 2064
||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3 cactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagc 62

Query: 2065 accaaccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacatt 2124
|||||||||||||||||||||||||||||||||||||||
Sbjct: 63 accaaccgggcaccttctcctctgatttcgccgccgc-atgatcaagatgggagacatt 121

Query: 2125 agtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaattt 2184
|||||||||||||||||||||||||||||||||||||||
Sbjct: 122 agtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaattt 181

Query: 2185 gattcagtccttgaatattaagggtcctacacatacgaagcaatttaattgtgtttaata 2244
||||||||||||||||||||||||||| |||||||||||||
Sbjct: 182 aattcagtccttgaatattaagggtcctacacatacgcagcaatttaattgtgtttaata 241

Query: 2245 agttgttaaaacatgttttggttgtattttggattcctagtgtagtttcggtgatcaatg 2304
||||||||||||||||||||||||||| |||||||||||||
Sbjct: 242 agttgttaaaacatgttttggttgtattttggattcctagtgtagtttcggtgatcaatg 301

Query: 2305 ccgtctacttttagtgtgttctacttccc 2332
|||||||||||||||||||

Sbjct: 302 ccgtctacttttagtgtgttctacttccc 329

>gb|FK018609.1| GLND133TF JCVI-SOY3 Glycine max cDNA 5', mRNA sequence
Length = 464

Score = 557 bits (281), Expect = e-154
Identities = 291/293 (99%), Gaps = 1/293 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgag 1848
|||||
Sbjct: 172 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgag 231

Query: 1849 accaacaatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 232 accaacaatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 291

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 292 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 351

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 352 tacttcaaggacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 411

Query: 2029 ggtgggtccaccgactcca-ttgtgcgtggctacagcaccaaccgggcacct 2080
|||||
Sbjct: 412 ggtgggtccaccgactccatttgcgtggctacagcaccaaccgggcacct 464

Score = 333 bits (168), Expect = 3e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgtagccaa 1537
|||||
Sbjct: 7 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgtagccaa 66

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 67 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 126

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645

|||||

Sbjct: 127 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 174

>gb|BU577048.1| sar71e12.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-7896 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 432

Score = 545 bits (275), Expect = e-151
Identities = 376/408 (92%), Gaps = 5/408 (1%)
Strand = Plus / Plus

Query: 1879 aggcagcaaagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgat 1938

|||||

Sbjct: 1 aggcaacaaagctgcccaagaacatcagggtcaggggacaataatcttgcaacgcttgat 60

Query: 1939 cttcaaactccaaccagctttgacaactactacttcaagaacctcggtcagaagaagggt 1998

|||||

Sbjct: 61 cttcaaactccaaccgaattcgacaactactacttcaagaatcttgttcagaagaagggt 120

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggc 2058

|||||

Sbjct: 121 ctctccactctgatcagcaactgttcaatgggtgggtccaccgactccattgtgcgtggc 180

Query: 2059 tacagcaccaacccgggcaccttctcctctgatttcgccgccgcatgatcaagatggga 2118

|||||

Sbjct: 181 tacagcaccaacttttttcttctcctctgacttcgccgccgcatgatcaagatggga 240

Query: 2119 gacattagtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaac 2178

|||||

Sbjct: 241 gacattagtcctctcactggctccaacggagaaatcaggaagaattgtagaaggattaac 300

Query: 2179 taatt--tgattcagtccttgaatattaagggtc---ctacacatacgcaagcaatttaac 2233

|||||

Sbjct: 301 taattactaattgagtcctcaatattaagggtcctactacacatacgcaagcaatttaac 360

Query: 2234 tgtgtttaataagttgttaaaacatgttttggttgatatttgattcc 2281

|||||
Sbjct: 361 tgtgtttaataagttgttaaacaatgttttggttggttttgattcc 408

>gb|BM093025.1| saj04a09.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl065-9257 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE ;, mRNA sequence
Length = 568

Score = 527 bits (266), Expect = e-145
Identities = 266/266 (100%)
Strand = Plus / Plus

Query: 519 atcaaacacaaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 578
|||||
Sbjct: 1 atcaaacacaaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 60

Query: 579 gttttgttctagattgacaatttgttggctctgtttgtcctcatatgggggagtgccaa 638
|||||
Sbjct: 61 gttttgttctagattgacaatttgttggctctgtttgtcctcatatgggggagtgccaa 120

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698
|||||
Sbjct: 121 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 180

Query: 699 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 758
|||||
Sbjct: 181 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 240

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 241 gttcttccacgattgctttgtcaatg 266

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 266 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 325

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||||
Sbjct: 326 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 385

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 386 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 445

Query: 1337 tctgttcagatt 1348
|||||||
Sbjct: 446 tctgttcagatt 457

Score = 218 bits (110), Expect = 1e-52
Identities = 110/110 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 458 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 517

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaact 1587
|||||||
Sbjct: 518 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaact 567

>gb|BE210375.1| so42h10.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-668 5' similar to TR:024336 024336
KOREAN-RADISH ISOPEROXIDASE ;, mRNA sequence
Length = 520

Score = 527 bits (266), Expect = e-145
Identities = 266/266 (100%)
Strand = Plus / Plus

Query: 519 atcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaattaactatggcttc 578
|||||||
Sbjct: 7 atcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaattaactatggcttc 66

Query: 579 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 638
|||||||

Sbjct: 67 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 126

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698
|||||

Sbjct: 127 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 186

Query: 699 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctccttcgctt 758
|||||

Sbjct: 187 atccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctccttcgctt 246

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||

Sbjct: 247 gttcttccacgattgctttgtcaatg 272

Score = 373 bits (188), Expect = 3e-99
Identities = 191/192 (99%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||

Sbjct: 272 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 331

Query: 1217 aaccccaacaggaactctgctcgatcgaggttattgacaacattaaatcagccgtg 1276
|||||

Sbjct: 332 aaccccaacaggaactctgctcgatcgaggttattgacaacattaaatcagccgtg 391

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 392 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 451

Query: 1337 tctgttcagatt 1348
|||||

Sbjct: 452 tctgttcagatt 463

Score = 97.6 bits (49), Expect = 3e-16
Identities = 55/57 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagc 1534
||||| ||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 464 cttggaagccctacatggaatgttaaacttgaaagaagagacgctagaactgctagc 520

>gb|EV263181.1| GLLA357TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 813

Score = 525 bits (265), Expect = e-145
Identities = 274/277 (98%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567
||||| ||||||||||||||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 3 acaccctttcaatcaaacacaaacactcgaagtactaagttagtgtgttcgagcaaatta 62

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
||||| ||||||||||||||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 63 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 122

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 123 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 182

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttct 747
||||| ||||||||||||||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 183 tcctctgtgaaatccgacagtgcgaatctgccatatctaaggagacccgcatgggtgcttct 242

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||||||||| |||||||||
Sbjct: 243 ctcttcgcttggttcttccacgattgctttgtcaatg 279

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||||||||||||||||||| ||||||||||||||||||||| |||||||||
Sbjct: 279 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 338

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 339 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 398

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 399 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 458

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 459 tctgttcagatt 470

Score = 333 bits (168), Expect = 3e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 471 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 530

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 531 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 590

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 591 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 638

Score = 270 bits (136), Expect = 4e-68
Identities = 178/184 (96%), Gaps = 6/184 (3%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgag 1848
|||||
Sbjct: 636 ggtggtcacacaattggacaagcaag-tgcacaaacttcagagcccgcattctacaacgag 694

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908

|||||
Sbjct: 695 accaacatag-aaccgcatttgcaaggacta-gcagcaaagctgccctagaacatca-gg 751

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||

Sbjct: 752 tcaggggacaacaatctggcaccacttgatcttc-aactccaaccagctttgac-actac 809

Query: 1969 tact 1972

||||
Sbjct: 810 tact 813

>gb|CF806168.1| psHB004x020f USDA-IFAFS:Expression of Phytophthora sojae genes
during infection and propagation Glycine max cDNA clone
sHB004020 5, mRNA sequence
Length = 397

Score = 523 bits (264), Expect = e-144

Identities = 264/264 (100%)

Strand = Plus / Plus

Query: 521 caaacacaaacacttgaagtactaagttagtgtgtttgagcaaattaactatggcttcgt 580
|||||

Sbjct: 9 caaacacaaacacttgaagtactaagttagtgtgtttgagcaaattaactatggcttcgt 68

Query: 581 tttgttctagattgacaattttgtttggctctgtttgtcctcatatgggggagtgccaatg 640
|||||

Sbjct: 69 tttgttctagattgacaattttgtttggctctgtttgtcctcatatgggggagtgccaatg 128

Query: 641 cacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaat 700
|||||

Sbjct: 129 cacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaat 188

Query: 701 ccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgt 760
|||||

Sbjct: 189 ccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgt 248

Query: 761 tttccacgattgctttgtcaatg 784

|||||
Sbjct: 249 tttccacgattgctttgtcaatg 272

Score = 250 bits (126), Expect = 3e-62
Identities = 126/126 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 272 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 331

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 332 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 391

Query: 1277 gagaaa 1282
|||||
Sbjct: 392 gagaaa 397

>gb|BI972311.1| sag89h02.y1 Gm-c1084 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1084-1515 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE ;, mRNA sequence
Length = 573

Score = 502 bits (253), Expect = e-138
Identities = 253/253 (100%)
Strand = Plus / Plus

Query: 532 acttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctaga 591
|||||
Sbjct: 1 acttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctaga 60

Query: 592 ttgacaatttggttgcctctgtttgtcctcatatgggggagtgccaatgcacaactttct 651
|||||
Sbjct: 61 ttgacaatttggttgcctctgtttgtcctcatatgggggagtgccaatgcacaactttct 120

Query: 652 acaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaa 711
|||||
Sbjct: 121 acaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaa 180

Query: 712 tctgccatatctaaggagacccgatgggtgcttctctccttcgcttgttcttccacgat 771
|||||
Sbjct: 181 tctgccatatctaaggagacccgatgggtgcttctctccttcgcttgttcttccacgat 240

Query: 772 tgctttgtcaatg 784
 |||||||
Sbjct: 241 tgctttgtcaatg 253

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||||
Sbjct: 253 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 312

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||||
Sbjct: 313 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 372

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
 |||||||
Sbjct: 373 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 432

Query: 1337 tctgttcagatt 1348
 |||||||
Sbjct: 433 tctgttcagatt 444

Score = 240 bits (121), Expect = 3e-59
Identities = 127/129 (98%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
 |||||||
Sbjct: 445 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 504

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
 |||||||
Sbjct: 505 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 564

Query: 1598 ttttagcgct 1606
|||||||
Sbjct: 565 ttttagcgct 573

>gb|BE209964.1| so37a08.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-111 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 391

Score = 490 bits (247), Expect = e-134
Identities = 247/247 (100%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 114 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 173

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 174 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 233

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 234 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 293

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 294 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 353

Query: 2029 ggtgggt 2035
|||||||
Sbjct: 354 ggtgggt 360

Score = 230 bits (116), Expect = 3e-56
Identities = 116/116 (100%)
Strand = Plus / Plus

Query: 1530 ctagccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactca 1589
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1 ctagccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactca 60

Query: 1590 tctcaagatttagcgctcttggactttccaccaaggacttggtcgcccttggtccggt 1645
|||||
Sbjct: 61 tctcaagatttagcgctcttggactttccaccaaggacttggtcgcccttggtccggt 116

>gb|BG725689.1| sae39d12.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-7487 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 499

Score = 464 bits (234), Expect = e-126
Identities = 285/302 (94%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 197 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 256

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
| |||||
Sbjct: 257 agcaacatagacaccgcatttgaaggacaaggcaacaaagctgccaagaacatcaggg 316

Query: 1909 tcaggggacaacaatcttggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 317 tcaggggacaataatcttgcaccgcttgatcttcaaactccaaccgaattcgacaactac 376

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 377 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 436

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 2088
|||||
Sbjct: 437 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgagctccttctcctct 496

Query: 2089 ga 2090
||
Sbjct: 497 ga 498

Score = 293 bits (148), Expect = 3e-75

Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 32 cttggaggccctagttggaatgttaaagtiggaagaagagacgctagaactgctagccaa 91

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 92 tctgctgctaacaatggcatccctccaccacacttcaaaccttaaccaactcatctcaaga 151

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgcttgtccggt 1645
||
Sbjct: 152 ttcagcgctcttggactttccaccaaggacttggtcgcttgtccggt 199

Score = 50.1 bits (25), Expect = 0.065
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 1319 gccatcgctgccagagactctgttcagat 1347
|||||
Sbjct: 2 gccatagctgccagagactctgttcagat 30

>gb|FG889629.1| UCRVU08_CCNS10828_g1 Cowpea IT97K-461-4 Mixed Tissue and Conditions
cDNA Library UCRVU08-1-2 Vigna unguiculata cDNA clone
CCNS10828.g1, mRNA sequence
Length = 670

Score = 444 bits (224), Expect = e-120
Identities = 341/380 (89%)
Strand = Plus / Minus

Query: 1800 aattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaacataga 1859
|||||
Sbjct: 670 aattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgagagcaacattga 611

Query: 1860 aaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcaggggacaa 1919
|||
Sbjct: 610 tacctcatttgccaggacaagacaatcaagctgccccagaacatcagggtcaggggacaa 551

Query: 1920 caatctggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaagaa 1979
||||||| ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 550 caatctggcaccgcttgatcttcagactccgaccacattcgacaactactacttcaggaa 491

Query: 1980 cctcgttcagaagaaggtctctccactctgatcagcaactgttcaacgggtgggtccac 2039
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 490 cctggttcagaagaaggtctctccactctgaccagcaactcttcaatgggtgggtccac 431

Query: 2040 cgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctctgatttcgccgc 2099
||||||| ||||| ||||| ||||| || ||||| ||||| |||||
Sbjct: 430 tgactccatagtgcgtgggtacagcaccaacccgagctccttttcctctgattttgtctc 371

Query: 2100 cgccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaa 2159
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 370 cgccattatcaagatgggagacattagtcctctcactggctccaaaggagaaatcagaaa 311

Query: 2160 gaattgtagaaggattaact 2179
||| || ||||| |||||
Sbjct: 310 gaactgcagaaggattaact 291

>gb|BE022389.1| sm85b11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-6838 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 571

Score = 438 bits (221), Expect = e-119
Identities = 278/297 (93%)
Strand = Plus / Plus

Query: 1834 cgcactctacaacgagaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgc 1893
||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 6 cgcactctacaacgagagcaacatagacaccgcatttgcaaggacaaggcaacaaagctgc 65

Query: 1894 cctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaacc 1953
|| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 66 ccaagaacatcagggtcaggggacaataatcttgcaacgcttgatcttcaaactccaacc 125

Query: 1954 agctttgacaactactacttcaagaacctcgttcagaagaaggtctcctccactctgat 2013
|| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 126 gaattcgacaactactacttcaagaatcttggttcagaagaaggtctcctccactctgat 185

Query: 2014 cagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccg 2073
|||||||
Sbjct: 186 cagcaactgttcaatgggtgggtccaccgactccattgtgcgtggctacagcaccaaccg 245

Query: 2074 ggcacctttctcctctgatttcgccgcccatgatcaagatgggagacattagtcct 2130
||
Sbjct: 246 agtcctttctcctctgacttcgccgcccatgatcaagatgggagacattagtcct 302

>gb|BG359695.1| sac27d09.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1051-3617 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE :, mRNA sequence
Length = 233

Score = 436 bits (220), Expect = e-118
Identities = 230/232 (99%), Gaps = 1/232 (0%)
Strand = Plus / Plus

Query: 533 cttgaagtactaagttagtgtgtttgagcaaattaactatggcttcgttttgttctagat 592
|||||||
Sbjct: 2 cttgaagtactaagttagtgtgtttgagcaaattaactatggcttc-ttttgttctagat 60

Query: 593 tgacaattttgtttggctctgtttgtcctcatatgggggagtgccaatgcacaactttcta 652
|||||||
Sbjct: 61 tgacaatttttttggctctgtttgtcctcatatgggggagtgccaatgcacaactttcta 120

Query: 653 caaaccttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgaat 712
|||||||
Sbjct: 121 caaaccttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgaat 180

Query: 713 ctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctt 764
|||||||
Sbjct: 181 ctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctt 232

>gb|EV265313.1| GLLAS95TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 652

Score = 412 bits (208), Expect = e-111
Identities = 260/277 (93%), Gaps = 4/277 (1%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567
||||| ||| ||||||||||||||||||||||||||| |||||||
Sbjct: 2 acaccctctcaagcaaacacaaacacttgaagtactaagttagtgtttttagcaaa--- 58

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
||||||||||||||||||||| ||||||||||||||| |
Sbjct: 59 -ctatggcttcgttttgttctagattgaccatttgtttggctctgtttgtcctcatattg 117

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||||||||| ||||||||||||||| ||||||||| |||||||||||
Sbjct: 118 gggagtgccaatgccaaactttctacaaacttctactaccattcgtgtccaaacctcttc 177

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttct 747
||| ||||||||||||||||||| |||||||||||
Sbjct: 178 tccactgtgaaatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttct 237

Query: 748 ctctctcgcttgttcttccacattgctttgtcaatg 784
|||| ||| |||||||||||||||||||
Sbjct: 238 ctctctcgcccggttcttccacattgctttgtcaatg 274

Score = 331 bits (167), Expect = 1e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||||||| |||||||||||||||
Sbjct: 274 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||||||||||||||||| ||||| |||||||||||||||
Sbjct: 334 aaccccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||| ||||||||||||| ||||||||||||||| |||||||||
Sbjct: 394 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 453

Query: 1337 tctgttcagat 1347
|||||||

Sbjct: 454 tctgttcagat 464

Score = 293 bits (148), Expect = 3e-75
Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 466 cttggaggccctagttggaatgttaaagttggaagaagagacgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||||
Sbjct: 526 tctgctgctaacaatggcatccctccacccacttcaaaccttaaccaactcatctcaaga 585

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645
||
Sbjct: 586 ttcagcgctcttggactttccaccaaggacttggtcgccttgtccggt 633

Score = 44.1 bits (22), Expect = 4.0
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaag 1810
|||||||
Sbjct: 631 ggtggtcacacaattggacaag 652

>gb|AW132280.1| se02a03.y1 Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1013-2309 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 552

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 151 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 210

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 211 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 270

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 271 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 330

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 331 tctgttcagatt 342

Score = 325 bits (164), Expect = 7e-85
Identities = 167/168 (99%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 343 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 402

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 403 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 462

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
| |||||
Sbjct: 463 ttagcgctcttggactttccaccaaggacttggcgccttgtccggt 510

Score = 299 bits (151), Expect = 4e-77
Identities = 151/151 (100%)
Strand = Plus / Plus

Query: 634 gccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctct 693
|||||
Sbjct: 1 gccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctct 60

Query: 694 gtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctcctt 753

|||||
Sbjct: 61 gtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctcctt 120

Query: 754 cgcttggttcttccacgattgctttgtcaatg 784

|||||
Sbjct: 121 cgcttggttcttccacgattgctttgtcaatg 151

Score = 83.8 bits (42), Expect = 5e-12
Identities = 44/45 (97%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcc 1833

|||||
Sbjct: 508 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcc 552

>gb|CF809087.1| psHB042xH14f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB042H14 5, mRNA sequence
Length = 364

Score = 373 bits (188), Expect = 3e-99
Identities = 188/188 (100%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

|||||
Sbjct: 177 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 236

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908

|||||
Sbjct: 237 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 296

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

|||||
Sbjct: 297 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 356

Query: 1969 tacttcaa 1976

|||||
Sbjct: 357 tacttcaa 364

Score = 333 bits (168), Expect = 3e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 12 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 71

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 72 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 131

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 132 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 179

>gb|BU577870.1| sar93g05.y1 Gm-cl074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl074-9922 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 426

Score = 373 bits (188), Expect = 3e-99
Identities = 231/245 (94%), Gaps = 4/245 (1%)
Strand = Plus / Plus

Query: 540 tactaagttagtgtgtttgagcaaattaactatggcttcgttttgttctagattgacaat 599
|||||
Sbjct: 1 tactaagttagtgtttttagcaaa----ctatggcttcgttttgttctagattgaccat 56

Query: 600 ttgtttggctctgtttgtcctcatatgggggagtccaatgcacaactttctacaaactt 659
|||||
Sbjct: 57 ttgtttggctctgtttgtcctcatattgggggagtccaatgcccaactttctacaaactt 116

Query: 660 ttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgaatctgccat 719
|||||
Sbjct: 117 ctactaccattcgtgtccaaacctcttctccactgtgaaatccacagtgaatctgccat 176

Query: 720 atctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgt 779
||| |||||

Sbjct: 177 atcaaaggagaccgcgatgggtgcttctctctccgcctgttcttccacgattgctttgt 236

Query: 780 caatg 784

|||||

Sbjct: 237 caatg 241

Score = 321 bits (162), Expect = 1e-83

Identities = 180/186 (96%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct: 241 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 300

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||

Sbjct: 301 aaccccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 360

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

||||||| ||||||||||||| ||||||||||||||||||||||| |||||||||||

Sbjct: 361 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 420

Query: 1337 tctgtt 1342

|||||

Sbjct: 421 tctgtt 426

>gb|AW432575.1| sh76b11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1015-5686 5' similar to SW:PERX_BRARA P00434

PEROXIDASE P7 ;, mRNA sequence

Length = 313

Score = 361 bits (182), Expect = 1e-95

Identities = 263/290 (90%)

Strand = Plus / Plus

Query: 1791 tggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagac 1850

||||| ||||||||||||||||| |||||||||||||||||||||||||||||||||

Sbjct: 1 tggtcgcacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagac 60

Query: 1851 caacatagaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtc 1910
|||| | ||| ||||| ||| ||||| |||| | ||||| ||||| |||||
Sbjct: 61 caacgtagagaccgcattggcatggactaggcggcaaaactgccctagaacatcagggtc 120

Query: 1911 aggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactacta 1970
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 121 aggggacagcaatctggcaccacttgataacttaaaactccgacatagtatgacaactagta 180

Query: 1971 cttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacgg 2030
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 181 cttgtagaacctcggttcataagaagggtctcctccactctgatcagcaactgttcaacgg 240

Query: 2031 tgggtccaccgactccattgtgcgtggctacagcaccaaccgggcacct 2080
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 241 tgggtccaccgactccgttgtgcgtggctacagcagcagcccgggcacct 290

>gb|FG825601.1| UCRVU04_CCNI8859_g1 Cowpea 524B Mixed Tissue and Conditions cDNA
Library UCRVU04-1-2 Vigna unguiculata cDNA clone
CCNI8859.g1, mRNA sequence
Length = 604

Score = 343 bits (173), Expect = 3e-90
Identities = 263/293 (89%)
Strand = Plus / Minus

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 589 aagctgccccagaacatcagggtcaggggacaacaatctggccccgcttgatcttcagac 530

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctcca 2006
||| ||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 529 tccgaccacattcgacaactactacttcaggaacctggttcagaagaagggtcttctcca 470

Query: 2007 ctctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcac 2066
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 469 ctctgaccagcaactcttcaatggtggtccactgactccatagtgcgtggctacagcac 410

Query: 2067 caaccgggcacctttctcctctgatttcgccgccgcatgatcaagatgggagacattag 2126
||||| || |||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 409 caaccgaagctcctttcctctgattttgtctccgcatatcaagatgggagacattag 350


```
Query: 2127 tcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaact 2179
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 349 tcccctcactggctccaaaggagaaatcagaaagaactgcagaaggattaact 297
```

>gb|FF387035.1| M00BI56TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 502

Score = 335 bits (169), Expect = 8e-88
Identities = 262/293 (89%)
Strand = Plus / Plus

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946
 |||||
 Sbjct: 31 aagctgccccagaacaccagggtcaggggacaacaatctggcaccgcttgatcttcagac 90

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctctcca 2006
||| ||| | | | | | | | | | | | | | | | | | | | |
Sbjct: 91 tccgaccacattcgacaactactacttcaggaacctgggtcagaagaagggtcttctcca 150

```
Query: 2007 ctctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcac 2066
          ||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 151 ctctgaccagcaactcttcaatgggtggctccactgactccatagtgcgtggctacagcac 210
```

```
Query: 2067 caaccgggcaccttctctctgatttcgccgcccatgatcaagatgggagacattag 2126
          |||||  || |||| ||||| ||| | ||||| ||||| ||||| |||||
Sbjct: 211  caaccgaagctccttttctctgatttgcctccgcattatcaagatgggagacattag 270
```

```
Query: 2127 tcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaact 2179
      ||| |||| |||||| ||||||||| |||| | | |||||||||
Sbjct: 271 tcccctcaccggctccaaaggagaaatcagaaagaactgcagaaggattaact 323
```

```
>gb|BE807926.1| ss31hl2.y1 Gm-c1061 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
      Gm-c1061-384 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;,
      mRNA sequence
      Length = 634
```

Score = 331 bits (167), Expect = 1e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 122 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 181

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 182 aaccccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 241

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 242 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 301

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 302 tctgttcagat 312

Score = 281 bits (142), Expect = 1e-71
Identities = 159/165 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 314 cttggaggccctagttggaatgttaaagttggaagaagagacgctagaactgctagccaa 373

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 374 tctgctgctaacaatggcatccctccacccacttcaaaccttaaccaactcatctcaaga 433

Query: 1598 tttagcgtcttggactttccaccaaggacttggcgccttgtcc 1642
|| |||||
Sbjct: 434 ttcagcgtcttggactntccaccaaggacttggcgccttgtcc 478

Score = 202 bits (102), Expect = 7e-48
Identities = 117/122 (95%)
Strand = Plus / Plus

Query: 663 ctaccattcatgtccaaaccttctctctctgtgaaatccacagtgaatctgcatatc 722
|||||

Sbjct: 1 ctaccattcgtgtccaaacctcttctccactgtgaaatccacagtgcaatctgccatatc 60

Sbjct: 61 aaaggagaccgcgcatgggtgcttctctcctccgcctgttcttccacgattgctttgtcaa 120

Sbjct: 121 tg 122

Query: 1790 gtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgaga 1849

Query: 1850 ccaacatagaaaccgcatttgcaggactaggcagcaaagctg-ccctagaacatcaggg 1908

Query: 1909 tcaggggacaa 1919

>gb|FF386168.1| M00BI56TRB M00 Vigna unguiculata cDNA, mRNA sequence
Length = 598

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctcca 2006

Sbjct: 91 tccgaccacattcgacaactactacttcaggaacctggttcagaagaagggtcttctcca 150

Query: 2007 ctctgatcagcaactgttcaa-cggtgggtccaccgactccattgtgcgtggctacagca 2065
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 151 ctctgaccagcaactcttcaataggtggctccactgactccatagtgcgtggctacagca 210

Query: 2066 ccaacccgggcacettctcctctgatttcgccgccgcatgatcaagatgggagacatta 2125
||||| || |||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 211 ccaaccaagctccttttctctgattttgtctccgcattatcaagatgggagacatta 270

Query: 2126 gtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaact 2179
|||| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| |||||

Sbjct: 271 gtccctcaccggtccaaaggagaaatcagaagaactgcagaaggattaact 324

>gb|AI441922.1| sa51f09.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1004-2850 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 480

Score = 291 bits (147), Expect = 1e-74
Identities = 165/171 (96%)
Strand = Plus / Plus

Query: 1177 attggatgacacatcaagcttcaccggagagaagaacgcaaaccccaacaggaactctgc 1236
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 6 attggatgacacatcaagcttcaccggagagaagaacgcaaaccccaacaggaactctgc 65

Query: 1237 tcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtccaggagt 1296
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 66 tcgtggatacagaggtcattgacaacattaaatcagccgtggagaaagcatgtccaggagt 125

Query: 1297 tgtttcctgcgcagatatccttgccatcgctgccagagactctgttcagat 1347
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 126 tgtctcctgcgcagatatccttgccatagctgccagagactctgttcagat 176

Score = 287 bits (145), Expect = 2e-73
Identities = 160/165 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Sbjct: 178 cttggaggccctagttggaatgttaaagttgaagaagagacgctagaactgctagccaa 237

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 238 tctgctgctaacaatggcatccctccacccacttcaaaccttaaccaactcatctcaaga 297

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtcc 1642
 |||
 Sbjct: 298 ttcagcgctcttggactttccaccaaggacttggtcgccttgtcc 342

Score = 206 bits (104), Expect = 5e-49
Identities = 129/136 (94%), Gaps = 1/136 (0%)
Strand = Plus / Plus

Query: 1790 gtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgaga 1849
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 344 gtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgaga 403

```
Query: 1850 ccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggt 1909
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 404 gcaacatagacaccgcatttgcaaggacaaggcaacaaagctgcccaagaacatca-ggt 462
```

```
Query: 1910 caggggacaacaatct 1925
          |||||
Sbjct: 463  caggggacaataatct 478
```

>gb|G0029196.1| LJMAW92T0 JCVI-LJ2 Lotus japonicus cDNA 3', mRNA sequence
Length = 887

Score = 289 bits (146), Expect = 4e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

```
Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
          ||||||||||||| ||||||||||| ||||| ||||||||| ||||||||| ||
Sbjct: 388 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 329
```

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 328 tacttcaagaacctgggttcagaacaaggcctcctacactccgaccagcaactcttcaac 269

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 268 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcatcttctctct 209

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||
Sbjct: 208 gatttcgcccagcgccatggtcaagatgggagatatcagtcctctcactggatccaacggt 149

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||
Sbjct: 148 gaaatcaggaagaattgcagaa 127

Score = 180 bits (91), Expect = 3e-41
Identities = 160/183 (87%)
Strand = Plus / Minus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 865 tgtgatggttcagttctacttgatgacacatcaagcttcaccgggagaagaatgcaaac 806

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 805 cccaacagaaactctgctcgcggatttgatgttattgacaacatcaagtcagcagtagag 746

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
||
Sbjct: 745 gcagcatgcccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 686

Query: 1340 gtt 1342
|||
Sbjct: 685 gtt 683

Score = 123 bits (62), Expect = 5e-24
Identities = 134/158 (84%)

Strand = Plus / Minus

Query: 1484 ggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgct 1543
||||| ||||||| ||| | ||||||| ||||||| ||||||| ||| ||

Sbjct: 670 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 611

Query: 1544 gctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| |||| | ||||||| ||||||| ||| | ||||||| ||||||| || ||

Sbjct: 610 gccaacacagggcatccctgcacccacttctagcttgagccaactcacctcaaggttcagt 551

Query: 1604 gctcttggactttccaccaaggacttggcgccttgtc 1641
||||| ||||||| ||| ||||||| || |||||

Sbjct: 550 gctcttggactttccagcaaagacttgggttcattgtc 513

>dbj|BP048143.1| BP048143 Lotus corniculatus var. japonicus pods (less than 20 mm in
length) Lotus japonicus cDNA clone SPD052d03_f 3', mRNA
sequence
Length = 472

Score = 289 bits (146), Expect = 4e-74

Identities = 233/262 (88%)

Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| ||||| ||||||| ||||||| ||| ||

Sbjct: 418 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 359

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||| ||||||| ||||||| ||||| ||||| ||||| || ||||||| |||||||

Sbjct: 358 tacttcaagaacctgggttcagaacaaggcctctacactccgaccagcaactcttcaac 299

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
||||| ||||||| ||||||| ||||||| ||||||| ||||| || |||||||

Sbjct: 298 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcatcttctcctct 239

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
||||||| ||||||| ||||||| ||||| ||||||| ||||||| ||||| ||

Sbjct: 238 gatttcgccagcgccatgggtcaagatgggagatatcagtcctctcactgggtccaacggt 179

Query: 2149 gaaatcaggaagaattgtagaa 2170

|||||
Sbjct: 178 gaaatcaggaagaattgcagaa 157

>dbj|BP048038.1| BP048038 Lotus corniculatus var. japonicus pods (less than 20 mm in
length) Lotus japonicus cDNA clone SPD051a08_f 3', mRNA
sequence
Length = 513

Score = 289 bits (146), Expect = 4e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 453 tcaggggacaacaatttggcaccacttgaccttcagactccaacctccttgacaacaac 394

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 393 tacttcaagaacctgggttcagaacaaggcctctacactccgaccagcaactcttcaac 334

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 333 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcatcttctcctct 274

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||
Sbjct: 273 gatttcgccagcgccatgggtcaagatgggagatatcagtcctctcactggatccaacggt 214

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||
Sbjct: 213 gaaatcaggaagaattgcagaa 192

>dbj|AV768169.1| AV768169 Lotus japonicus Young plants (two-weeks old) Lotus japonicus
cDNA clone MWM225a08_f 3', mRNA sequence
Length = 587

Score = 289 bits (146), Expect = 4e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

|||||
Sbjct: 452 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 393

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 392 tacttcaagaacctgggttcagaacaagggcctcctacactccgaccagcaactcttcaac 333

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 332 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcattttcctct 273

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||

Sbjct: 272 gatttcgcccagcgccatggtcaagatgggagatatcagtcctctcactggatccaacggt 213

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||

Sbjct: 212 gaaatcaggaagaattgcagaa 191

>dbj|BP048158.1| BP048158 Lotus corniculatus var. japonicus pods (less than 20 mm in
length) Lotus japonicus cDNA clone SPD052e08_f 3', mRNA
sequence
Length = 495

Score = 274 bits (138), Expect = 2e-69
Identities = 231/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||

Sbjct: 442 tcaggggacaacaatttggcaccactggaccttcagactcccacctcctttgacaacaac 383

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 382 tacttcaagaacctgggttcagaacaagggcctcctacactccgaccagcaactcttcaac 323

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 322 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcattttcctct 263

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||| || ||||||||| ||||| ||
Sbjct: 262 gatttcgccagcgccatggtcaagatgggagatatcagtcctctcactggatccaacggt 203

Query: 2149 gaaatcaggaagaattgtagaa 2170
||||||| |||||
Sbjct: 202 gaaatcaggaagaattgcagaa 181

>gb|G0017605.1| LJGBF85T0 JCVI-LJ1 Lotus japonicus cDNA 3', mRNA sequence
Length = 420

Score = 266 bits (134), Expect = 6e-67
Identities = 230/262 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||| ||||| ||||| || ||||| || ||||| ||
Sbjct: 265 tcaggggacaacaatttggcaccacttgaccttcagacaccaacctccttcgacaacaac 206

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||| ||||| ||||| || ||||| ||||| ||||||||| |||||
Sbjct: 205 tactttaagaacctggttcaaaacaaggcctcctacactctgatcagcaacttttcaac 146

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
||||| || ||||| ||||||||| ||||| || || |||||
Sbjct: 145 ggtggtccgccgactccaccgtgcgtggctacagcaccaacccgagctcattttctct 86

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||| || ||||||||| ||||| ||
Sbjct: 85 gatttcgccagcgccatggtcaagatgggagatatcagtcctctcactggatccaacggt 26

Query: 2149 gaaatcaggaagaattgtagaa 2170
||||||| |||||
Sbjct: 25 gaaatcaggaagaattgcagaa 4

>gb|G0023584.1| LJMCD71TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA sequence
Length = 630

Score = 262 bits (132), Expect = 9e-66
Identities = 210/236 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 387 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 446

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 447 tacttcaagaacctgggttcagaacaaggcctcctacactccgaccagcaactcttcaac 506

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 507 ggtgggtccaccgactccaccgtgcgtggctacagcaccaacccgagctcattttcctct 566

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaa 2144
|||||
Sbjct: 567 gatttcgccagcgccatgggtcaagatgggagatatcagtcctctcactgggtccaa 622

Score = 123 bits (62), Expect = 5e-24
Identities = 134/158 (84%)
Strand = Plus / Plus

Query: 1484 ggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaatctgct 1543
|||||
Sbjct: 105 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 164

Query: 1544 gctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| |||
Sbjct: 165 gccaacacaggcatccctgcacccacttctagcttgagccaactcacctcaaggttcagt 224

Query: 1604 gctcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 225 gctcttggactttccagcaaagacttgggttcattgtc 262

Score = 69.9 bits (35), Expect = 7e-08
Identities = 77/91 (84%)
Strand = Plus / Plus

```
Query: 1312  tatccttgccatcgctgccagagactctgtt 1342
           |||||  |||||  |||||  |||||  |||||
Sbjct: 62    tatcctcgccatctctgctagagactctgtt 92
```

Score = 246 bits (124), Expect = 5e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||
 Sbjct: 318 aacccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 377

```
Query: 1337 tctgttca 1344
      |||||
Sbjct: 438 tctgttca 445
```

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Sbjct: 450 cttggaggccctagttggaatgttaaacttgaagaagagatgctagaactgctagccaa 509

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||||||| ||||||| ||||||||||||||||||||| |||
Sbjct: 510 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 569

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgct 1641
|| || ||||| |||||||||||||||||||||||||||||
Sbjct: 570 ttcagtgcctctaggactttccaccaaggacttggtcgccttgct 613

Score = 234 bits (118), Expect = 2e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
||||||||||||||||||| || || ||||| ||||||||||||| || |||
Sbjct: 45 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 104

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
||| ||||||||||||||||| |||| ||||| ||| || ||||| ||| |||||
Sbjct: 105 tgtgtcaatgcacaactttctactgacttctactacagttcttgcctctctcc 164

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
||||||| ||||||||||||||||| |||||||||||||||||||||
Sbjct: 165 actgtgagatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttctctc 224

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
|| |||||||||||||||||||||||||||||
Sbjct: 225 ctccgcttggttcttccacgattgctttgtcaatg 258

Score = 83.8 bits (42), Expect = 5e-12
Identities = 48/50 (96%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcat 1838
||||| ||||||||||||||||||||||||||||| |||||||||
Sbjct: 615 ggtgggcacacaattggacaagcaaggtgcacaaatttcagagcccgcat 664

>gb|FF394030.1| MOODS81TF MOO Vigna unguiculata cDNA 5', mRNA sequence
Length = 786

Score = 246 bits (124), Expect = 5e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 274 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||| ||||||||| || || ||||| ||| |||||||||
Sbjct: 334 aaccccaacagaaactctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
||||||||| ||||||||| || ||||||||| || |||||||||
Sbjct: 394 gagaaagtgtgtccaggagttgtttcctgtgcggatatccttgctattgctgccagagac 453

Query: 1337 tctgttca 1344
|||||||
Sbjct: 454 tctgttca 461

Score = 238 bits (120), Expect = 1e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 466 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||||||| ||||||| ||||||||| ||||||||| |||
Sbjct: 526 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 585

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgctc 1641
|| || ||||| ||||||||| ||||||||| |||||||||
Sbjct: 586 ttcagtgtcttaggactttccaccaaggacttggctgccttgctc 629

Score = 234 bits (118), Expect = 2e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
|||||
Sbjct: 61 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 120

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 121 tgtgtcaatgcacaactttctactgacttctactacagttcttgcccaaaactcctctcc 180

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||
Sbjct: 181 actgtgagatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttctctc 240

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 241 ctccgcttggttcttccacgattgctttgtcaatg 274

Score = 180 bits (91), Expect = 3e-41
Identities = 140/155 (90%), Gaps = 1/155 (0%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 631 ggtggccacacaattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgag 690

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|
Sbjct: 691 agcaacatagatacctcattagccaggacaagacaatcaagctgccccagaaacatcaggg 750

Query: 1909 tcaggggacaacaatctggcaccacttgatcttca 1943
|||
Sbjct: 751 tca-gggacaacaatctggcaccgcttgatcttca 784

>gb|FF387818.1| M00C268TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 625

Score = 246 bits (124), Expect = 5e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 226 ggatgtgacggttcgattcctttggatgacacgtcaagcttcaccggggagaagaacgca 285

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||| || ||||||||| || || ||||||| || |||||||||
Sbjct: 286 aaccccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 345

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||| || || ||||||| || |||||||||
Sbjct: 346 gagaaagtgtgtccaggagttgtttcctgctgcgatatccttgccattgctgccagagac 405

Query: 1337 tctgttca 1344
|||||||
Sbjct: 406 tctgttca 413

Score = 226 bits (114), Expect = 5e-55
Identities = 189/214 (88%)
Strand = Plus / Plus

Query: 571 atggtctcgttttgttctagattgacaatttgtttggtctgtttgtcctcatatggggg 630
||||||| ||||||| || || ||||||| ||||||||| || |||
Sbjct: 13 atggtctcgttttgttctagattaactatcagtttggtgctgtttgtcctcgtactgggt 72

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
||| ||||||| ||||| ||||| ||| || ||||| || |||||
Sbjct: 73 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 132

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 133 actgtgagatccacagtgaatctgccatatcaaaggagacccgcatgggtgcttctctc 192

Query: 751 cttcgcttgcttctccacgattgctttgtcaatg 784
|| ||||||| ||||||| ||||||| |||||||

Sbjct: 193 ctccgcttggtttcttccacgattgctttgtcaatg 226

Score = 131 bits (66), Expect = 2e-26
Identities = 102/114 (89%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||||| ||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct: 512 ggtgggcacacaattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgag 571

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaaca 1902
| ||||||||| ||| ||||||| ||||| || | || ||||||||| |||||
Sbjct: 572 agcaacatagatacctcatttgccaggacaagacaatcaagctgccccagaaca 625

Score = 97.6 bits (49), Expect = 3e-16
Identities = 64/69 (92%)
Strand = Plus / Plus

Query: 1573 aaaccttaaccaactcatctcaagatttagcgctcttggactttccaccaaggacttgg 1632
||||||||||||||||||||| ||||| || ||||| ||| |||||||||||||||
Sbjct: 442 aaaccttaaccaactcatctctagattcagtgctctaggattttccaccaaggacttgg 501

Query: 1633 cgccttggtc 1641
|||||||
Sbjct: 502 cgccttggtc 510

>gb|FF383796.1| M00B233TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 498

Score = 246 bits (124), Expect = 5e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||||| ||||||||||||| |||||||||
Sbjct: 146 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 205

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||
Sbjct: 206 aacccaacagaaattctgtctgtggatatgaagtcattgacagcataaaatcagccgtg 265

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 266 gagaaagtgtgtccaggagttgtttcctgtgctggatatccttgccattgctgccagagac 325

Query: 1337 tctgttca 1344

|||||
Sbjct: 326 tctgttca 333

Score = 216 bits (109), Expect = 5e-52
Identities = 148/161 (91%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

|||||
Sbjct: 338 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccga 397

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

|||||
Sbjct: 398 tctgctgccaacaatggcattcctgcaccttctcaaaccttaaccaactcatctctaga 457

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgcctt 1638

|| || |||||
Sbjct: 458 ttcagtgtcttaggactttccaccaaagacttggctgcctt 498

Score = 178 bits (90), Expect = 1e-40
Identities = 132/146 (90%)
Strand = Plus / Plus

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698

|||||
Sbjct: 1 tgcacaactttctactgacttctactacagttcttgcceaaactcctctccactgtgag 60

Query: 699 atccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 758

|||||
Sbjct: 61 atccacagtgcgaatctgccatatcaaaggagaccgcgatgggtgcttctctccccgctt 120

Query: 759 gttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 121 gttcttccacgattgctttgtcaatg 146

>dbj|FS240762.1| FS240762 RPSC Glycyrrhiza uralensis cDNA clone KAN050-D13.F 5', mRNA
 sequence
 Length = 554

Score = 244 bits (123), Expect = 2e-60
Identities = 174/191 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||
Sbjct: 246 ggatgtgatggttcaattctactggatgacacatcaagctttacagggagaagaacgca 305

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||
Sbjct: 306 aaccggaacaggaactcagctcgtgggttcgaagtcacgacaacatcaagtcagccgta 365

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
 |||||
Sbjct: 366 gagaaagtgtgccctggagttgtttcctgcgcgtgatatccttgccatcgctgccagagac 425

Query: 1337 tctgttcagat 1347
 ||
Sbjct: 426 tccgttcagat 436

Score = 178 bits (90), Expect = 1e-40
Identities = 159/182 (87%)
Strand = Plus / Plus

Query: 603 tttggctctgtttgtcctcatatgggggagtgccaatgcacaactttctacaaactttta 662
 |||||
Sbjct: 65 tttggctctctctgtttctcataatgggggagtgccaatgcacaactctctacaaactteta 124

Query: 663 ctaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaatctgccatatc 722
 || |

Sbjct: 125 ctccagttcttgtccaaaactggtttccactgtaaaatccacagtacaatccgccatatac 184

Query: 723 taaggagaccgcgatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaa 782
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 185 aaaggagaccgcgatgggtgcttccctcctccgcttggttcttccatgattgctttgtcaa 244

Query: 783 tg 784
||

Sbjct: 245 tg 246

Score = 137 bits (69), Expect = 4e-28
Identities = 105/117 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 438 cttggaggacctacttggaatgttaaacttggaagaagagacgctaagacggctagccag 497

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctca 1594
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 498 tctgctgccaacaacggcatccctcctcccacttctaacctcaaccaactcatctca 554

>gb|FG889628.1| UCRVU08_CCNS10828_b1 Cowpea IT97K-461-4 Mixed Tissue and Conditions
cDNA Library UCRVU08-1-2 Vigna unguiculata cDNA clone
CCNS10828.b1, mRNA sequence
Length = 692

Score = 238 bits (120), Expect = 1e-58
Identities = 171/188 (90%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 257 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 316

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||| || ||||| ||||| || || ||||| ||| ||||| |||||

Sbjct: 317 aaccccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 376

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcgagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 377 gagaaagtgtgtccaggagttgtttcctgtgcgagatatccttgctattgctgccagagac 436

Query: 1337 tctgttca 1344
|||||||
Sbjct: 437 tctgttca 444

Score = 238 bits (120), Expect = 1e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 449 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccaa 508

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||||
Sbjct: 509 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 568

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
|| ||
Sbjct: 569 ttcagtgccttaggactttccaccaaggacttggctgccttgtc 612

Score = 226 bits (114), Expect = 5e-55
Identities = 189/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgtttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
|||||||
Sbjct: 44 atggcttcgtttgttctagattaactttcagtttggttctgtttgtcctcgactgggt 103

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 104 tgtgtcaatgcacaactttctactgacttctactacagtcttgcceaaaactcctctcc 163

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||

Sbjct: 164 actgtgagatccacagtgaatctgccatatcaaaggagacccgcatgggtgcttctctc 223

Query: 751 cttcgcttggtttccacgattgctttgtcaatg 784

|| ||||||||||||||||||||||||||||||||

Sbjct: 224 ctccgcttggtttccacgattgctttgtcaatg 257

Score = 111 bits (56), Expect = 2e-20

Identities = 65/68 (95%)

Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||

Sbjct: 614 ggtggccacacaattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgag 673

Query: 1849 accaacaat 1856

| |||||

Sbjct: 674 agcaacaat 681

>gb|FF403045.1| M00F734TF M00 Vigna unguiculata cDNA 5', mRNA sequence

Length = 745

Score = 238 bits (120), Expect = 1e-58

Identities = 153/164 (93%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

||||||||||| ||||||||||||||||||||||||| |||||||||||||||||

Sbjct: 465 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccaa 524

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

||||||| ||||||||| ||||||| ||||||||||||||||||||||||| |||

Sbjct: 525 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 584

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgcttgtc 1641

|| || ||||| |||||||||||||||||||||||||

Sbjct: 585 ttcagtgtctaggactttccaccaaggacttggtcgcttgtc 628

Score = 234 bits (118), Expect = 2e-57

Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggettcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
|||||

Sbjct: 61 atggettcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 120

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||

Sbjct: 121 tgtgtcaatgcacaactttctactgacttctactacagtcttgcccaaaactcctctcc 180

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||

Sbjct: 181 actgtgagatccacagtgaatctgccatatcaaaggagacccgcatgggtgcttctctc 240

Query: 751 cttegcttggttcttccacgattgctttgtcaatg 784
||

Sbjct: 241 ctccgcttggttcttccacgattgctttgtcaatg 274

Score = 222 bits (112), Expect = 8e-54
Identities = 170/188 (90%), Gaps = 1/188 (0%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||

Sbjct: 274 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccgggagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||

Sbjct: 334 aaccccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgtttcctgtgcgagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 394 gagaaagtgtgt-caggggttggtttcctgtgcggatatccttgccattgctgccagagac 452

Query: 1337 tctgttca 1344
|||||

Sbjct: 453 tctgttca 460

Score = 127 bits (64), Expect = 3e-25
Identities = 103/116 (88%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggatgcacaaacttcagagcccgcatctacaacgag 1848
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 630 ggtgggcacacaattggacaagcaaagtgcacaaatttcagagcccgcatctacaacgag 689

```
Query: 1849  accaacaatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatc 1904
              | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 690    agcaacatagatacctcatttgccaggacaagacaatcaagctgccccagaacatc 745
```

>gb|FF392448.1| M00CV65TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 607

Score = 238 bits (120), Expect = 1e-58
Identities = 171/188 (90%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 272 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 331

```
Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
          |||||
Sbjct: 332 aacccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 391
```

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336
 |||||||
 Sbjct: 392 gagaaagtgtgtccaggagttgtttcctgcgagatatcctcgccattgctgccagagac 451

```
Query: 1337 tctgttca 1344
      |||||
Sbjct: 452 tctgttca 459
```

Score = 234 bits (118), Expect = 2e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttggttggtctgtttgtcctcatatggggg 630
|||||
Sbjct: 59 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 118

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 119 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 178

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||
Sbjct: 179 actgtgagatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttctctc 238

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 239 ctccgcttggttcttccacgattgctttgtcaatg 272

Score = 198 bits (100), Expect = 1e-46
Identities = 133/144 (92%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 464 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccaa 523

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 524 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 583

Query: 1598 tttagcgctcttggaactttccacc 1621
||
Sbjct: 584 ttcagtgccttaggaactttccacc 607

>gb|FF399144.1| M00EV84TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 345

Score = 234 bits (118), Expect = 2e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttggttggtctgtttgtcctcatatggggg 630
|||||||
Sbjct: 64 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 123

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 124 tgtgtcaatgcacaactttctactgacttctactacagttcttgcctccaaactcctctcc 183

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||
Sbjct: 184 actgtgagatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttctctc 243

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 244 ctccgcttggttcttccacgattgctttgtcaatg 277

Score = 89.7 bits (45), Expect = 8e-14
Identities = 63/69 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 277 ggatgtgacggttcgattcttttggatgacacgtcaagcttccccggggagaagaacgca 336

Query: 1217 aacccaac 1225
|||||||
Sbjct: 337 aacccaac 345

>gb|G0019707.1| LJMAW92TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA sequence
Length = 663

Score = 208 bits (105), Expect = 1e-49
Identities = 180/205 (87%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttggttggtctgtttgtcctcatatgggggagtgccaat 639
|||||||
Sbjct: 71 ttttgttctagattaactatctgtttgtcctcttctgtcctcatattgggggagtgccaat 130

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699
|| ||||| ||||| || || ||||| ||||| || |||||
Sbjct: 131 gctcaactttctacaaacttctattctagttcttgtccaaacctctttccactgtgaaa 190

Query: 700 tccacagtgcgaatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttg 759
||| ||||| ||||| ||||| | ||||| ||||| |||||
Sbjct: 191 tcctcagtgcgaatccgccatatcaaaggaggctcgcatgggtgcttctctcctccgcttg 250

Query: 760 ttcttccacgattgctttgtcaatg 784
||| ||||| |||||
Sbjct: 251 ttcttccatgattgcttcgtcaatg 275

Score = 180 bits (91), Expect = 3e-41
Identities = 160/183 (87%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 278 tgtgatggttcagttctacttgatgacacatcaagcttcaccgggagaagaatgcaaac 337

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
||| ||||| ||||| ||||| || ||||| ||||| || ||||| || |||
Sbjct: 338 cccaacagaaactctgctcgcggatttgatgttattgacaacatcaagtcagcagtagag 397

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 398 gcagcatgccaggagttgtatcctgcgctgatatacctcgccatctctgctagagactct 457

Query: 1340 gtt 1342
|||
Sbjct: 458 gtt 460

Score = 123 bits (62), Expect = 5e-24
Identities = 134/158 (84%)
Strand = Plus / Plus

Query: 1484 ggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaatctgct 1543
||||| ||||||||| || | ||||||||| ||||||||| || ||
Sbjct: 473 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 532

Query: 1544 gctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| |||| | ||||||||| || || | ||||||| ||||||| || ||
Sbjct: 533 gccaacacaggcatccctgcacccacttctagcttgagccaactcacctcaagttcagt 592

Query: 1604 gctcttggactttccaccaaggacttggcgccttgtc 1641
||||||| ||||| || ||||| || |||||
Sbjct: 593 gctcttggactttccagcaaagacttggttgcatgtc 630

>dbj|AV412875.1| AV412875 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MWM225a08_r 5', mRNA sequence
Length = 282

Score = 208 bits (105), Expect = 1e-49
Identities = 180/205 (87%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggtctgtttgtcctcatatgggggagtgccaat 639
||||||| || || ||||| ||||| ||||||||| |||||||||
Sbjct: 53 ttttgttctagattaactatctgtttgtctctttgtcctcatattggggagtgccaat 112

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699
|| ||||||||| || | || ||||||| ||||| || |||||||
Sbjct: 113 gctcaactttctacaaacttctattctagttcttgtccaaaactcttttccactgtgaaa 172

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
||| ||||||||| ||||||| ||||| | ||||||||| |||||||
Sbjct: 173 tctcagtgcaatccgccatatcaaaggagctcgcatgggtgcttctctcctccgcttg 232

Query: 760 ttcttccacgattgctttgtcaatg 784
||||||| ||||||| |||||||
Sbjct: 233 ttcttccatgattgcttcgtcaatg 257

>dbj|AV771838.1| AV771838 Lotus japonicus Pods (20-30 mm in length) Lotus japonicus
cDNA clone MPD027c11_f 3', mRNA sequence
Length = 430

Score = 202 bits (102), Expect = 7e-48

Identities = 208/242 (85%), Gaps = 1/242 (0%)
Strand = Plus / Minus

Query: 1925 tggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaagaacctcg 1984
|||||
Sbjct: 428 tggcaccacttgaccttcagactccaacctcctttgactaccactacttcaagtacctgg 369

Query: 1985 ttcagaagaagggtctcctccactctgatcagcaactgttcaacggtgggtccaccgact 2044
|||||
Sbjct: 368 ttcagaaccagggcctccgacactccgaccagcaactcttcaacggtgggtccaccgact 309

Query: 2045 ccattgtgcgtgggtacagcaccaacccgggcaccttctcctctgatttcgccgccgcca 2104
|||
Sbjct: 308 ccaccgtgcgtgggtacagcaccaacccgagctcatttctcctctgatttcgccagcgcca 249

Query: 2105 -tgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||
Sbjct: 248 ctggtccagatgggagatatcagtcctctcactggatccaacggtgaaatcaggaagaat 189

Query: 2164 tg 2165
||
Sbjct: 188 tg 187

>dbj|BW620524.1| BW620524 Lotus japonicus protoplasts from suspension-cultured cells
Lotus japonicus cDNA clone LjFL1-sab-002-BB11 5', mRNA
sequence
Length = 480

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 211 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 270

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 271 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 330

sequence
Length = 482

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 145 tgtgatggttcaattctacttggatgacacatcaagcttcaccgggagaagaatgcaaac 204

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 205 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 264

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatataccttgccatcgtgccagagactct 1339
||
Sbjct: 265 gcagcatgcccaggagttgtatcctgcgctgatatacctcgccatctctgctagagactct 324

Query: 1340 gtt 1342
|||
Sbjct: 325 gtt 327

Score = 127 bits (64), Expect = 3e-25
Identities = 100/112 (89%)
Strand = Plus / Plus

Query: 673 tgtccaaacctcttctcctctgtgaaatccacagtgcattctgccatatctaaggagacc 732
|||||
Sbjct: 31 tgtccaaacctctttccactgtgaaatcctccgtgcattccgccatatcaaaggagct 90

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 91 cgcattgggtgcttctctccttcgcttgttcttccatgattgcttcgtcaatg 142

Score = 119 bits (60), Expect = 8e-23
Identities = 117/136 (86%)
Strand = Plus / Plus

```
Query: 1484  ggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaatctgct 1543
           ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 340    ggccccacatggaatgtgaaagttggaagaagagacgctaaaactgctagccagtcgcc 399
```

```

Query: 1604 gctcttggactttcca 1619
          |||||
Sbjct: 460  gctcttggactttcca 475

```

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
 ||||||| ||||||||| ||||||| ||||||||| || ||||| || ||
 Sbjct: 336 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 395

```
Query: 1340 gtt 1342
      |||
Sbjct: 456 gtt 458
```


Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaat 639
|||||

Sbjct: 69 ttttgttctagattaactatctgttttgcctcttctgtcctcatattggggagtgcta 128

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699
|||

Sbjct: 129 gctcaactttctacaaacttctattctagttcttgcctccaaactcttttccactgtgaaa 188

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
|||

Sbjct: 189 tcctccgtgcaatccgccatatcaaaggaggctcgcatgggtgcttctctcctccgcttg 248

Query: 760 ttcttccacgattgctttgtcaatg 784
|||||

Sbjct: 249 ttcttccatgattgcttcgtcaatg 273

>dbj|BW628107.1| BW628107 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-019-CE07 5', mRNA
sequence
Length = 471

Score = 196 bits (99), Expect = 4e-46

Identities = 162/183 (88%)

Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||

Sbjct: 278 tgtgatggttcaattctacttgatgacacatcaagcttcaccgggagaagaatgcaaac 337

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||

Sbjct: 338 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 397

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|||

Sbjct: 398 gcagcatgcccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 457

Query: 1340 gtt 1342

|||
Sbjct: 458 gtt 460

Score = 192 bits (97), Expect = 7e-45
Identities = 178/205 (86%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggtctgtttgtcctcatatgggggagtccaat 639
||||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 71 ttttgttctagattaactatctgtttgtctctttgtcctcatattggggagtgcta 130

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctctctcctctgtgaaa 699
|| ||||| ||||| || | ||| ||||| ||||| || |||||
Sbjct: 131 gctcaactttctacaaacttctattctagtcttgtccaaaactctttccactgtgaaa 190

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttg 759
||| | ||||| ||||| ||||| | ||||| ||||| ||||| |||||
Sbjct: 191 tctccgtgcaatccgccatatcaaaggaggctcgcatgggtgcttctctcctccgcttg 250

Query: 760 ttcttccacgattgctttgtcaatg 784
||||||| ||||| |||||
Sbjct: 251 ttcttccatgattgcttcgtcaatg 275

>dbj|BW627140.1| BW627140 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-017-AA04 5', mRNA
sequence
Length = 480

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaa 1219
||||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 286 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaa 345

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
||||||| ||||| ||||| ||||| ||||| ||||| || ||||| || |||
Sbjct: 346 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 405

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|| || |||||||||| ||||||| ||||||| |||||| | ||| |||||||
Sbjct: 406 gcagcatgcccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 465

Query: 1340 gtt 1342
|||
Sbjct: 466 gtt 468

Score = 184 bits (93), Expect = 2e-42
Identities = 177/205 (86%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggtctctgtttgtcctcatatgggggagtgccaat 639
|||||||||||| || || ||||| ||||| |||||||||||| ||||||| |||
Sbjct: 79 ttttgttctagattaactatctgtttgtctctttgtcctcatattggggagtgctaata 138

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699
|| |||||||||||||| || | ||| |||||| | |||| | |||||||
Sbjct: 139 gctcaactttctacaaacttctattctagttctctgtccaaaactcttttccactgtgaaa 198

Query: 700 tccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
||| | ||||||| ||||||| ||||| | ||||||| ||||||| |||||||
Sbjct: 199 tcttccgtgcaatccgccatatcaaaggaggctcgcatgggtgcttctctccttcgcttg 258

Query: 760 ttcttccacgattgctttgtcaatg 784
||||||| ||||||| |||||||
Sbjct: 259 ttcttccatgattgcttcgtcaatg 283

>dbj|BW624354.1| BW624354 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-009-BC11 5', mRNA
sequence
Length = 483

Score = 196 bits (99), Expect = 4e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||||||||||||| | ||||||| ||||||| ||||||| |||||||

Sbjct: 290 tgtgatggttcaattctacttgatgacacaccaagcttcaccggggagaagaatgcaaac 349

Sbjct: 350 cccaacaggaactctgctcgcgattcgatgttattgacaacatcaagtcagcagtagag 409

Sbjct: 410 gcagcatgccaggagttgtatcctgcgctgatatcctgccatctctgctagagactct 469

Sbjct: 470 gtt 472

Query: 580 ttttgttctagattgacaattttgtttggctctgtttgtcctcatatgggggagtgccaat 639

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759

Query: 760 ttcttcacgattgctttgtcaatg 784
|||

>dbj|BW595840.1| BW595840 Lotus japonicus suspension-cultured cells Lotus japonicus
cDNA clone LjCa-005-DD12 5', mRNA sequence
Length = 485

Identities = 177/203 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||

Sbjct: 283 tcaggggacaacaatttggcaccacttgaccttcagacaccaacctccttcgacaacaac 342

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 343 tactttaagaacctgggttcaaacaagggcctcctacactctgatcagcaacttttcaac 402

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 403 ggtgggtccgccgactccaccgtgcgtgggtacagcaccaacccgagctcattttcctct 462

Query: 2089 gatttcgccgcgccatgatcaa 2111
|||||

Sbjct: 463 gatttcgccgcgccatggtcaa 485

Score = 127 bits (64), Expect = 3e-25
Identities = 130/152 (85%)
Strand = Plus / Plus

Query: 1490 acatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgtaac 1549
|||||

Sbjct: 7 acatggaatgtgaaagtgggaagaagagacgctaaaactgctagccagtcgccccaac 66

Query: 1550 aatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctctt 1609
|

Sbjct: 67 acaggcatccctgcacccacttctagcttgagccaactcacctcaaggttcagtgtctt 126

Query: 1610 ggactttccaccaaggacttgggtgccttgtc 1641
|||||

Sbjct: 127 ggactttccagcaaagacttgggtgcatgtc 158

>gb|EY976963.1| EST 83 Alfalfa aluminum suppression subtractive library Medicago
sativa cDNA clone E2B11, mRNA sequence
Length = 971

Score = 190 bits (96), Expect = 3e-44
Identities = 147/164 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||| ||| ||||||||||||||| ||||||| ||||| ||
Sbjct: 437 cttggaggcccaacatgggatgtgaaacttggaagaagagatgctagaacagctagtaaa 496

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||| ||||||||||||||| ||||||||||||| || |||||||||||||||
Sbjct: 497 tcagctgcaaacatggcatcccagcaccacttcaagcctcaaccaactcatctcaagg 556

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||| ||||||||||||||||||| ||||||||| |||||
Sbjct: 557 tttaatgctcttggactttccaccaaggatttggtcgcattgtc 600

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||||| | ||||||||||||||||||||||||| ||
Sbjct: 245 ggatgtgatggttcaattcttctcggatgacacatcaagcttcaccggagagaaaactgcc 304

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
|| ||||||||| || || || ||||||||||||| || || ||||| || ||||||||| ||
Sbjct: 305 aatcccaacagaaattcggcccgatggattcgaagtgatcgacaaaatcaaatacagcagtg 364

Query: 1277 gagaaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||| | ||||| || || ||||||||| ||||||| ||||| |||||||
Sbjct: 365 gagaaagtatgtccagggtgcagtttcatgtgctgatatcctcgccatcactgctagagac 424

Query: 1337 tctgttcagat 1347
||||||| |||||
Sbjct: 425 tctgttgagat 435

Score = 111 bits (56), Expect = 2e-20
Identities = 71/76 (93%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 170 caatctgccatatcaaaggagacccgcatgggtgcttctcttctacgtttgttcttccac 229

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 230 gattgctttgttaatg 245

Score = 63.9 bits (32), Expect = 4e-06
Identities = 32/32 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcac 1820
|||||
Sbjct: 602 ggtggtcacacaattggacaagcaaggtgcac 633

>gb|EH613355.1| EST 02 Alfalfa aluminum suppression subtractive library Medicago
sativa cDNA clone A4 5', mRNA sequence
Length = 748

Score = 190 bits (96), Expect = 3e-44
Identities = 147/164 (89%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 545 cttggaggcccaacatgggatgtgaaacttggaagaagagatgctagaacagctagtaaa 486

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|| |||||
Sbjct: 485 tcagctgcaaacaatggcatccagcaccacttcaagcctcaaccaactcatctcaagg 426

Query: 1598 ttttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 425 tttaatgctcttggactttccaccaaggatttggctgcattgtc 382

Score = 149 bits (75), Expect = 9e-32
Identities = 162/191 (84%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 737 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 678

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 677 aatcccaacagaaattcggcccggtgattcgaaagtgatcgacaaaatcaaatcagcagtg 618

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 617 gagaaagtatgtccagggtgcagtttcatgtgtgatatcctcgccatcactgctagagac 558

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 557 tctgttgagat 547

Score = 99.6 bits (50), Expect = 8e-17
Identities = 212/266 (79%)
Strand = Plus / Minus

Query: 1900 acatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt 1959
|||||
Sbjct: 269 acatcagggtccggggacaataatttggcacctcttgatcttgcaacaccaacatccttt 210

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
|||||
Sbjct: 209 gacaatcactatttcaagaacctagttgacagtaagggaactactccactccgaccaacaa 150

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcacc 2079
||
Sbjct: 149 ctcttcaatggtggatccactgattccatagtgcatgaatatggcttgtatccaagctct 90

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||
Sbjct: 89 tttctcctctgatttcgtcaccgcccatgatcaagatgggagacattagtcctcctcaccgt 30

Query: 2140 tccaatggagaaatcaggaagaattg 2165
 |||||

>dbj|BB913062.1| BB913062 Trifolium pratense three week-old plant Trifolium pratense
cDNA clone RCE12415, mRNA sequence
Length = 582

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctcctcca 2006

Query: 2007 ctctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcac 2066

Query: 2067 caaccgggcaccttctcctctgatttcgccgcgccatgatcaagatgggagacattag 2126

Query: 2127 tcctctcactggctccaatggagaaatcaggaagaattgtagaa 2170
 ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

>gb|BI969832.1| GM830009A23A12 Gm-r1083 Glycine max cDNA clone Gm-r1083-3096 3', mRNA
sequence
Length = 678

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||| ||||||||||||||||||||||||| ||| ||||||| ||||| |||||
Sbjct: 585 ggtcatacaattggacaagcaaggtgcacaacctttagagcccgaatctacnnngagagc 526

Query: 1852 aacatagaaaccgcatTTTgcaaggactaggcagcaaagctgccttagaacatcagggtca 1911
||||||| | | | ||||| | | ||| | | | ||| ||||| |||
Sbjct: 525 aacatagatagctctTTTgcccgcgatgagacaatctaggtgtccccgaacctcaggatca 466

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctTTTgacaactactac 1971
||||||| || | ||||| |||| | | ||||| | | ||||||||| |||||
Sbjct: 465 ggggacaacaaccttgcacccattgactTTTgccactcccactTTTctTTTgacaaccactac 406

Query: 1972 ttcaagaacctcgTTtcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
||||||| ||||| ||||||| |||| | | ||||| | | ||||| |||||
Sbjct: 405 ttcaagaacctcattcagaagaagggtctcatccattccgaccaagaactcttcaatggt 346

Query: 2032 gggTccaccgactccattgtgcgtggctacagcaccaacccgggcacTTTctcctctgat 2091
|| ||||| ||||| | ||||| ||||||| ||||||| | ||||| | | |||
Sbjct: 345 ggtTccactgactcctTggTgcgtacctacagcaccaacccggcctcTTTttcgccgat 286

Query: 2092 ttTcgccgcccatgatcaagatgggagacattagTcctctcactggctccaatggagaa 2151
||| ||||||| ||||| ||||||| ||||||| ||||||| |||||
Sbjct: 285 ttTcgccgcccatgatcaggatgggagacattagTcccctcactggctcccgcggagaa 226

Query: 2152 atcaggaagaattgtagaaggattaactaatt 2183
|| ||| |||| | | ||| | |||||
Sbjct: 225 ataagggagaactgcaggagggtcaactaatt 194

Score = 50.1 bits (25), Expect = 0.065
Identities = 25/25 (100%)
Strand = Plus / Minus

Query: 1611 gactttccaccaaggactTggtcgc 1635
|||||||||||||||||
Sbjct: 620 gactttccaccaaggactTggtcgc 596

>gb|BI700509.1| sag61f05.y1 Gm-c1082 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1082-1041 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE

;, mRNA sequence
Length = 472

Score = 180 bits (91), Expect = 3e-41
Identities = 282/343 (82%), Gaps = 2/343 (0%)
Strand = Plus / Plus

Query: 1801 attggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaacatagaa 1860
|||||
Sbjct: 1 attggacaagcaaggtgcacaacctttagagcccgaatctacaacgagaccaacatagat 60

Query: 1861 accgcatttgcaaggactaggcagcaaaagctgccctagaacatcagggtcaggggacaac 1920
| | |
Sbjct: 61 agctcttttctcgcgatgagacaatctaggtgtccccgaacctcagggtcaggggacaac 120

Query: 1921 aatctggcaccacttgatcttcaa-actccaaccagctttgacaactactacttcaagaa 1979
| | |
Sbjct: 121 aaactagcaccattga-cttcgccactcccaggttctttgacaaccactacttcaagaa 179

Query: 1980 cctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacggtgggtccac 2039
| | |
Sbjct: 180 cctcattcagaagaagggcctcatcattccgaccaacaactcttcaatggtggttccac 239

Query: 2040 cgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctgatttcgccgc 2099
| | |
Sbjct: 240 tgactccatagtgcgtacctacagcaccaaccgggcctcctttttcgccgatttctccgc 299

Query: 2100 cgccatgatcaagatgggagacattagtcctctcactggctcc 2142
| | |
Sbjct: 300 cgccatgatccgatgggagacattagtcctctcactggctcc 342

>gb|BU578183.1| sar49a02.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-5404 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 271

Score = 176 bits (89), Expect = 4e-40
Identities = 134/149 (89%)
Strand = Plus / Plus

Query: 630 gagtgcgaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctc 689

|||||
Sbjct: 1 gagtccaatgcccaactttctacaaacttctactaccattcatggccaaacctcttctc 60

Query: 690 ctctgtgaaatccacagtgcaatctgccatatctaaggagacccgcatgggtgcttctct 749
 | | | | |

Sbjct: 61 cactgtgaaatccaccagcaatctgccatatcagaagagacccgcatggctgcttctct 120

Query: 750 ccttcgcttggttcttccacgattgctttg 778

 ||| | | | |

Sbjct: 121 cctccacctgttcttccaccattgctttg 149

Score = 107 bits (54), Expect = 3e-19

Identities = 99/114 (86%)

Strand = Plus / Plus

Query: 1159 atgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaa 1218

 | | | | | | | |

Sbjct: 157 atgtgatgggtcaattctattggatgacacctcgagcttcgccgagagaaaaacgcgaa 216

Query: 1219 ccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagc 1272

 | | | | | | | |

Sbjct: 217 ccccaacaagaactctgctcctggataccaggtccttgaccacctaaatcagc 270

>gb|G0258927.1| VBL1_16_M09_E001.g1 Normalized cDNA library from cotyledon and young
 leaves of peanut Arachis hypogaea cDNA, mRNA sequence
Length = 616

Score = 174 bits (88), Expect = 2e-39

Identities = 226/272 (83%)

Strand = Plus / Plus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969

 | | | | | | | | | | |

Sbjct: 3 caggggacaacaaccttgcgccgcttgatctccaaacacccacggccttcgacaacaact 62

Query: 1970 acttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029

 | | | | | | | |

Sbjct: 63 acttcaggaaccttggttcagaacaaggggtgctccactccgaccagcaactcttcaacg 122

Identities = 193/228 (84%)
Strand = Plus / Plus

[illegible]

Sbjct: 67 ctttgacaaccactacttcaagaacctcattcagaagaagggtctcatccattccgacca 126

Query: 2016 gcaactgtttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccggg 2075

Sbjct: 127 agaactcttcaatggtggttccactgactccttggtgcgtacctacagcaccaaccggc 186

Query: 2076 caccttcicctctgatttcgccgccgccatgatcaagatgggagacattagtcctctcac 2135

Sbjct: 187 ctcttttttcgccgattttctccgccgcatgatcaggatgggagacattagtagtcccctcac 246

Query: 2136 tggctccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 247 tggctcccgcgagaaataagggagaactgcaggagggtcaactaatt 294

>gb|AW350788.1| GM210009A20D5 Gm-r1021 Glycine max cDNA clone Gm-r1021-3226 3', mRNA
sequence
Length = 507

Score = 174 bits (88), Expect = 2e-39
Identities = 193/228 (84%)
Strand = Plus / Minus

Query: 1956 ctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatca 2015

Sbjct: 444 ctttgacaaccactacttcaagaacctcattcagaagaagggtctcatccattccgacca 385

Query: 2016 gcaactgtttcaacgggtgggtccaccgactccattgtgctggctacagcaccaacccggg 2075

Sbjct: 384 agaacttttcaatggtggttccactgactccttagtgcgctacctacagcaccaacccggc 325

Query: 2076 caccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcac 2135

Sbjct: 324 ctcttttttcgccgattttctccgccgcatgatcaggatgggagacattagtcacctcac 265

Query: 2136 tggctccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183

Score = 163 bits (82), Expect = 6e-36

Identities = 139/158 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 65 cttggtggcccaacttggaacgtgaaacttggaagaagagactccagaacagcaagccaa 124

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 125 tctgctgccaacaatggcatcccacgaccacttcaaaccttaaccaactcatctccaga 184

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgc 1635
|| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 185 ttcaactctcttggactttcctccaaggacttggctgc 222

Score = 67.9 bits (34), Expect = 3e-07
Identities = 46/50 (92%)
Strand = Plus / Plus

Query: 1295 gttgtttcctgcgcatatccttgccatcgctgccagagactctgttca 1344
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 11 gttgtttcctgtgccgatatccttgccattgctgccagagattctgttca 60

>gb|EY476317.1| METAQ01TF JCVI-MT3 Medicago truncatula cDNA 5', mRNA sequence
Length = 716

Score = 167 bits (84), Expect = 4e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 492 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctagtaaa 551

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 552 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 611

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641

Sbjct: 612 |||| |||||||| |||||||||||||| |||||||| ||||| 655

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||
 Sbjct: 300 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 359

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 || |||||| | || || | | | | | | | |
Sbjct: 360 aatccaacaaaaattcggcccgtaggcgatcgacaaaatcaaatcagcagtg 419

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336
 ||||| ||||| | |||| |||| | ||||| ||||| ||||| |||||
 Sbjct: 420 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 479

```
Query: 1337 tctgttcagat 1347
        ||||| |||
Sbjct: 480 tctgttgagat 490
```

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

```
Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggtctttccac 768
          |||||
Sbjct: 225 caatctgccatatcaaaagagactcgcatgggtgcttctctctgcgttggtctttccac 284
```

```
Query: 769 gattgctttgtcaatg 784
      |||||
Sbjct: 285 gattgctttgttaatg 300
```

Score = 63.9 bits (32), Expect = 4e-06
Identities = 50/56 (89%)

Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||||
Sbjct: 660 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacga 715

>gb|EX530374.1| MTGland_A066_2007-06-28/MTGlandA066_C04_014_1 Medicago truncatula A17
glandular trichome Medicago truncatula cDNA, mRNA
sequence
Length = 1023

Score = 167 bits (84), Expect = 4e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 487 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 546

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| |||||
Sbjct: 547 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 606

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||||
Sbjct: 607 tttaatgctcttggctttccaccaaggatttggtcgcattgtc 650

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 295 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 354

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 355 aatcccaacaaaaattcggcccgatggattcgaagtgatcgacaaaatcaaatcagcagtg 414

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336
||||||| ||||||| | ||||| ||||| | ||||||| ||||| ||||| |||||
Sbjct: 415 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 474

Query: 1337 tctgttcagat 1347
||||| ||||
Sbjct: 475 tctgttgagat 485

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttccac 768
||||||| || ||||| ||||||| ||||| || || ||||||| |||||
Sbjct: 220 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgttgttcttccac 279

Query: 769 gattgctttgtcaatg 784
||||||| ||||
Sbjct: 280 gattgctttgttaatg 295

Score = 93.7 bits (47), Expect = 5e-15
Identities = 204/257 (79%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||||| ||||||| || || ||||| || ||||||| ||
Sbjct: 655 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 714

Query: 1852 aacatagaaaccgcatTTGcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| || | ||||| | || ||||| | || ||||| || ||
Sbjct: 715 aacatagatacttctttgctcgcaaggcaatcagggtgccccagacatcnggttcc 774

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactac 1971
||||||| || ||||||| ||||||| || ||||| || ||||||| || ||
Sbjct: 775 ggggacaataatttggcacccttgatcttgcaacaccaacatcctttgacaaccattac 834

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
||||||| |||| | | ||||| || ||||||| || || ||||| || || |||||

Sbjct: 835 ttcaagaacctagttgacagtaagggactactccactccgaccaacaactctttaatggt 894

Sbjct: 895 ggntccaccgattccat 911

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 ||||||| ||||| ||| ||||| ||||| || ||||| ||||| ||
 Sbjct: 439 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 498

Query: 1598 ttttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 559 tttaatgctcttggcttttccaccaaggatttggtcgcatgtc 602

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 ||||||||||||||| | ||||||||||||||||||||||||| ||
 Sbjct: 247 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 306

```
Query: 1337 tctgttcagat 1347
        ||||| |||
Sbjct: 427 tctgttgagat 437
```

```
Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttcac 768
      |||||
Sbjct: 172 caatctgccatatcaaaagagaactcgcatgggtgcttctctccttcgcttggttcttcac 231
```

```
Query: 769 gattgctttgtcaatg 784
      |||||
Sbjct: 232 gattgctttgttaatg 247
```

Score = 167 bits (84), Expect = 4e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 ||||||||| ||||| ||| ||||| ||||| || ||||| ||||| ||
 Sbjct: 461 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 520

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 521 tcagctgcaaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 580

```
Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
           |||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct: 581  tttaatgctcttggcttttccaccaaggatttggtcgcattgtc 624
```

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 269 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 328

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 329 aatcccaacaaaaattcggcccggtggattcggaagtgatcgacaaaatcaaacagcagtg 388

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 389 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 448

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 449 tctgttgagat 459

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttcac 768
|||||||
Sbjct: 194 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttcac 253

Query: 769 gattgctttgtcaatg 784
|||||||
Sbjct: 254 gattgctttgttaatg 269

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851

|||||
Sbjct: 629 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacgactcc 688

Query: 1852 aacataga 1859

|||||
Sbjct: 689 aacataga 696

>gb|AW268020.1| EST306242 DSIR Medicago truncatula cDNA clone pDSIR-8B8, mRNA
sequence
Length = 702

Score = 167 bits (84), Expect = 4e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 447 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 506

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| |||||
Sbjct: 507 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 566

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgct 1641
|||||
Sbjct: 567 tttaatgctcttggctttccaccaaggatttggtcgcattgtc 610

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 255 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 314

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 315 aatcccaacaaaattcggcccgatggattcgaagtgatcgacaaaatcaaatcagcagtg 374

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||| | ||||| ||||| | ||||||| ||||| ||||| |||||
Sbjct: 375 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 434

Query: 1337 tctgttcagat 1347
||||||| |||||
Sbjct: 435 tctgttgagat 445

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttccac 768
||||||| ||||| ||||||| ||||||| || || ||||||| |||||
Sbjct: 180 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 239

Query: 769 gattgctttgtcaatg 784
||||||| |||||
Sbjct: 240 gattgctttgttaatg 255

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||||| ||||||| || || ||||||| || ||||||| ||
Sbjct: 615 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 674

Query: 1852 aacataga 1859
|||||||
Sbjct: 675 aacataga 682

>gb|BI969294.1| GM830007B20G07 Gm-r1083 Glycine max cDNA clone Gm-r1083-2630 3', mRNA
sequence
Length = 779

Score = 165 bits (83), Expect = 2e-36
Identities = 161/187 (86%)
Strand = Plus / Minus

Query: 1956 ctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactctgatca 2015

Query: 2016 gcaactgtttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccggg 2075

Query: 2076 caccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcac 2135

Query: 2136 tggctcc 2142
 |||||

Score = 111 bits (56), Expect = 2e-20
Identities = 65/68 (95%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851

Query: 1852 aacataga 1859
 |||

>gb|FG998035.1| GLPA295TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 740

Score = 163 bits (82), Expect = 6e-36
Identities = 136/154 (88%)
Strand = Plus / Plus

Query: 1482 gaggcctacatggaatgttaaacttggagaagagacgctagaactgctagccaatctg 1541

Query: 1542 ctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagattta 1601
|||||
Sbjct: 543 ctgccaacaatggcatcccaagaccacttcaaacctcaaccaacttatatccagattta 602

```

Query: 1602 gcgctcttggactttccaccaaggacttggtcgc 1635
          |||||
Sbjct: 603  acactctcggactttccaccaaggacttggtcgc 636

```

Score = 159 bits (80), Expect = 1e-34
Identities = 161/188 (85%)
Strand = Plus / Plus

```
Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
          ||||| || ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 290 tgtgatgggtcgattctacttggatgacacatcaagcttcaccggagagaagaacgcggga 349
```

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
 || ||||| |||| ||||| || || || || || ||||| |||||
 Sbjct: 350 cctaacaggaattctgcccgaggattgaagtgatcgaccaaatcaaatcagctgtggag 409

Query: 1280 aaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagactct 1339
 |||
 Sbjct: 410 aaagtgtgtccgggtgtggtttcttgcgctgacattcttgccatcgctgccagagactct 469

```
Query: 1340 gttcagat 1347
      ||| |||
Sbjct: 470  gttgagat 477
```

Score = 121 bits (61), Expect = 2e-23
Identities = 85/93 (91%)
Strand = Plus / Plus

```
Query: 692 ctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctcc 751
      |||||  ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 195 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcgatgggtgcttctctcc 254
```

Age Group	Number of People
0-10	18
11-20	12
21-30	10
31-40	8
41-50	6
51-60	4
61-70	2
71-80	1
81-90	1
91-100	1

Score = 87.7 bits (44), Expect = 3e-13

>gb|EY477044.1| METAY48TF JCVI-MT3 *Medicago truncatula* cDNA 5', mRNA sequence

Score = 163 bits (82), Expect = 6e-36

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	52
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[illegible]

Score = 141 bits (71), Expect = 2e-29

Identities = 161/191 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 302 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 361

Query: 1217 aacccaacaggaactctgctcgaggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 362 aatccaacaaaaattcgcccgaggattcgaagtgatcgacaaaatcaaatcagcagtg 421

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 422 gagaaagtgtgtccagggtgcagtttctgtgcgtgacatccttaccatcactgctagagac 481

Query: 1337 tctgttcagat 1347
||||||
Sbjct: 482 tctgttgagat 492

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttcac 768
|||||||
Sbjct: 227 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgttgttcttcac 286

Query: 769 gattgctttgtcaatg 784
|||||||
Sbjct: 287 gattgctttgttaatg 302

Score = 63.9 bits (32), Expect = 4e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||||||
Sbjct: 662 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacga 717

>gb|BG448404.1| NF024B09EC1F1074 Elicited cell culture Medicago truncatula cDNA clone

NF024B09EC 5', mRNA sequence
Length = 673

Score = 155 bits (78), Expect = 2e-33
Identities = 138/158 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| ||||| ||| ||||||||| || ||||| ||||| ||
Sbjct: 481 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 540

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||| ||||| ||||| ||||||||| || ||||||||| |||||
Sbjct: 541 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 600

Query: 1598 tttagegctcttggactttccaccaaggacttggtcgc 1635
||| ||||| ||||||||| |||||
Sbjct: 601 gttaatgctcttggctttccaccaaggatttggtcgc 638

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| | ||||||||| ||||||||| || ||
Sbjct: 289 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 348

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| ||||| || || || ||||||||| || || ||||| || ||||| |||||
Sbjct: 349 aatcccaacaaaaattcgcccggtgattcgaagtgatcgacaaaatcaaatcagcagtg 408

Query: 1277 gagaaagtgtgtccaggagttgttctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 409 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 468

Query: 1337 tctgttcagat 1347
||||| ||||
Sbjct: 469 tctgttgagat 479

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 214 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 273

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 274 gattgctttgttaatg 289

Score = 48.1 bits (24), Expect = 0.26
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaagg 1815
|||||
Sbjct: 649 ggtcacacaattggacaagcaagg 672

>gb|BF644619.1| NF017G06EC1F1051 Elicited cell culture Medicago truncatula cDNA clone
NF017G06EC 5', mRNA sequence
Length = 684

Score = 155 bits (78), Expect = 2e-33
Identities = 142/164 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 479 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctagtaaa 538

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 539 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaang 598

Query: 1598 tttagcgctcttggactttccaccaaggacttgggtcgcttctgtc 1641
||||
Sbjct: 599 tttaatgctcttggcttttccaccaangatttgggtcgcatgtgc 642

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 287 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 346

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 347 aatcccaacaaaattcggcccgaggattcgaagtgatcgacaaaatcaaatcagcagtg 406

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 407 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 466

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 467 tctgttgagat 477

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttccac 768
|||||||
Sbjct: 212 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 271

Query: 769 gattgctttgtcaatg 784
|||||||
Sbjct: 272 gattgctttgttaatg 287

Score = 58.0 bits (29), Expect = 3e-04
Identities = 29/29 (100%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcac 1820
|||||
Sbjct: 647 ggtcacacaattggacaagcaaggtgcac 675

>gb|CA919059.1| EST636777 MTUS Medicago truncatula cDNA clone MTUS-7C2, mRNA sequence
Length = 802

Score = 151 bits (76), Expect = 2e-32
Identities = 143/164 (87%), Gaps = 1/164 (0%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 754 cttggaggcccaacatgggatgtgaaact-ggaagaagagatgcaagaacagctagtaaa 696

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 695 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 636

Query: 1598 tttagegctcttggactttccaccaaggacttggcgcttgtc 1641
||||
Sbjct: 635 tttaatgctcttggctttccaccaaggatttggcgcatgtgc 592

Score = 117 bits (59), Expect = 3e-22
Identities = 284/359 (79%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 587 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 528

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
|||||
Sbjct: 527 aacatagatacttccttggctgcacaaggcaatcagggtgccccagacatcggttcc 468

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactac 1971
|||||
Sbjct: 467 ggggacaataatttggcacccttgatcttgaacaccaacatcctttgacaaccattac 408

Query: 1972 ttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
||||||| ||| | | ||||| || ||||| || | | ||||| || | | |||
Sbjct: 407 ttcaagaacctagttgacagtaagggtactccactccgaccaacaactctttaatggt 348

Query: 2032 ggggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctctgat 2091
|| ||||| ||||| |||| | | || || | | || ||||| |||||
Sbjct: 347 ggatccaccgattccatagtcacgaatatagcttgatccaagctcttttctcctctgat 288

Query: 2092 ttgcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatggaga 2150
|||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 287 ttgtcaccgcccatgatcaagatgggagacattagtcctctcactggctccaatggaga 229

>gb|AW830120.1| sm23a02.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-4707 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 573

Score = 151 bits (76), Expect = 2e-32
Identities = 154/180 (85%)
Strand = Plus / Plus

Query: 1160 tgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||||| || ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 232 tgtgatgggtcgattctacttgatgacacatcaagcttcaccggagagaagaacgcggga 291

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 292 cctaacaggaattctgcccgtggatttgaagtatcgaccaaataaatcagctgtggag 351

Query: 1280 aaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagactct 1339
||||||| || || ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 352 aaagtgtgtccgggtgtggtttcttgctgacattcttgccatcgctgccagagactct 411

Score = 121 bits (61), Expect = 2e-23
Identities = 85/93 (91%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctcc 751
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 137 ctgtgaaacgcacagtggaatcggccatatcaaaggagaccgcgatgggtgcttctctcc 196

Score = 75.8 bits (38), Expect = 1e-09
Identities = 87/102 (85%), Gaps = 1/102 (0%)
Strand = Plus / Plus

Query: 1542 ctgctaacaatggcatccctgcaccacttcaaaccttaacc 1583
 ||| ||| ||||| || ||||| ||||| |||||
 Sbjct: 485 ctgccaacgatggcattccaagaccacttc-aaccttaacc 525

Score = 149 bits (75), Expect = 9e-32
Identities = 162/191 (84%)
Strand = Plus / Plus

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 || ||||| || || || ||||| || || ||||| ||||| |||||
 Sbjct: 350 aatccaacagaaattcgcccggtgattcgaggtatcgacaaaatcaaacagcagtg 409

Query: 1337 tctgttcagat 1347

Score = 111 bits (56), Expect = 2e-20
Identities = 71/76 (93%)
Strand = Plus / Plus

[illegible]

Score = 93.7 bits (47), Expect = 5e-15
Identities = 83/95 (87%)
Strand = Plus / Plus

[illegible]

Length = 602

Score = 147 bits (74), Expect = 4e-31
Identities = 158/186 (84%)
Strand = Plus / Minus

```
Query: 2077  acccttctcctctgatttcgccgcgcccatgatcaagatgggagacattagtcctctcact 2136
              ||||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 393    tcctttttcgccgatttttcgccgcgcccatgatcaggatgggagacattagtcctctcact 334
```

>gb|C0516034.1| s13dSG64B1200101_445396 Glandular trichomes *Medicago sativa* cDNA,
mRNA sequence
Length = 495

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 ||||||| ||||| ||||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 298 ggatgtgatggatcaattctcttggatgacacatcaagctttaccggtgagaagaatgca 357

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 418 gagaacgtatgccccggagttgtctcatgtgccgatataccttgctattgctgccgagac 477

Score = 129 bits (65), Expect = 9e-26
Identities = 134/157 (85%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||| ||||| | | | ||||| || ||||
Sbjct: 142 gggagtaccaatgcacaactttctacaagttttactccaaaacttgccccaaactctct 201

Query: 688 tcctctgtgaaatccacagtgcattctgccatatctaaggagaccgcgatgggtgcttct 747
|| | ||||||||||| | ||| ||||||||| ||||| |||| | ||| |||||||
Sbjct: 202 accacagtgaaatccacactacaaactgccatatcaaaggaggcccgatgagtgcttct 261

Query: 748 ctctctcgcttggttcttccacgattgctttgtcaatg 784
|||||||||||||||||||||||||||||||||
Sbjct: 262 atctctcgcttggttcttccacgattgctttgtcaatg 298

>gb|C0514259.1| s13dSG76D0500042_157180 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 549

Score = 147 bits (74), Expect = 4e-31
Identities = 158/186 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatgggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||||||||||||||||| ||||| ||||||| |||
Sbjct: 297 ggatgtgatggatcaattctcttggatgacacatcaagctttaccggtgagaagaatgca 356

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| || | ||||||||||||||||| || || | ||||||| || |||||||
Sbjct: 357 aacccaaatagaaactctgctcgtggatttgatgtcatcgacaacataaagacagccgta 416

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||| || | || || ||||||||| || || || ||||||||| || ||||||| |||||
Sbjct: 417 gagaacgtatgccccggagttgtctcatgtgccgatatccttgctattgctgccgagac 476

Query: 1337 tctgtt 1342
|||||
Sbjct: 477 tctgtt 482

Score = 137 bits (69), Expect = 4e-28
Identities = 135/157 (85%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||| ||||| | | ||||| || |||
Sbjct: 141 gggagtaccaatgcacaactttctacaagttttactccaaaacttgtcccaaactctct 200

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttct 747
|| | ||||||||| | || ||||||||| ||||| ||| |||||||||
Sbjct: 201 accacagtgaaatccacactacaaactgccatatcaaaggaggcccgatgggtgcttct 260

Query: 748 ctcttcgcttggttcttccacgattgcttgtcaatg 784
||||||||||| ||||||||| |||||||||
Sbjct: 261 atcttcgcttggttcttccacgattgcttgtcaatg 297

Score = 58.0 bits (29), Expect = 3e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| || | ||||||| ||||||||| ||||| ||| ||||| |||
Sbjct: 489 cttggaggtccaacctggaatgtaaaacttggaagaagagatgctaaaacggctagtcaa 548

Query: 1538 t 1538
|
Sbjct: 549 t 549

>gb|AW686470.2| NF041G08NR1F1000 Nodulated root Medicago truncatula cDNA clone
NF041G08NR 5', mRNA sequence
Length = 481

Score = 145 bits (73), Expect = 1e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||||||||| ||||||||| ||||| | | ||||| || |||
Sbjct: 118 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgtcccaaactctct 177

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttct 747
|| | ||||||||| ||||| ||||||||| ||||| ||| ||||||| |||

Sbjct: 178 accacagtgaaatccacactgcaaactgccatatcaaaggaggcccgaaatgggtgctct 237

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784

||||| |||||||||||||||||||||||||||||||

Sbjct: 238 atctccgcttggttcttccacgattgctttgtcaatg 274

Score = 123 bits (62), Expect = 5e-24

Identities = 155/186 (83%)

Strand = Plus / Plus

Query: 1157 ggatgtgatgggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||| ||||||| || ||||||||||||||||||| ||||| ||||||| |||

Sbjct: 274 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 333

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggtattgacaacattaaatcagccgtg 1276

|| || || || ||||| ||||||||||| || || || || ||||||| || |||||||

Sbjct: 334 aatccaaatagaaactccgctcgatggatttgatgtcatcgacaacataaagacagccgta 393

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

||||| || || || || ||||||| || || || || ||||||| ||||| ||||||| |||||

Sbjct: 394 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 453

Query: 1337 tctgtt 1342

|||||

Sbjct: 454 tctgtt 459

>gb|BF639633.1| NF015A12IN1F1097 Insect herbivory Medicago truncatula cDNA clone

NF015A12IN 5', mRNA sequence

Length = 516

Score = 145 bits (73), Expect = 1e-30

Identities = 136/157 (86%)

Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687

||||||||||||||||||||||||||||||||| || || ||||| || |||||

Sbjct: 61 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgtccaaactctct 120

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747

>gb|CX530413.1| s13dNF99F02MJ016_246858 Methyl Jasmonate-Elicited Root Cell
Suspension Culture Medicago truncatula cDNA, mRNA
sequence
Length = 585

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 341 aatcccaacaaaaattcggcccgatcgaggttattgacaacattaaatcagccgtg 400

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 401 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 460

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 461 tctgttgagat 471

Score = 113 bits (57), Expect = 5e-21
Identities = 99/113 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 473 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctagtaaa 532

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcat 1590
||
Sbjct: 533 tcagctgcaacaatgacatcccgacccacttcaagcctcaaccaactcat 585

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||||
Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 265

Query: 769 gattgctttgtcaatg 784
|||||||
Sbjct: 266 gattgctttgttaatg 281

>gb|CX529528.1| s13dNF97C05MJ034_245107 Methyl Jasmonate-Elicited Root Cell
Suspension Culture Medicago truncatula cDNA, mRNA
sequence
Length = 545

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 290 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 349

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 350 aatcccaacaaaaattcggcccgatggaagtgatcgacaaaatcaaatacagcagtg 409

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 410 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 469

Query: 1337 tctgttcagat 1347
|||||||
Sbjct: 470 tctgttgagat 480

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttcac 768
||||||| || ||||| ||||| ||||| || || ||||| |||||
Sbjct: 215 caatctgccatatcaaaagagactcgcatgggtgcttctctctgcgttgttcttcac 274

Query: 769 gattgctttgtcaatg 784
||||||| |||||
Sbjct: 275 gattgctttgttaatg 290

Score = 63.9 bits (32), Expect = 4e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctag 1533
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 482 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctag 537

>gb|BF647501.1| NF068D03EC1F1029 Elicited cell culture Medicago truncatula cDNA clone
NF068D03EC 5', mRNA sequence
Length = 658

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 288 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 347

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
|| ||||| || || || ||||| || || ||||| || ||||| |||||
Sbjct: 348 aatcccaacaaaaattcggcccgatggattcgaagtgatcgacaaaatcaaatcagcagtg 407

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||| || ||||| ||||| || ||||| ||||| |||||
Sbjct: 408 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 467

Query: 1337 tctgttcagat 1347
||||| |||||

Sbjct: 468 tctgttgagat 478

Score = 141 bits (71), Expect = 2e-29
Identities = 142/165 (86%), Gaps = 1/165 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 ||||||| ||||| ||| ||||||||| ||| ||| ||| ||| |||
 Sbjct: 480 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 539

Query: 1538 tctgtgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 540 tcagctgcaaacaatgacatcccagcaccacttcaagcctcaaccaactcatctnaagg 599

```
Query: 1598 ttttagcgct-cttggactttccaccaaggacttggtcgccttgtc 1641
          |||  ||  ||||  |||  |||||  |||  |||||  |||||  |||||
Sbjct: 600  tttaatgctccttggctctttncaccaaggatttggtcgcattgtc 644
```

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

```
Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttccac 768
          |||||
Sbjct: 213 caatctgccatatcaaaagagactcgcatgggtgcttctctccttcgcttggttcttccac 272
```

```
Query: 769 gattgctttgtcaatg 784
      |||||
Sbjct: 273 gattgctttgttaatg 288
```

>gb|BF645317.1| NF030B11EC1F1092 Elicited cell culture Medicago truncatula cDNA clone
NF030B11EC 5', mRNA sequence
Length = 603

Score = 141 bits (71), Expect = 2e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 341 aatcccaacaaaaattcggcccggtggattcgaagtgatcgacaaaatcaaactcagcagtg 400

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 401 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 460

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 461 tctgttgagat 471

Score = 107 bits (54), Expect = 3e-19
Identities = 108/125 (86%), Gaps = 1/125 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 473 cttggaggcccaacatgggatgtgaaactnggaagaagagatgcaagaacagctagtaaa 532

Query: 1538 tctgctgctaacaatggcat-ccctgcacccacttcaaacccttaaccaactcatctcaag 1596
|| |||||
Sbjct: 533 tcagctgcaacaatgacatccccagcaccacttcaagcctcaaccaactcatctcaag 592

Query: 1597 attta 1601
||||
Sbjct: 593 gttaa 597

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttggttctccac 768
|||||

Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 265

Query: 769 gattgctttgtcaatg 784

|||||||

Sbjct: 266 gattgctttgttaatg 281

>gb|C0515766.1| s13dSG77F0400043_419681 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 572

Score = 139 bits (70), Expect = 9e-29

Identities = 157/186 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||||

Sbjct: 299 ggatgtgatgatcaattctcttggatgacacatcaagctttaccggtgagaagaatgca 358

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||

Sbjct: 359 aacccaaatagaaactctgctcgtggttgggtgtcatcgacaacataaagacagccgta 418

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

|||||

Sbjct: 419 gagaacgtatgccccggagttgtctcatgtgccgatatccttgctattgctgccgcagac 478

Query: 1337 tctgtt 1342

|||||

Sbjct: 479 tctgtt 484

Score = 137 bits (69), Expect = 4e-28

Identities = 135/157 (85%)

Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687

|||||

Sbjct: 143 gggagtaccaatgcacaactttctacaaagtttttactccaaaacttgccccaaactctct 202

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagacccgcatgggtgcttct 747

Sbjct: 280 tttaatgctctcggactttccaccaaagacttggtcgc 317

Score = 111 bits (56), Expect = 2e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 328 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 387

Query: 1852 aacataga 1859
|||||
Sbjct: 388 aacataga 395

Score = 93.7 bits (47), Expect = 5e-15
Identities = 128/155 (82%)
Strand = Plus / Plus

Query: 1193 agcttcaccggagagaagaacgcaaaccacaacaggaactctgctcgtggattcgaggtt 1252
|||||
Sbjct: 4 agcttcaccggagagaaaaacgcaggacctaacaggaactctgcccgtggttttgaagtg 63

Query: 1253 attgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagat 1312
|| || |||||
Sbjct: 64 atcgatcaaattaagtcagctgtggaaaaagtgtgtccgggtgtggtctcttgcgctgac 123

Query: 1313 atccttgccatcgctgccagagactctgttcagat 1347
|||||
Sbjct: 124 atccttgccatcgctgcaagagactccgttgagat 158

>gb|AW703873.1| sk25b09.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-3186 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 397

Score = 139 bits (70), Expect = 9e-29
Identities = 136/158 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

|||||
Sbjct: 136 cttggaggcccaacttgggatgtgaaacttgggaagaagagactccaggacggcaagccaa 195

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 196 tctgctgccaacaatgacatcccaagaccacttcaaacctcaaccaacttatttccaga 255

Query: 1598 tttagcgctcttggactttccaccaaggacttgggtcgc 1635
|||||

Sbjct: 256 tttaatgctctcggactttccaccaaagacttgggtcgc 293

Score = 111 bits (56), Expect = 2e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||

Sbjct: 304 ggtcacacaattggacaagcaaggtgcacaaactttagagcccgatctacaacgagacc 363

Query: 1852 aacataga 1859
|||||

Sbjct: 364 aacataga 371

Score = 73.8 bits (37), Expect = 4e-09
Identities = 103/125 (82%)
Strand = Plus / Plus

Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|||||

Sbjct: 10 aacaggaactctgcccgtggttttgaagtgatcgatcaaattaagtcagctgtggaaaaa 69

Query: 1283 gtgtgtccaggagtgttttctgcgcagatatccttgccatcgctgccagagactctgtt 1342
|||||

Sbjct: 70 gtgtgtccgggtgtggtctcttgcgctgacatccttgccatcgctgcaagagactccgtt 129

Query: 1343 cagat 1347
|||||

Sbjct: 130 gatat 134

>gb|AI495213.1| sb02b01.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1004-7586 5' similar to TR:Q41326 Q41326 PEROXIDASE
;, mRNA sequence
Length = 448

Score = 139 bits (70), Expect = 9e-29
Identities = 169/202 (83%)
Strand = Plus / Plus

Query: 1985 ttcagaagaagggtctctccactctgatcagcaactgttcaacgggtgggtccaccgact 2044
|||||
Sbjct: 4 ttcagaagaagggtctcatccattccgaccaagaactcttcaatgggtgggtccactgact 63

Query: 2045 ccattgtgctgggtacagcaccaacccgggcaccttctcctctgatttcgccgccgcca 2104
|||
Sbjct: 64 ccttagtgctacactacagcaccaacccgggectctttttcgccgatttctccgccgcca 123

Query: 2105 tgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaatt 2164
|||||
Sbjct: 124 tgatcaggatgggagacattagtcctctcactggctcccgaggagaaataagggagaact 183

Query: 2165 gtagaaggattaactaatttga 2186
|||
Sbjct: 184 gcaggagggtcaactaatttga 205

>gb|AW830098.1| sm22c01.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-4633 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 434

Score = 137 bits (69), Expect = 4e-28
Identities = 150/177 (84%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 258 tgtgatgggtcgattctacttgatgacacatcaagcttcaccggagagaagaacgcggga 317

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||

Sbjct: 318 cctaacaggaattctgcccgatgtgaagtgatcgaccaaataaatcagctgtggag 377

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| || || ||||| ||||| || || ||||| ||||| |||||

Sbjct: 378 aaagtgtgtccgggtgtggtttcttgcgctgacattcttgccatcgctgccagagac 434

Score = 121 bits (61), Expect = 2e-23
Identities = 85/93 (91%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgcgaatcgccatatctaaggagacccgcatgggtgcttctctcc 751
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 163 ctgtgaaacgcacagtggaatcgccatatcaaaggagacccgcatgggtgcttctctcc 222

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
| || ||||| ||||| ||||| ||||| |||||

Sbjct: 223 tacgtttgttcttccacgattgctttgttaatg 255

>gb|AW704238.1| sk18d12.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-2544 5' similar to TR:024336 024336
KOREAN-RADISH ISOPEROXIDASE ;, mRNA sequence
Length = 566

Score = 135 bits (68), Expect = 1e-27
Identities = 158/188 (84%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 243 tgtgatgggtcaattctacttgatgacacatcaagcttcaccggagagaaaaacgcagga 302

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|| ||||| ||||| ||||| || || || || || || ||||| ||||| |||||

Sbjct: 303 cctaacaggaactctgcccggtgtttgaagtgatcgatcaaattaagtcagctgtggaa 362

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactct 1339
||||||| || || || || ||||| || ||||| ||||| ||||| |||||

Sbjct: 363 aaagtgtgtccgggtgtggtctcttgcgctgacatccttgccatcgctgcaagagactcc 422

Query: 1340 gttcagat 1347

Sbjct: 423 gttgagat 430

Score = 129 bits (65), Expect = 9e-26

Identities = 86/93 (92%)

Query: 692 ctgtgaaatccacagtgc aatctgccatatctaaggagacccgcatgggtgcttctctcc 751

Sbjct: 148 ctgtgaaacgcacagtggaatcggccatatcaaaggagacccgcatgggtgcttctctcc 207

Query: 752 ttcgcttggttcttcacgattgctttgtcaatg 784

Sbjct: 208 tacgtttgttcttcacgattgctttgtcaatg 240

Score = 95.6 bits (48), Expect = 1e-15

Identities = 105/124 (84%)

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Sbjct: 432 cttggaggcccaacttgggatgtgaaacttgaagaagagactccaggacggcaagccaa 491

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597

Sbjct: 492 tctgctgccacaatgacatcccaagaccacttcagacctcaaccaacttatttcaga 551

Query: 1598 tttta 1601

Sbjct: 552 ttta 555

>emb|CU524253.1| CU524253 STSSHWB2Sb_KZ0ACB Theobroma cacao cDNA clone KZ0ACB3Y012FM1,

mRNA sequence

Score = 133 bits (67), Expect = 6e-27

Identities = 229/283 (80%)

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 243 ctgcccgaaggacaacaggctcaggggacaacaacttggcacccttgatatccagactcc 302

Query: 1950 aaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactc 2009
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 303 aacattttttgacaacaactacttcaagaacctcatcaacaggaggggactcctccactc 362

Query: 2010 tgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtgggtacagcaccaa 2069
|| ||| ||||| || ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 363 cgaccaacacgtgttcaatgggggctccacggattccatcgtgcggggttacagcaacaa 422

Query: 2070 cccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtc 2129
|||| || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 423 cccgagctccttcagttctgactttgtcaccggcatgatcaagatgggagacatcagtc 482

Query: 2130 tctcactggctccaatggagaaatcaggaagaattgtagaagg 2172
||||||| ||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 483 cctcactggatcaaggggagagatcaggaagaactgcagaagg 525

Score = 58.0 bits (29), Expect = 3e-04
Identities = 101/125 (80%)
Strand = Plus / Plus

Query: 1508 ggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccctgcaccc 1567
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 7 ggaaggagagatgctaggactgctagccaggctgctgccaacaacagcattcctcctcca 66

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
||||| ||| || ||| ||||| || ||||| || ||||| ||||| ||||| |||||

Sbjct: 67 acttctaacttgaacagactcatttctagattcaatgctcttggactttccaccaggac 126

Query: 1628 ttggt 1632
||||

Sbjct: 127 atggt 131

>dbj|AV771209.1| AV771209 Lotus japonicus Pods (20–30 mm in length) Lotus japonicus

cDNA clone MPD018a07_f 3', mRNA sequence
Length = 375

Score = 133 bits (67), Expect = 6e-27
Identities = 125/143 (87%), Gaps = 1/143 (0%)
Strand = Plus / Minus

Query: 2024 tcaacggtgggtccaccgactccattgtgcgtgggtacagcaccaaccgggcacattct 2083
 |||
 Sbjct: 339 tcaacggtgggtccaccgactccaccgtgcgtgggtacagcaccaaccgagctcatttt 280

Query: 2084 cctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcca 2143
 |||||
 Sbjct: 279 cctctgatttcgccagcgccatgggtcaagatgggagatatcagtcctctcactggatcca 220

```
Query: 2144 atggagaaat-caggaagaattg 2165  
      | ||||| |||||||||  
Sbjct: 219 acggtgaaatccaggaagaattg 197
```

>gb|C0516246.1| s13dSG69B0900075_445820 Glandular trichomes *Medicago sativa* cDNA,
mRNA sequence
Length = 516

Score = 131 bits (66), Expect = 2e-26
Identities = 156/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 ||||||| ||||| ||||||||| ||| || ||||| |||
 Sbjct: 162 ggatgtgatggatcaattctcttggatgacacatcaagcttactggtgagaagaatgca 221

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 ||||| || || ||||| ||||| ||||| || || || ||||| || || |||||
 Sbjct: 222 aacccaatatagaactctgctcgtggatttgatgtcatcgacgacataaagacagccgta 281

Query: 1277 gagaagtggtgccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336
 ||||| || || || ||||| || || || ||||| ||||| ||||| |||||
 Sbjct: 282 gagaacgtatgccccggagttgtctcatgtgctgatatccttgctattgctgccgagac 341

Query: 1337 tctgtt 1342
 |||

Sbjct: 342 tctgtt 347

Score = 121 bits (61), Expect = 2e-23
Identities = 133/157 (84%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||| ||||||| | | | ||||| || ||||
Sbjct: 6 gggagtaccaatgcacaactttctacaagtttttactccaaaacttgcccaaactctct 65

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcgcatgggtgcttct 747
|| | |||||||||||| | ||| || ||||||| |||||| |||| |||||||||||||
Sbjct: 66 accacagtgaaatccacactacaaactaccatatcaaaggaggcccgaatgggtgcttct 125

Query: 748 ctctctcgcttggttcttccacgattgctttgtcaatg 784
|||| |||||||||||||||||||||||||||||
Sbjct: 126 atcctccgcttggttcttccacgattgctttgtcaatg 162

Score = 103 bits (52), Expect = 5e-18
Identities = 130/156 (83%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| || || ||||||| ||||||||||||||||| |||| ||| ||||| |||
Sbjct: 354 cttggagggtccaaacctggaatgtaaaacttgaagaagagatgctaaaacggctagtcaa 413

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||||||| || |||||| ||||| ||||| ||||| || ||||| |||||
Sbjct: 414 tccgctgctaacaactgccatcccagcaccaacttccaacctcaatacactcacctcaatg 473

Query: 1598 tttagcgctcttggactttccaccaaggacttggtc 1633
||||||| |||| |||||| |||||||
Sbjct: 474 tttagcgccgttggtctttccagcaaggatttggtc 509

>gb|BF071209.1| st04h08.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1065-376 5' similar to TR:Q9XFL7 Q9XFL7 PEROXIDASE 6
;, mRNA sequence
Length = 319

Score = 131 bits (66), Expect = 2e-26
Identities = 114/130 (87%)
Strand = Plus / Plus

Query: 1218 accccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtgg 1277
||||| |||| |||||||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 81 accccaataggatctctgctcgtggatacagaggtcattgactacattagatcatccgtgt 140

Query: 1278 agaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatgctgccagagact 1337
|||| | ||||||| | |||| |||||||||||| ||||||| ||||||| ||||
Sbjct: 141 agaatgcgtgtccagtatttgtctcctgcgcagatatgcttgccatagctgccagatact 200

Query: 1338 ctgttcagat 1347
|||||||||
Sbjct: 201 ctgttcagat 210

Score = 58.0 bits (29), Expect = 3e-04
Identities = 66/77 (85%), Gaps = 1/77 (1%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||||||| | | ||||||| ||||||| ||||||| ||||||| ||||| |||||
Sbjct: 212 cttggaggccctagtttgtatgttaaagttggaagatgagacgctagatctgcttgcccta 271

Query: 1538 tctgctgctaacaatgg 1554
|||| || |||||||
Sbjct: 272 tctggtg-taacaatgg 287

>gb|EX660929.1| JS1BF51JG Salt stressed *Fragaria vesca* (strain Hawaii-4) cDNA library
Fragaria vesca cDNA clone JS1BF51, mRNA sequence
Length = 758

Score = 129 bits (65), Expect = 9e-26
Identities = 214/263 (81%), Gaps = 3/263 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
||||||||||| |||| |||||||||||| ||||| ||||| ||||| |||||
Sbjct: 238 tcaggggacaacaacttggtccacttgatcttcaatctccaacagccttcgacaacaac 297

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttc--- 2025
||||| ||| || || | ||||| | ||||||||||||||| ||||||| |||||
Sbjct: 298 tactacaataatcttatcaagaacagagggtctcctccactccgatcagcagttgttcttg 357

Query: 2026 aacggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcc 2085
|| ||||| ||||||| ||||| ||||||||||||||| || || | ||||| ||| |
Sbjct: 358 aatggtgggtccaccgattccatagtgctgggtacagcagcagccagagcacattcaca 417

Query: 2086 tctgatttcgcgcgcccatgatcaagatgggagacattagtcctctcactgggtccaat 2145
||||| || || ||||| ||||||||||||||| ||||| | || ||||||| |||||||
Sbjct: 418 tctgactttgctgccgcaatgatcaagatgggaaacatcaacccgctcactggatccaat 477

Query: 2146 ggagaaatcaggaagaattgtag 2168
||||| || ||||||| |||||
Sbjct: 478 ggagagattaggaagaactgtag 500

Score = 61.9 bits (31), Expect = 2e-05
Identities = 52/59 (88%)
Strand = Plus / Plus

Query: 1574 aaccttaaccaactcatctcaagatttagcgctcttggactttccaccaaggacttggt 1632
||||| ||||| ||||||| ||||| | ||||||| ||||||| ||||| |||||
Sbjct: 46 aacctaaaccagctcatctccagattcaacgctcttggcctttccaccaaggacatggt 104

>gb|DN950706.1| 0st2T_331 Oak tissue culture growing 2 days in hypertonic medium
Quercus robur cDNA 5', mRNA sequence
Length = 852

Score = 129 bits (65), Expect = 9e-26
Identities = 98/109 (89%)
Strand = Plus / Plus

Query: 676 ccaaacctcttctcctctgtgaaatccacagtgcaatctgccatatctaaggagacccgc 735
||||| ||||| || ||||||||||| ||||||||||||||| ||||| |||||
Sbjct: 151 ccaaaactctttccactgtgaaatccaccgtgcaatctgccatatcaaaggaagccga 210

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||||| ||||||| ||||||||||| |||||||||||||||

Sbjct: 211 atgggtgcctctctcctgcgcttggttcttccatgattgctttgtcaatg 259

Score = 101 bits (51), Expect = 2e-17
Identities = 120/143 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
|||||
Sbjct: 466 tggaatgttaaacttggaagaagagatgctaggactgcgagccaggctgctgctaataat 525

Query: 1553 ggcattccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612
|||
Sbjct: 526 agcattcctcctccaacttctaacctaaaccaactcatttctagatttaacaatttgga 585

Query: 1613 ctttccaccaaggacttggtcgc 1635
|||
Sbjct: 586 ctttccactaggacatggtcgc 608

Score = 81.8 bits (41), Expect = 2e-11
Identities = 59/65 (90%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
|||
Sbjct: 622 cacacaattgggcaagcaaggtgtacatccttcagagctcgcatatacaacgagaccaac 681

Query: 1855 ataga 1859
|||
Sbjct: 682 ataga 686

>gb|C0511866.1| s13dSG02H0700064_103632 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 483

Score = 129 bits (65), Expect = 9e-26
Identities = 149/177 (84%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 307 gatgggtcaatcctactagatgacacatcaaattttaccggagagaagaacgcactcccc 366

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||| ||||| || ||||| ||||| || ||||| |||||
Sbjct: 367 aataggaactctgttcgaggattcgatgtcattgacaacataaagacagccgtagagaac 426

Query: 1283 gtgtgtccaggagtgttttctgcgcagatatccttgccatcgctgccagagactct 1339
| ||||| ||||| || || || ||||| ||||| ||||| |||||
Sbjct: 427 atatgtccaggagtgttatcatgtgctgatatcctagccattgctgccacagactct 483

Score = 87.7 bits (44), Expect = 3e-13
Identities = 166/206 (80%), Gaps = 3/206 (1%)
Strand = Plus / Plus

Query: 582 ttgttctagattgacaattt---gtttggctctgtttgtcctcatatgggggagtgccaa 638
||||| ||||| ||||| | ||||| ||| ||| ||||| ||||| |||||
Sbjct: 96 ttgttctagattaacaatgttcagtttggttctatttttcctcataataggagtgccaa 155

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698
||||| ||||| ||||| ||||| | | ||||| || ||| ||| |
Sbjct: 156 tgcacaactctctacaaacttttactcaaaaactgtccaaactcttccattgtcca 215

Query: 699 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 758
| | ||||| || ||||| ||||| | || ||||| ||||| || |||
Sbjct: 216 acgccaagtgaatccgctatatcaaaggaggcacgaatgggtgcttctattctccgatt 275

Query: 759 gttcttccacgattgctttgtcaatg 784
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 276 gttcttccacgattgctttgtcaatg 301

>gb|BF650349.1| NF096E02EC1F1017 Elicited cell culture Medicago truncatula cDNA clone
NF096E02EC 5', mRNA sequence
Length = 474

Score = 129 bits (65), Expect = 9e-26
Identities = 154/184 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 291 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 350

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 351 aatcccaacaaaaattcggcccgaggattcgaagtgatcnacaaaatcaaatacagcagtg 410

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 411 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 470

Query: 1337 tctg 1340
|||
Sbjct: 471 tctg 474

Score = 95.6 bits (48), Expect = 1e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctctccttcgcttgttcttcac 768
|||||
Sbjct: 216 caatctgccatatcaaaagagactcgcatgggtgcttctctctcgcgttgttcttcac 275

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 276 gattgctttgttaatg 291

>gb|BE022178.1| sm68f01.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-9074 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 352

Score = 129 bits (65), Expect = 9e-26
Identities = 86/93 (92%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgcattctgccatatctaaggagaccgcgatgggtgcttctctcc 751
|||||

Sbjct: 45 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcatgggtgcttctctcc 104

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784

| | | | | | | | | | | | | | | | | | | | | |

Sbjct: 105 tacgtttgttcttccacgattgctttgtcaatg 137

Score = 60.0 bits (30), Expect = 7e-05

Identities = 54/62 (87%)

Strand = Plus / Plus

Query: 1181 gatgacacatcaagcttcaccggagagaagaacgcaaaccaccaaggaactctgctcgt 1240

| | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 161 gatgacgcatcaagcttcaccggagagaagacgcaggacctaacaggaactctgcccgt 220

Query: 1241 gg 1242

| |

Sbjct: 221 gg 222

>gb|AW666186.1| sk33d05.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1028-3970 5' similar to SW:PERX_BRARA P00434

PEROXIDASE P7 ;, mRNA sequence

Length = 329

Score = 125 bits (63), Expect = 1e-24

Identities = 120/139 (86%)

Strand = Plus / Plus

Query: 1497 atgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556

| | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 8 atgtgaaacttggaagaagagactccaggacggcaagccaatctgctgccaacaatgaca 67

Query: 1557 tccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgacttt 1616

| | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 68 tcccaagaccacttcaaaccttaaccaacttatttcagatttaatgctctcgacttt 127

Query: 1617 ccaccaaggacttggtcgc 1635

| | | | | | | | | |

Sbjct: 128 ccaccaaagacttggtcgc 146

Score = 111 bits (56), Expect = 2e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 157 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 216

Query: 1852 aacataga 1859
|||||
Sbjct: 217 aacataga 224

>gb|AW685593.1| NF029D05NR1F1000 Nodulated root Medicago truncatula cDNA clone
NF029D05NR 5', mRNA sequence
Length = 677

Score = 117 bits (59), Expect = 3e-22
Identities = 284/359 (79%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 592 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 533

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
|||||
Sbjct: 532 aacatagatacttctttgctcgcaaggcaatcagggtgcccccaagacatcgggttcc 473

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactac 1971
|||||
Sbjct: 472 ggggacaataatttggcaccccttgatcttgcaacaccaacatcctttgacaaccattac 413

Query: 1972 ttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
|||||
Sbjct: 412 ttcaagaacctagttgacagtaagggtactccactccgaccaacaactctttaatggt 353

Query: 2032 ggggccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctctgat 2091
|||
Sbjct: 352 ggatccaccgattccatagtcacgaatatagcttgatccaagctcttttctcctctgat 293

Query: 2092 ttgccgcccgcgatgatcaagatgggagacattagtcctctcactggctccaatggaga 2150
||||| | ||||||||||||||||||||||||||||||| ||||| || || |||||||||
Sbjct: 292 ttgctaccgccgatgatcaagatgggagacattagtcctctcaccggttcaaattggaga 234

Score = 81.8 bits (41), Expect = 2e-11
Identities = 72/81 (88%), Gaps = 1/81 (1%)
Strand = Plus / Minus

Query: 1562 gcaccacacttcaaaccttaaccaactcatctcaagatttagcgctc-ttggactttccac 1620
||||||| ||| ||||||||||||||||||| |||| |||| |||| |||||||||
Sbjct: 677 gcaccacacttcaagcctcaaccaactcatctcaaggtttaatgctctttggtctttccac 618

Query: 1621 caaggacttggtcgcttctgtc 1641
|||||| |||||||| |||||
Sbjct: 617 caaggatttggtcgcatctgtc 597

>dbj|FS263447.1| FS263447 RPSC Glycyrrhiza uralensis cDNA clone S02198-34-013 5', mRNA
sequence
Length = 146

Score = 113 bits (57), Expect = 5e-21
Identities = 72/77 (93%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||||| ||||||| || || || |||||||||
Sbjct: 70 ggatgtgatggttcaattctactggatgacacatcaagctttacaggggagaagaacgca 129

Query: 1217 aaccccaacaggaactc 1233
||||| |||||||||
Sbjct: 130 aacccgaacaggaactc 146

Score = 107 bits (54), Expect = 3e-19
Identities = 66/70 (94%)
Strand = Plus / Plus

Query: 715 gccatatctaaggagacccgcgatgggtgcttctctccttcgcttggttcttccacgattgc 774
||||||| ||||||| ||||||| ||||| ||||||| ||||||| |||||

Sbjct: 1 gccatatcaaaggagaccgcatgggtgcttccctcctccgcttgttcttccatgattgc 60

Query: 775 tttgtcaatg 784

|||||||

Sbjct: 61 tttgtcaatg 70

>gb|BF650698.1| NF099E07EC1F1053 Elicited cell culture Medicago truncatula cDNA clone
NF099E07EC 5', mRNA sequence
Length = 501

Score = 113 bits (57), Expect = 5e-21

Identities = 157/191 (82%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||| | |||||||

Sbjct: 283 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 342

Query: 1217 aacccaacaggaactctgctcgtggattcgagttattgacaacattaaatcagccgtg 1276

|| ||||| || || || ||||| | || || ||||| || ||||| || ||

Sbjct: 343 aatccaacaaaaattcgcccggtgattccaagtgatcgacaaaatcaatcancagng 402

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

||||||| ||||| | ||||| || | || ||||| ||||| ||||| |||||

Sbjct: 403 gagaaagtatgtccagggtgcagtttcatgcctgacatccttaccatcactgctagagac 462

Query: 1337 tctgttcagat 1347

||||| |||

Sbjct: 463 tctgttgagat 473

Score = 95.6 bits (48), Expect = 1e-15

Identities = 69/76 (90%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttcttccac 768

||||||| || ||||| ||||||| || || ||||| |||||

Sbjct: 208 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 267

Query: 769 gattgctttgtcaatg 784

|||||
Sbjct: 268 gattgctttgttaatg 283

>gb|EV262518.1| MTYEW71TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 742

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
|||||
Sbjct: 287 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccc 346

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|||
Sbjct: 347 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 406

Query: 1283 gtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|||
Sbjct: 407 gtatgccccgagttgtatcatgtgctgatatccttgccattgctgccacagactc 462

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
|||||
Sbjct: 202 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 261

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 262 ccacgattgctttgtcaatg 281

Score = 71.9 bits (36), Expect = 2e-08
Identities = 132/164 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||| || | ||||||| |||
Sbjct: 473 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 532

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| | | |||| || ||||| || ||||| ||||||| ||||| |||||
Sbjct: 533 tctgatacgaacactgccatcccaagaccaacttccaaccttaataactcacctcaatg 592

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgcttgtc 1641
|||| | |||| ||||||||||||||||| ||||| |||||
Sbjct: 593 tttagaatgttggcttttccaccaaggacttagtcgcatgtc 636

Score = 63.9 bits (32), Expect = 4e-06
Identities = 62/72 (86%)
Strand = Plus / Plus

Query: 1788 aggtgggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||||||||||||||||||||| |||| | || | || ||||||| ||
Sbjct: 637 agtgctcacacaattggacaagcaagggtgtacaacatttaggtacgaatctacaatga 696

Query: 1848 gaccaacataga 1859
|||||||||||
Sbjct: 697 gaccaacataga 708

>gb|EV260463.1| MTYE803TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 773

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||||||| | ||||||||||||| || ||||||||||||||||| |||
Sbjct: 310 gatgggtcaattctactagatgacacatcaactttaccggagagaagaacgcactcccg 369

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||||| || ||||||| || ||||||||| || | || || |||||
Sbjct: 370 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaa 429

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|| || || ||||| || || || ||||| ||||| |||||
Sbjct: 430 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 485

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttctt 764
||||| ||||| ||||| | || || ||||| ||||| |||||
Sbjct: 225 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 284

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 285 ccacgattgctttgtcaatg 304

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||| | || || ||||| ||||| ||||| || || ||||| |||
Sbjct: 496 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 555

Query: 1538 tctgctgctaacaatggcatccctgcaccacattcaaaccttaaccaactcatctcaaga 1597
||| || ||| || ||||| || ||||| ||||| |||||
Sbjct: 556 tctgatgcgaacactgccatcccaagaccaactccaaccttaataactcacctcaatg 615

Query: 1598 tttagcgctcttggaactttccaccaaggacttggtcgcttgtc 1641
||| | ||| ||||| ||||| |||||
Sbjct: 616 tttaagaatgttggtctttccaccaaggacttagtcgcattgtc 659

Score = 63.9 bits (32), Expect = 4e-06
Identities = 62/72 (86%)
Strand = Plus / Plus

Query: 1788 agtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847

||||| |||||||||||||||||| ||||||| || || | || ||||||| ||
Sbjct: 660 aggtgctcacacaattggacaagcaaagtgcacaacatttaggtacgaatctacaatga 719

Query: 1848 gaccaacataga 1859

|||||||||||
Sbjct: 720 gaccaacataga 731

>gb|EV258111.1| MTYDG59TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 677

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||||||| | ||||||||||||| ||| ||||||||||||||||| |||
Sbjct: 305 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccg 364

Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | |||||||| ||| |||||||| | ||||||||||||| || | || || |||||
Sbjct: 365 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 424

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|| || | |||||||| || || || ||||||||||||| ||||||| |||||
Sbjct: 425 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 480

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttctt 764
||||||||| |||||||| ||||| | || || ||||||||| |||| |||||||||
Sbjct: 220 agtgcaatccgccatatcaaggaggcacgaattggtgcttctatcctccgcttggttctt 279

Query: 765 ccacgattgctttgtcaatg 784
|||||||||||
Sbjct: 280 ccacgattgctttgtcaatg 299

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| |||||||||||||||| || | ||||||| |||
Sbjct: 491 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacaactgctagtcaa 550

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || ||||||| ||| ||||| ||||||| ||||| |||||
Sbjct: 551 tctgatgcgaacactgccatcccaagaccgacttccaaccttaataactcacctcaatg 610

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||| | |||| |||||||||||||||| ||||| |||||
Sbjct: 611 tttagaatgttggctttccaccaaggacttagtcgcattgtc 654

>gb|DW017370.1| EST1226331 MTY Medicago truncatula cDNA clone MTYAS77, mRNA sequence
Length = 793

Score = 111 bits (56), Expect = 2e-20
Identities = 203/252 (80%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| |||||||||||||||||||||||| || || | || ||||||| |||
Sbjct: 307 agtgctcacacaattggacaagcaaggtgcacaacatttaggtacgaatctacaatga 366

Query: 1848 gaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagg 1907
|||||||||| || | ||||| || || ||||| | ||||| | |||||||
Sbjct: 367 gaccaacatagatacttcttttgctagcacaaggcaatctaattgcccaaagacatcagg 426

Query: 1908 gtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaacta 1967
|||||||||||||| ||||||| ||||||| || ||||| || |||||||
Sbjct: 427 atcaggggacaacaatttggcacctcttgatctccatactccacttctttgacaactg 486

Query: 1968 ctacttcaagaacctcggttcagaagaaggtctcctccactctgatcagcaactgttcaa 2027
||||| || ||||||| ||||| || ||||||| || || || || || ||||| |||||
Sbjct: 487 ctactacaggaacctgtttcaaaacaaggtcttcttcattcagaccaacaacttttcaa 546

Query: 2028 cgggtgggtccac 2039

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

[illegible]

Score = 54.0 bits (27), Expect = 0.004
Identities = 84/103 (81%)
Strand = Plus / Plus

[illegible]

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Length = 773

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
||||| ||||||| | |||||||||||| || |||||||||||||||| |||
Sbjct: 311 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccg 370

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||||| || ||||||| || |||||||||||| || | || || |||||
Sbjct: 371 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 430

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|| || || ||||||| || || || |||||||||||||| ||||||| |||||
Sbjct: 431 gtatgccccgagttgtatcatgtgctgatatccttgccattgctgccacagactc 486

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||||| ||||||| ||||| | || || |||||||| |||| |||||||||
Sbjct: 226 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 285

Query: 765 ccacgattgctttgtcaatg 784
||||||| |||||||
Sbjct: 286 ccacgattgctttgtcaatg 305

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| |||||||||||||||| || | |||||||| |||
Sbjct: 497 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 556

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || ||||| || ||||| ||||||| ||||| |||||
Sbjct: 557 tctgatgcgaacactgccatcccaagaccaacttccaaccttaataactcacctcaatg 616

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgcttgtc 1641
|||| | |||| |||||||||||||| |||| |||||

Sbjct: 617 tttaagaatgttggtctttccaccaaggacttagtcgcattgtc 660

Score = 71.9 bits (36), Expect = 2e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||||||||||||||||||||||||| || || | || |||||||| ||
Sbjct: 661 aggtgctcacacaattggacaagcaaggtgcacaacatttagggtacgaatctacaatga 720

Query: 1848 gaccaacataga 1859
|||||||||||
Sbjct: 721 gaccaacataga 732

>gb|C0513179.1| s13dSG23G0900068_129522 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 561

Score = 111 bits (56), Expect = 2e-20
Identities = 169/206 (82%), Gaps = 3/206 (1%)
Strand = Plus / Plus

Query: 582 ttgttctagattgacaattt---gtttggctctgtttgtcctcatatgggggagtgccaa 638
||||||||||| |||| | |||||| || || || |||||||| |||||||||
Sbjct: 102 ttgttctagattaacaatgttcagtttggttctatttctcctcataatagggagtgccaa 161

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698
||||||||| |||| ||||||||| | | | |||| | |||| || |||| |
Sbjct: 162 tgcacaactctctacgaacttttactccaaaacttgccccaaactctcttccactgtcca 221

Query: 699 atccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 758
| | |||||||| || |||| |||||| | || |||||||||||| |||| |||||
Sbjct: 222 acgccaagtgcgaatccgctatatcgaaggaggcacgaatgggtgcttctatcctccgctt 281

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||||||||||||||||
Sbjct: 282 gttcttccacgattgctttgtcaatg 307

Score = 111 bits (56), Expect = 2e-20
Identities = 149/180 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 313 gatgggtcaatcctactagatgacacatcaaattttaccggagagaagaacgcactcccg 372

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||||| ||| ||||| || || ||||| ||||| || ||||| |||||
Sbjct: 373 aataggaactctgttcgaggatttgatgtcattgacaacataaagacagccgtagagaac 432

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactctgtt 1342
| ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 433 atatgtccaggagttgtatcatgtgtgatatcctagccattgctgccacatactctgtt 492

Score = 54.0 bits (27), Expect = 0.004
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| | ||||| ||||| ||||| ||||| || || ||||| |||||
Sbjct: 499 cttggaggcccaaactggaatgttaaacttggaagaagagatgccacgactgctagtcaa 558

Query: 1538 tct 1540
|||
Sbjct: 559 tct 561

>gb|C0512465.1| s13dSG100C120008_114444 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 614

Score = 111 bits (56), Expect = 2e-20
Identities = 149/180 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || || ||||| ||||| |||||
Sbjct: 77 gatgggtcaatcctactagatgacacatcaaattttactggagagaagaacgcactcccg 136

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||| ||||| || ||||| || ||| ||| |||||
Sbjct: 137 aataggaactctgttcgaggattcgatgtcattgacaacataaagacagtcgtagagaac 196

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactctgtt 1342
| ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 197 atatgtccaggagttgtatcatgtgctgatatcctagccattgctgccacagactctgtt 256

Score = 87.7 bits (44), Expect = 3e-13
Identities = 134/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||| ||||| ||||| ||||| ||| ||||| |||
Sbjct: 263 cttggtggcccaacctggaatgtaaaacttgggagaagagatgccacgactgctagtcaa 322

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaactcatctcaaga 1597
||||||| |||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 323 tctgctgcgaacactgccatcccagcaccaacttccaaccttaatggactcacctcaatg 382

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||| | ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 383 tttagaatgttggctttccaccaaggacttagtcgcattgtc 426

Score = 71.9 bits (36), Expect = 2e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 427 aggtgctcacacaattggacaagcaaggtgcacaacatttagggctcgaatctacaatga 486

Query: 1848 gaccaacataga 1859
|| |||||
Sbjct: 487 gaacaacataga 498

Score = 69.9 bits (35), Expect = 7e-08
Identities = 59/67 (88%)
Strand = Plus / Plus

Query: 718 atatctaaggagacccgcatgggtgcttctctccttcgcttggttcttccacgattgcttt 777
||||| ||||| | || ||||| ||||| | || || ||||| ||||| |||||
Sbjct: 5 atatcaaaggaggcacgaatgggtgcttctattctccgattgttcttccacgattgcttt 64

Query: 778 gtcaatg 784
|||||||
Sbjct: 65 gtcaatg 71

>gb|BG456493.1| NF082E02PL1F1017 Phosphate starved leaf Medicago truncatula cDNA
clone NF082E02PL 5', mRNA sequence
Length = 675

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
||||| ||||| || ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 280 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcaactccc 339

Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||| || ||||| || ||||| || || || || |||||
Sbjct: 340 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 399

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|| || | ||||| || || || ||||| ||||| ||||| |||||
Sbjct: 400 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 455

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttggttctt 764
||||||| ||||| ||||| | || || ||||| ||||| |||||
Sbjct: 195 agtgcaatccgccatatcaaaggaggcacgaattgggtgcttctatcctccgcttggttctt 254

Query: 765 ccacgattgctttgtcaatg 784

Score = 71.9 bits (36), Expect = 2e-08
Identities = 87/104 (83%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaa 1581

Score = 61.9 bits (31), Expect = 2e-05
Identities = 34/35 (97%)
Strand = Plus / Plus

Query: 1788 aggtgggtcacacaattggacaagcaaggtgcacaa 1822

>gb|BG456057.1| NF073F02PL1F1025 Phosphate starved leaf *Medicago truncatula* cDNA
clone NF073F02PL 5', mRNA sequence
Length = 663

Score = 111 bits (56), Expect = 2e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282

Score = 109 bits (55), Expect = 8e-20
Identities = 112/131 (85%)
Strand = Plus / Minus

Query: 1502 aaacttggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccct 1561
|||||
Sbjct: 230 aaacttggaagaagagatgcaagaagtgctagccagctcgcggctaataatggcattccct 171

Query: 1562 gcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||||
Sbjct: 170 gcaccaacttcgaacttgaaccaactcattccaggttcaatgctcttggactttccacc 111

Query: 1622 aaggacttggt 1632
|
Sbjct: 110 agggacttggt 100

Score = 75.8 bits (38), Expect = 1e-09
Identities = 50/54 (92%)
Strand = Plus / Minus

Query: 731 cccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 499 cccgaatgggtgcttctctgcttcgattgttcttccacgactgctttgtcaatg 446

Score = 56.0 bits (28), Expect = 0.001
Identities = 118/148 (79%)
Strand = Plus / Minus

Query: 1195 cttcaccggagagaagaacgcaaaccaccaaggaactctgctcgtggattcgaggttat 1254
|||||
Sbjct: 408 cttcaccggagagaaaaatgctatcccgaatcggaactcagctcgcggattcgatgttgt 349

Query: 1255 tgacaacattaaatcagccgtggagaaagtgtgtccaggagttgttctcgcgcagatat 1314
|||
Sbjct: 348 tgataacatcaagtgcgtgttgagaatgtttgccctggtgtagtttcttgtgctgatat 289

Query: 1315 ccttgccatcgctgccagagactctgtt 1342
|

Sbjct: 288 cttggccattactgctagagactctgtt 261

>gb|DW481566.1| GH_RMIRS_031_E08_056_F Cotton Normalized Library random primed
Gossypium hirsutum cDNA, mRNA sequence
Length = 716

Score = 109 bits (55), Expect = 8e-20
Identities = 112/131 (85%)
Strand = Plus / Plus

Query: 1502 aaacttggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccct 1561
|||||
Sbjct: 486 aaacttggaagaagagatgcaagaagtgctagccagtctgcggtataataatggcattcct 545

Query: 1562 gcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||||
Sbjct: 546 gcaccaacttcgaacttgaaccaactcattccaggttcaatgctcttggactttccacc 605

Query: 1622 aaggacttggt 1632
|
Sbjct: 606 aaggacttggt 616

Score = 75.8 bits (38), Expect = 1e-09
Identities = 50/54 (92%)
Strand = Plus / Plus

Query: 731 cccgcatgggtgcttctctcttcgcttgttcttccacgattgcttgtcaatg 784
|||||
Sbjct: 217 cccgaatgggtgcttctctgcttcgattgttcttccacgactgcttgtcaatg 270

Score = 56.0 bits (28), Expect = 0.001
Identities = 118/148 (79%)
Strand = Plus / Plus

Query: 1195 cttcaccggagagaagaacgcaaaccccaacaggaactctgctcgtggattcgaggttat 1254
|||||
Sbjct: 308 cttcaccggagagaaaaatgctatcccgaatcgaactcagctcgcggattcgatgttgt 367

Query: 1255 tgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatat 1314
||| |||| | |||| | |||| | || | || | || |||| | || ||||
Sbjct: 368 tgataacatcaagtcagctgttgagaatgtttgccctgggtgtagtttcttgctgatata 427

Query: 1315 ccttgccatcgctgccagagactctgtt 1342
| | |||| | || |||||||||
Sbjct: 428 cttggccattactgctagagactctgtt 455

>gb|DV443257.1| CV01009B1D06.f1 CV01-normalized library Manihot esculenta cDNA clone
CV01009B1D06.f1, mRNA sequence
Length = 753

Score = 107 bits (54), Expect = 3e-19
Identities = 108/126 (85%)
Strand = Plus / Plus

Query: 1497 atgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556
||||||| ||||| |||| | ||||| || |||| |
Sbjct: 422 atgttaaacttgaagaagagatgctagaactgcaagcctttctgctgcaataatggta 481

Query: 1557 tccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgacttt 1616
| ||| | || |||| | |||| | ||||| ||||| | ||||| || ||||
Sbjct: 482 ttctctccaacttctaacctcaaccaactcatctcaagattcaacgctctcggccttt 541

Query: 1617 ccacca 1622
| ||||
Sbjct: 542 caacca 547

Score = 65.9 bits (33), Expect = 1e-06
Identities = 45/49 (91%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgctgttcttccacgattgctttgtcaatg 784
||||||| || | ||||| ||||| ||||| ||||| ||||
Sbjct: 163 atgggtgcttccctcgcttcgctgttcttccatgattgctttgttaatg 211

Score = 56.0 bits (28), Expect = 0.001
Identities = 70/84 (83%)
Strand = Plus / Plus

Query: 1256 gacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatatac 1315
||||| || ||||| || || ||||| ||||| ||||| || || || |||||
Sbjct: 310 gacaatataaaatccgcagttgagaaagcttgcctggagtagtctcatgtgctgatatac 369

Query: 1316 cttgccatcgctgccagagactct 1339
||||||| |||||
Sbjct: 370 cttgccatcgctgctagagactct 393

Score = 54.0 bits (27), Expect = 0.004
Identities = 27/27 (100%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
||||||| |||||
Sbjct: 574 cacacaattggacaagcaaggtgcaca 600

>gb|DY633234.1| Medicago--03-I06.g1 Subtracted medicago cDNA library specific for
UV-B irradiation Medicago truncatula cDNA clone
Medicago--03-I06, mRNA sequence
Length = 290

Score = 105 bits (53), Expect = 1e-18
Identities = 122/145 (84%)
Strand = Plus / Plus

Query: 1901 catcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttg 1960
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 104 catcaggatcaggtgacaacaatttggcacctcttgatcttcagactcctagttcttttg 163

Query: 1961 acaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaac 2020
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 164 acaacaactacttcaagaaccttgttcagaacaagggtcttctcattcagaccaacaac 223

Query: 2021 tgttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 224 tttttaacggcgggtccaccaactc 248

>gb|DY633115.1| Medicago--03-I06.b1 Subtracted medicago cDNA library specific for

UV-B irradiation Medicago truncatula cDNA clone
Medicago--03-I06, mRNA sequence
Length = 290

Score = 105 bits (53), Expect = 1e-18
Identities = 122/145 (84%)
Strand = Plus / Minus

Query: 1901 catcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttg 1960
||||||| ||||| ||||||||| ||||||| ||||||||| ||||| | |||||
Sbjct: 187 catcaggatcaggtgacaacaatttggcacctcttgatcttcagactcctagttcttttg 128

Query: 1961 acaactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaac 2020
||||| ||||||||||||||| ||||||| ||||||| ||||| || || |||||
Sbjct: 127 acaacaactacttcaagaaccttggttcagaacaagggtcttctccattcagaccaacaac 68

Query: 2021 tgttcaacgggtgggtccaccgactc 2045
| || ||||| ||||||||| |||||
Sbjct: 67 tttttaacggcgggtccaccaactc 43

>gb|BG359643.1| sac26g07.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-3398 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 633

Score = 105 bits (53), Expect = 1e-18
Identities = 120/133 (90%), Gaps = 7/133 (5%)
Strand = Plus / Plus

Query: 1508 ggaagaagagacgc-tagaa-ctgctagcc-aatctgct-gctaacaatggca-tccctg 1562
||||||||||||| ||||| ||||||| || ||||||||| ||||||||||||| |||||
Sbjct: 334 ggaagaagagacgcctagaaactgctaaccaatctgcttgctaacaatggcaattcctc 393

Query: 1563 caccacttcaaa-ccttaaccaactcatctcaagatttagcgctcttgactttcca-c 1620
||||||||||||| ||||||||||||||||||||| || ||||||||||||||||| |
Sbjct: 394 caccacttcaaaaccttaaccaactcatctcaagattcaccgctcttgactttccacc 453

Query: 1621 caaggacttggtc 1633
||| |||||||||
Sbjct: 454 caaagacttggtc 466

Score = 91.7 bits (46), Expect = 2e-14
Identities = 109/124 (87%), Gaps = 12/124 (9%)
Strand = Plus / Plus

Query: 1162 tgatggttcaattcta-ttggatgacacatcaag--cttcaccggagagaagaa--cgca 1216
|||||
Sbjct: 87 tgatggttcaattctatttggatgacacatcaagnncttcaccggagagaagaanncgca 146

Query: 1217 aaccccaacagg---aactctgctcgtggat--tcgaggttattgaca--acattaaatc 1269
|||||
Sbjct: 147 aaccccaacaggggaacctctgctcgtggatacccgaggtcattgacannacattaaatc 206

Query: 1270 agcc 1273
||||
Sbjct: 207 agcc 210

>gb|GT138697.1| METCC85TF JCVI-MT3 Medicago truncatula cDNA 5', mRNA sequence
Length = 726

Score = 103 bits (52), Expect = 5e-18
Identities = 70/76 (92%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 227 caatctgccatatcaaaagagaccgcgatgggtgcttctcttctgcgtttgttcttccac 286

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 287 gattgctttgttaatg 302

Score = 91.7 bits (46), Expect = 2e-14
Identities = 208/262 (79%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 410 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 469

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtca 1911
 ||||| || | |||| | || |||| | | |||| | |||| | ||
 Sbjct: 470 aacatagatacttcctttgctcgcacaaaggcaatcagggtgcccaagacatcgggttcc 529

```
Query: 1972 ttcaagaacctcggttcagaagaagggtctctccactctgatcagcaactgttcaacggt 2031
          |||||
Sbjct: 590 ttcaagaacctagttgacagtaagggactactccactccgaccaacaactctttaatggt 649
```

Score = 77.8 bits (39), Expect = 3e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

```
Query: 1631 gtcgccttgtc 1641
      ||||| |||||
Sbjct: 395 gtcgcattgtc 405
```

```
Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagc 1195  
      |||||  
Sbjct: 302 ggatgtgatggttcaattcttcgatgacacatcaagc 340
```

Gm-c1028-658 5' similar to TR:P93548 P93548 PEROXIDASE
PRECURSOR ;, mRNA sequence
Length = 286

Score = 103 bits (52), Expect = 5e-18
Identities = 103/120 (85%)
Strand = Plus / Plus

Query: 2023 ttcaacggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttc 2082
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 16 ttcaatggtggttccactgactccatagtgctacctacagcaccaacccggcctccttt 75

Query: 2083 tcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctcc 2142
| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76 ttgccgatttctccgccgcatgatccgatgggagacattagtcctcctcaccggctcc 135

>emb|CU485516.1| CU485516 CUSHIONC_KZOACAC Theobroma cacao cDNA clone KZOACAC4Y017FM1,
mRNA sequence
Length = 540

Score = 101 bits (51), Expect = 2e-17
Identities = 225/283 (79%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 516 ctgcccgaaggacaacaggttcaggggacaacaacttggcacccttgatatccagactcc 457

Query: 1950 aaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactc 2009
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 456 aacattttttgacaacgattacttcaagaacctcatcaacaggagaggactcctccactc 397

Query: 2010 tgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaa 2069
|| || || ||||| || || ||||| || ||| ||||| || ||||| |||||
Sbjct: 396 cgaccaacagctgttcaatgggggtccacggattccttcgtgcggggttacagcaacaa 337

Query: 2070 cccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtc 2129
|||| || ||||| || ||| || || || ||||| ||||| ||||| |||||
Sbjct: 336 cccgagctccttcagttttgactttgtcaccggcatgatcaagatgggagacatcagtc 277

Query: 2130 tctcactggctccaatggagaaatcaggaagaattgtagaagg 2172

||||||| || | |||| | ||||| || || |||||
Sbjct: 276 cctcactggatcaaggggagagatcaggaagaactgcagaagg 234

>gb|BG454205.1| NF108A01LF1F1001 Developing leaf Medicago truncatula cDNA clone
NF108A01LF 5', mRNA sequence
Length = 630

Score = 101 bits (51), Expect = 2e-17
Identities = 144/175 (82%)
Strand = Plus / Plus

Query: 1181 gatgacacatcaagcttcaccggagagaagaacgcaaaccccaacaggaactctgctcgt 1240
||||||| ||||| ||||| ||||| || || || ||||| |||||
Sbjct: 7 gatgacacatcaagctttaccggtgagaagaatgcaaatacgaactccgctcgt 66

Query: 1241 ggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtccaggagtgtt 1300
||||| || || || ||||| || ||||| ||||| || || |||||
Sbjct: 67 ggatttgatgtcatcgacaacataaagacagccgtagagaacgtatgccccggagttgta 126

Query: 1301 tcctgcgcagatatccttgccatcgctgccagagactctgttcagattgtaagt 1355
|| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 127 tcatgtgctgatatcctagccattgctgccgagactctgttgcaattgtaagt 181

Score = 95.6 bits (48), Expect = 1e-15
Identities = 90/104 (86%)
Strand = Plus / Plus

Query: 1475 tagcttgaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagc 1534
||||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 256 tagcttgagggtccaacctggaatgtaaaacttgaagaagagatgctaaaacggctagt 315

Query: 1535 caatctgctgctaacaatggcatccctgcacccacttcaaacct 1578
||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 316 caatccgctgctaactgcatcccgccaccaacttcaaacct 359

Score = 77.8 bits (39), Expect = 3e-10
Identities = 57/63 (90%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
|||||
Sbjct: 556 cacacaattggacaagcaaggtgtacaaatcttagggcacgaatctacaacgagaccaac 615

Query: 1855 ata 1857
|||
Sbjct: 616 ata 618

>gb|BE943474.1| EST423053 MGHG Medicago truncatula cDNA clone pMGHG-15J14, mRNA
sequence
Length = 480

Score = 101 bits (51), Expect = 2e-17
Identities = 138/167 (82%)
Strand = Plus / Plus

Query: 1172 attctattggatgacacatcaagcttcaccggagagaagaacgcaaaccaccaaggaac 1231
|||||
Sbjct: 1 attctactagatgacacatcaaactttaccggagagaagaacgcactcccgataagaac 60

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
|||||
Sbjct: 61 tctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaacgtatgcccc 120

Query: 1292 ggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|||||
Sbjct: 121 ggagttgtatcatgtgctgatatccttgccattgctgccacagactc 167

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 178 cttgggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 237

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 238 tctgatgcgaacactgccatcccaagaccaacttccaaccttaataactcacctcaatg 297

Query: 1598 ttttagcgctcttggactttccaccaaggacttggtgccttgtc 1641
||| | ||| ||||| |||||
Sbjct: 298 tttaagaatggttgctttccaccaaggacttagtcgcatgtgc 341

Score = 71.9 bits (36), Expect = 2e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

```
Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
          ||||| ||||||||| ||||||||| || || | || ||||| ||
Sbjct: 342 aggtgctcacacaattggacaagcaaggtgcacaaacatttagggtacgaatctacaatga 401
```

```
Query: 1848 gaccaacataga 1859
      |||||
Sbjct: 402 gaccaacataga 413
```

```
>gb|ES840062.1| UFL_061_05 Cotton fiber 0-10 day post anthesis Gossypium hirsutum
      cDNA, mRNA sequence
      Length = 1368
```

Score = 99.6 bits (50), Expect = 8e-17
Identities = 221/278 (79%)
Strand = Plus / Plus

Query: 1906 gggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaac 1965
 ||||||| || ||| |||| | || ||||| |||||
 Sbjct: 204 gggtcaggggacaacaattgtcacgcgttgacatccagactccaacatattttgacaac 263

Query: 1966 tactacttcaagaacctcggtcagaagaagggtctcctcactctgatcagcaactgttc 2025
 | ||||| | |||| | ||| || | ||||| |||| | |||||
 Sbjct: 264 aagtaacttcaacaacctcatcggaagagggggtgctccactcggaatcaagagttgttc 323

Query: 2026 aacggtgggtccaccgactccattgtgcgtggctacagcaccaacctgggcaccttcttc 2085
|| || | ||||||| ||||| | | ||||| | ||||| |
Sbjct: 324 aatgggggatccaccgactccattgtaaggccttacagtaaaaacctgagctccttcagc 383

Query: 2086 tctgatttcgcgcgcgcatgatcaagatgggagacattagtcctctcactggctccaat 2145

Sbjct: 384 tctgattttgttacagccatgattaagatgggagacattagtcactcactggatcaaag 443

Query: 2146 ggagaaatcaggaagaattgtagaaggattaactaatt 2183

||||| ||||||||| || |||||| |||||

Sbjct: 444 ggagagatcaggaagaactgcagaagggttaattaatt 481

>gb|BI262826.1| NF091E03EC1F1023 Elicited cell culture Medicago truncatula cDNA clone
NF091E03EC 5', mRNA sequence
Length = 409

Score = 99.6 bits (50), Expect = 8e-17

Identities = 108/128 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||| ||||||||| | ||||||||| ||||||||| || ||

Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|| ||||||| || || || || ||||||||| || || || || || || || || || || ||

Sbjct: 341 aatcccaacaaaaattcngcccggtgattcnaagtgatcgacaaaatcaaatcagcagtg 400

Query: 1277 gagaaagt 1284

|||||||

Sbjct: 401 gagaaagt 408

Score = 83.8 bits (42), Expect = 5e-12

Identities = 67/76 (88%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttcac 768

||||||| || ||||| ||||||||| || || || || || || || ||

Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttntgcgtttgttcttnac 265

Query: 769 gattgctttgtcaatg 784

||||||| ||||

Sbjct: 266 gattgctttgttaatg 281

>gb|AW666202.1| sk33f05.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1028-3994 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 329

Score = 99.6 bits (50), Expect = 8e-17
Identities = 112/133 (84%)
Strand = Plus / Plus

Query: 1497 atgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556
||||| ||||||||||||||||| | || || || ||||||||||||||| ||||||| ||
Sbjct: 8 atgtgaaacttggagaagagactccaggacggcaagccaatctgctgccaacaatgaca 67

Query: 1557 tccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgacttt 1616
||||| ||||||||||||||||| ||||||| || || ||||||| ||||| |||||
Sbjct: 68 tcccaagaccacttcaaaccttaaccaacttatttccagatttaatgctctncaacttt 127

Query: 1617 ccaccaaggactt 1629
||||||| |||||
Sbjct: 128 ccaccaaagactt 140

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||||||||||| ||||||| ||||||| ||| ||| ||| ||||||||| |||||
Sbjct: 157 ggtcacacaattgaacaagcaaggtgcacaacctttagaacccaaatctacaacaagacc 216

Query: 1852 aacataga 1859
|||||||
Sbjct: 217 aacataga 224

>gb|G0006531.1| LJGBF85TF JCVI-LJ1 Lotus japonicus cDNA 5', mRNA sequence
Length = 292

Score = 97.6 bits (49), Expect = 3e-16
Identities = 139/165 (84%), Gaps = 3/165 (1%)
Strand = Plus / Plus

Query: 586 tctagattgacaatttgtttggtctgtttgtcctcatatgggggagtgccaatgcacaa 645

Sbjct: 77 tctagattaactatctgttttgcctctctttgtcctcatattggggagtgctaattgctcaa 136

Query: 646 ctttctacaaactttttactaccattcatgtccaaacctcttctcctctgtgaaatccaca 705

Sbjct: 137 ctttctacaaacttctattctagttcttctgtccaaa-ctcttttccactgtgaaatcctcc 195

Query: 706 gtgcaatctgccatatctaaggagacccgcatgggtgcttctctc 750

Sbjct: 196 gtgc-atccg-catatcaaaggaggtcgcgatgggtgcttctctc 238

>gb|C0511819.1| s13dSG02D0500046_103538 Glandular trichomes *Medicago sativa* cDNA,
mRNA sequence
Length = 468

Score = 97.6 bits (49), Expect = 3e-16
Identities = 118/141 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552

[illegible]

Query: 1553 ggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612

Sbjct: 356 gccatcccagcaccaacttccaacctcaatacactcacctcaatgtttagcgccgttggt 415

Query: 1613 ctttccaccaaggacttggtc 1633

Sbjct: 416 ctttccagcaaggatttggtc 436

>gb|BF648119.1| NF027G10EC1F1083 Elicited cell culture Medicago truncatula cDNA clone
NF027G10EC 5', mRNA sequence
Length = 420

Score = 97.6 bits (49), Expect = 3e-16
Identities = 108/128 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

Sbjct: 289 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaaactgcc 348

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 349 natcccaacaaaaattcgcccggtggattcggaagtgatcgacaaaatcaaatacagcagtg 408

Query: 1277 gagaaagt 1284
| | | | | | | |

Sbjct: 409 gagaaagt 416

Score = 89.7 bits (45), Expect = 8e-14
Identities = 68/76 (89%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctctccttcgcttgttcttccac 768
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 214 caatctgccatatcaaaagagactcgcatgggtgcttctcttctctgcgtttgttcttccac 273

Query: 769 gattgctttgtcaatg 784
| | | | | | | | | | | | | |

Sbjct: 274 nattgctttgttaatg 289

>gb|AW309606.1| sf21h05.x1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-658 3' similar to TR:P93548 P93548 PEROXIDASE
PRECURSOR ;, mRNA sequence
Length = 419

Score = 97.6 bits (49), Expect = 3e-16
Identities = 102/120 (85%)
Strand = Plus / Minus

Query: 2023 ttcaacggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttc 2082
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 410 ttcaatggtggttcactgactccatagtgcgtaacntacagcaccaacccggcctccttt 351

Query: 2083 tcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactggetcc 2142
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 350 ttgccgatttctccgccgcatgatccgatgggagacattagtcctcaccggctcc 291

>gb|C0513848.1| s13dSG73C1100082_156358 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 629

Score = 95.6 bits (48), Expect = 1e-15
Identities = 135/164 (82%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||| || | ||||||| |||
Sbjct: 162 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacgactgctagtcaa 221

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaactcatctcaaga 1597
||||||| |||| | |||||| | |||| | |||||| | |||| | ||||
Sbjct: 222 tctgctggaacactgccatcccagcaccaactccaaccttaatgtactcacctcaatg 281

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtc 1641
|||| | |||| ||||||||||||||||| |||| | ||||
Sbjct: 282 tttagaatgttggctctttccaccaaggacttagtcgcattgtc 325

Score = 89.7 bits (45), Expect = 8e-14
Identities = 132/161 (81%)
Strand = Plus / Plus

Query: 1900 acatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt 1959
||||||| ||||||||| || ||||||| ||||||| || ||||| || |||
Sbjct: 438 acatcaggatcaggggacaataatttggcacctcttgatctccatactcccacttctttt 497

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
||||||| |||| | |||||| | |||| | ||||||| || || | || | |||
Sbjct: 498 gacaactgtactacaggaaccttgttcaaaacaagggtcttcttcattcagaccaacaa 557

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggcta 2060
|| ||||||| ||||||||| |||| | || | |||||||
Sbjct: 558 cttttcaacggcggtccaccaactcaatagtgagtggtgcta 598

Score = 81.8 bits (41), Expect = 2e-11
Identities = 116/141 (82%)
Strand = Plus / Plus

Query: 1202 ggagagaagaacgcaaaccaccaaggaactctgctcgtggattcgaggttattgacaac 1261
|||||
Sbjct: 15 ggagagaagaacgcactcccgaataggaactctgttcgaggattcgatgtcattgacaac 74

Query: 1262 attaaatcagccgtggagaaagtgtgtccaggagtgtttcctgcgcagatatccttgcc 1321
|||
Sbjct: 75 ataaagacagatgtagagaacatatgtccaggggtgtatcatgtgctgatatcctagcc 134

Query: 1322 atcgtgccagagactctgtt 1342
||
Sbjct: 135 attgctgccacagactctgtt 155

>gb|AW691930.2| NF050G04ST1F1000 Developing stem Medicago truncatula cDNA clone
NF050G04ST 5', mRNA sequence
Length = 372

Score = 95.6 bits (48), Expect = 1e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
|||||
Sbjct: 215 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 274

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 275 ccacgattgctttgtcaatg 294

Score = 67.9 bits (34), Expect = 3e-07
Identities = 49/54 (90%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 300 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgca 353

>emb|AJ548283.1| AJ548283 MTAPHEU Medicago truncatula cDNA clone mtaehac110006d12,
mRNA sequence

Score = 87.7 bits (44), Expect = 3e-13
Identities = 62/68 (91%)
Strand = Plus / Minus

```
Query: 2143  aatggaga  2150
          |||||
Sbjct: 131   aatggaga  124
```

Score = 87.7 bits (44), Expect = 3e-13
Identities = 143/176 (81%)
Strand = Plus / Plus

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
 ||| ||||| ||| ||||| ||| ||||| ||| ||| ||| |||
 Sbjct: 78 aataagaactctgttcgaggattcgcattgcattgacaacataaagacggcggtagagaac 137

Score = 79.8 bits (40), Expect = 7e-11
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Sbjct: 204 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 263

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 264 tctgatgcgaacctgccatcccaagaccaacttccaaccttaataatactcacctcaatg 323

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
||||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 324 tttagaatgttggctctttccaccaaggacttagtcgcattgtc 367

Score = 75.8 bits (38), Expect = 1e-09
Identities = 131/162 (80%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 368 aggtgctcacacaattggacaagcaaggtgcacaacatttaggtacgaatctacaatga 427

Query: 1848 gaccaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcagg 1907
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 428 gaccaacatagatacttcttttgcctagcacaaggcaatctaattgcccaaagacatcatg 487

Query: 1908 gtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 488 atcaggggacaacaatttggcacctcttgatctccatactcc 529

>emb|FN039861.1| FN039861 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs21P0001M16_R.ab1 2007-08-10, mRNA sequence
Length = 485

Score = 85.7 bits (43), Expect = 1e-12
Identities = 118/143 (82%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 400 tcaggttcaggggacaacaacttagcaccacttgatcttcaaactcctacaaactttgac 341

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||||||||| ||| | | ||||||| || | ||||||| |||||
Sbjct: 340 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 281

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 280 tttaatggtggatccactgactc 258

>emb|FN039860.1| FN039860 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs21P0001M16_F.ab1 2007-08-10, mRNA sequence
Length = 485

Score = 85.7 bits (43), Expect = 1e-12
Identities = 118/143 (82%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||||||||||| | ||||||||||||||||||| || | |||||||
Sbjct: 85 tcaggttcaggggacaacaacttagcaccacttgatcttcaaactcctacaaactttgac 144

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||||||||| ||| | | ||||||| || | ||||||| |||||
Sbjct: 145 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 204

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 205 tttaatggtggatccactgactc 227

>gb|EG559283.1| CR03032H04 Root CR03 cDNA library Catharanthus roseus cDNA clone
CR03032H04 5', mRNA sequence
Length = 560

Score = 85.7 bits (43), Expect = 1e-12
Identities = 109/131 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||||||||||||||||| || | ||||| ||||| |||||||||||||
Sbjct: 376 tggaatgtgaaacttggaagaagagatgcaacaactgcaagccaagctgctgctaacaat 435

Query: 1553 ggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612
 ||| ||| | || ||||| ||| ||| ||||| | |||||
 Sbjct: 436 agcattcctcctcctactttctaaccttaatgcctcgtctccagattcaacgctcttgggt 495

```
Query: 1613 ctttcaccaa 1623
          |||||
Sbjct: 496 ctttcaaccaa 506
```

Score = 67.9 bits (34), Expect = 3e-07
Identities = 49/54 (90%)
Strand = Plus / Plus

Query: 731 cccgcatgggtgcttctctccttcgcttggtcttccacgattgctttgtcaatg 784
 |||| |||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 116 ccggaatgggagcctccctccttcgcttggtcttccatgattgctttgtcaatg 169

>gb|DW500373.1| GH_TMIRS_045_H05_F Cotton Normalized Library dT primed Gossypium
hirsutum cDNA, mRNA sequence
Length = 545

Score = 85.7 bits (43), Expect = 1e-12
Identities = 234/295 (79%), Gaps = 2/295 (0%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaactctggcaccacttgatcttcaaactcc 1949
 ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 18 ctgccaagaacaacaggctcaggggacaacaacttgccacctcttgatatccaaactcc 77

```
Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaag-ggtctctccact 2008
           ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 78   aacatcttttgacaacaactacttcaagaacct-aatcagtc aaagagggtcttctccact 136
```

Query: 2009 ctgatcagcaactgttcaacggtgggtccaccgactccattgtgcgtggctacagcacca 2068
 ||||| || ||||| ||||| || ||||| || || || || ||
 Sbjct: 137 ctgatcaacagttgttcaatggtggatccacggattccatcggttcggttacggttaaca 196

```
Query: 2069 acccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtc 2128
          ||| || |||| | || | || | ||||| ||||| ||||| ||||| |||||
Sbjct: 197  gcccaagctccttcaattcggaacttgtttctgccatgatcaagatgggagacattagtc 256
```

Query: 2129 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183
| ||||| || || ||||| || ||||| || |||||
Sbjct: 257 ccctcactggatcacgtggggagatcaggaagaactgcagaagggtgaactaatt 311

>dbj|CI189311.1| CI189311 Oryza sativa (japonica cultivar-group) root of seedlings
Oryza sativa Japonica Group cDNA clone 035-M100R-G10 3',
mRNA sequence
Length = 520

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 15 tcacaccattggacaagcacgatgcacaaacttcagagctcacatatacaacgaaccaa 74

Query: 1854 catagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| || ||||| || ||||| ||||| |||||
Sbjct: 75 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 134

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||| ||||| || ||||| || ||||| || ||||| |||||
Sbjct: 135 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 194

Query: 1974 caagaacctcggtcagaagaagggtctcctccactctgatcag 2016
||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 195 caagaacctcgctcgtcaagaaggggtcctcctgcactctgatcag 237

>dbj|CI256090.1| CI256090 Oryza sativa (japonica cultivar-group) Panicles mixture of
one, two, three weeks after flowering and supermix Oryza
sativa Japonica Group cDNA clone 044-M077R-H03 3', mRNA
sequence
Length = 650

Score = 85.7 bits (43), Expect = 1e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 5 tcacaccattggacaagcacgatgcacaaacttcagagctcacatatacaacgaaaccaa 64

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| | ||||| | ||||| |||||

Sbjct: 65 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 124

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||| ||||| | ||||| || ||||| || |||||

Sbjct: 125 tgacaacaatctggcacctttggatcttcagacgccaaccgtgttcgagaacaactacta 184

Query: 1974 caagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| ||||| |||||

Sbjct: 185 caagaacctcgtcgtcaagaaggggtcctgcactctgatcag 227

>gb|C0498078.1| G.h.fbr-sw07468 G.h.fbr-sw Gossypium hirsutum cDNA, mRNA sequence
Length = 491

Score = 85.7 bits (43), Expect = 1e-12
Identities = 73/83 (87%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 322 gccatgatcaagatgggagacatcagtcctcactggatcaatgggagagatcaggaag 381

Query: 2161 aattgtagaaggattaactaatt 2183
|| ||||| |||||

Sbjct: 382 aactgtagaagggttaattaatt 404

>gb|EY707107.1| CS00-C3-701-064-H11-CT.F Sweet orange fruit, development stadium (2
of 6) Citrus sinensis cDNA, mRNA sequence
Length = 837

Score = 83.8 bits (42), Expect = 5e-12
Identities = 123/150 (82%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 152 cttggaggcccaagctggcaagtaaaactcgggaaggagagatgctagaactgcaagccta 211

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| | | |||| | || | | |||| | | | ||||| ||
Sbjct: 212 tctgctgctaatacgcgcatctctgctcctacctcaaacttgaatcaactcatctctagg 271

Query: 1598 tttagcgctcttggactttccaccaaggac 1627
|| | ||||| ||||| |||||
Sbjct: 272 ttcaacgctctcggactttccaacaaggac 301

Score = 73.8 bits (37), Expect = 4e-09
Identities = 181/229 (79%)
Strand = Plus / Plus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||| ||||| ||||| ||||| ||||| || | ||||| ||
Sbjct: 438 cagggcacaacaacttggcaccgcttgatctgcaaactcctacttgtttgacaacaatt 497

Query: 1970 acttcaagaacctcggtcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
||||| ||||| || | | |||| | || ||||| || ||||| ||
Sbjct: 498 acttcaggaacctggtcaacagaaagggttgcttcaactctgatcaacagctgttcaatg 557

Query: 2030 gtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctctg 2089
||||||| || || || || |||| | ||||| ||||| |||||
Sbjct: 558 gtgggtccacagattcacaagtcgcacgtacagtaacaacccgagcaccttcagctctg 617

Query: 2090 atttcgccgccgccatgatcaagatgggagacattagtcctctcactgg 2138
||| | |||| | ||||| ||||| || || || |||||
Sbjct: 618 attttgtgccggcatgatcaagatgggagatatcagcccactcactgg 666

>gb|FD423297.1| RT00024R_T3_024_F11_31MAY2004_085_ab1 CrUniGene root Catharanthus
roseus cDNA similar to peroxidase, mRNA sequence
Length = 672

Score = 83.8 bits (42), Expect = 5e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgccgccatgatcaagatgggagacattagtcctctcactggc 2139
||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 341 ttctactctgattttgctgccgccatgatcaagatgggagatattagtcctttgactggt 400

```
Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
          || ||||| || ||||| ||||| ||||| |||||
Sbjct: 401 tcaaatggagaggttaggaaaaattgtaggagggttaa 438
```

Score = 46.1 bits (23), Expect = 1.0
Identities = 26/27 (96%)
Strand = Plus / Plus

```
Query: 1795  cacacaattggacaaggaaggtgcaca  1821
          |||||
Sbjct: 56    cacacaattggtcaaggaaggtgcaca  82
```

>gb|FD422675.1| RT00017R_T3_017_E10_31MAY2004_072_ab1 CrUniGene root Catharanthus
roseus cDNA similar to peroxidase, mRNA sequence
Length = 714

Score = 83.8 bits (42), Expect = 5e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
 ||| ||||| || ||||| ||||| ||||| ||||| |||||
 Sbjct: 380 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 439

```
Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
          || ||||| || | ||||| ||||| ||| |||
Sbjct: 440 tcaaattggagaggttagaaaaaattgtaggagggttaa 477
```

Score = 46.1 bits (23), Expect = 1.0
Identities = 26/27 (96%)
Strand = Plus / Plus

```
Query: 1795  cacacaattggacaaggaaggtgcaca 1821
           |||||
Sbjct: 95    cacacaattggtcaaggaaggtgcaca 121
```

```
>gb|FD422951.1| RT00020R T3 020 G01 31MAY2004 003 ab1 CrUniGene root Catharanthus
```

roseus cDNA similar to peroxidase, mRNA sequence
Length = 708

Score = 83.8 bits (42), Expect = 5e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 376 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 435

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||| || ||||| ||||| || |||||
Sbjct: 436 tcaaatggagaggttaggaaaaattgtaggagggttaa 473

Score = 46.1 bits (23), Expect = 1.0
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
||||| ||||| ||||| |||||
Sbjct: 91 cacacaattggtcaagcaaggtgcaca 117

>gb|FD420140.1| 1_SM-JB_R10-G12_T3__G12_3100394_14_ab1 CrUniGene root Catharanthus
roseus cDNA similar to peroxidase, mRNA sequence
Length = 494

Score = 83.8 bits (42), Expect = 5e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 266 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 325

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||| || ||||| ||||| || |||||
Sbjct: 326 tcaaatggagaggttaggaaaaattgtaggagggttaa 363

>gb|DW508346.1| GH_TMIRS_123_D07_F Cotton Normalized Library dT primed Gossypium

hirsutum cDNA, mRNA sequence
Length = 325

Score = 81.8 bits (41), Expect = 2e-11
Identities = 74/85 (87%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||||
Sbjct: 160 gccatgatcaagatgggagacattagtcctctcactggatcacgtgggagatcaggaag 219

Query: 2161 aattgtagaaggattaactaatttg 2185
|| || |||||
Sbjct: 220 aactgcagaagggtgaactaatttg 244

>gb|GT143205.1| METCC85TR JCVI-MT3 Medicago truncatula cDNA 3', mRNA sequence
Length = 534

Score = 79.8 bits (40), Expect = 7e-11
Identities = 61/68 (89%)
Strand = Plus / Minus

Query: 2083 tcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcc 2142
|||||
Sbjct: 326 tcctctggttcgtcaccgcccatgatcaagatgggagacattagtcctctcactggctcc 267

Query: 2143 aatggaga 2150
|||||||
Sbjct: 266 aatggaga 259

>gb|DR280730.1| 157654 CERES-148 Arabidopsis thaliana cDNA clone 124846 5', mRNA
sequence
Length = 461

Score = 79.8 bits (40), Expect = 7e-11
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||||
Sbjct: 229 cgcatgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>gb|CN910539.1| 030128ABLC005555HT (ABLC) Braeburn cell culture three days after
subculture Malus x domestica cDNA clone ABLC005555, mRNA
sequence
Length = 643

```
Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
          ||||| || ||||| ||||| ||||| ||||| || || || ||||| ||
Sbjct: 15    tcaggagataacaatttggtccacttgaccttcaaaccctacttctttcgacaacaac 74
```

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcacettctcctct 2088
 ||||| ||||| || || ||| | | ||||| || | | ||||| |||
 Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagttct 194

```
Query: 2149 gaaatcaggaagaattgtag 2168
          || || |||||
Sbjct: 255 gagattaggaagaattgtag 274
```

Score = 79.8 bits (40), Expect = 7e-11
Identities = 205/260 (78%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcggtcagaagaagggtctctccactctgatcagcaactgttcaac 2028
 ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 75 tacttcaaaaacctaatccagaataaagggtctctccactctgaccagcagctcttcaat 134

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 2088
 ||||| ||||| || ||||| || ||||| || || ||||| || || ||||| ||
 Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagtct 194

Query: 2089 gatttcgcccgcgatgatcaagatgggagacattagtctctcactggctccaatgga 2148
|| || | ||||||| ||| |||
Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

```
Query: 2149 gaaatcaggaagaattgtag 2168
      || || |||||
Sbjct: 255 gagattaggaagaattgtag 274
```

```
>gb|CN908310.1| 030109ABLC001919HT (ABLC) Braeburn cell culture three days after
subculture Malus x domestica cDNA clone ABLC001919, mRNA
sequence
Length = 627
```

Score = 79.8 bits (40), Expect = 7e-11
Identities = 205/260 (78%)
Strand = Plus / Plus

```
Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
          ||||| || ||||| ||||| ||||| ||||| || || || ||||| ||
Sbjct: 15    tcaggagataacaatttggctccacttgaccttcaaaccctacttctttcgacaacaac 74
```

Query: 1969 tacttcaagaacctcggtcagaagaagggtctctccactctgatcagcaactgttcaac 2028
 ||||| |||| | |||| || ||||| ||||| ||||| ||||| |||||
 Sbjct: 75 tacttcaaaaacctaatccagaataaaggtctctccactctgaccagcagctcttcaat 134

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 2088
 ||||| ||||| || || ||| | | ||||| || | | ||||| |||
 Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagttct 194

Query: 2089 gatttcgccgcgcgatgatcaagatgggagacattagtctctcactggctccaatgga 2148

Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Query: 2149 gaaatcaggaagaattgtag 2168

|| || |||||

Sbjct: 255 gagattaggaagaattgtag 274

>dbj|AU238571.1| AU238571 RAFL17 Arabidopsis thaliana cDNA clone RAFL17-40-J20 5',
mRNA sequence
Length = 647

Score = 79.8 bits (40), Expect = 7e-11

Identities = 49/52 (94%)

Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784

|||||

Sbjct: 226 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 277

>emb|FN019009.1| FN019009 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0005I02_R.ab1 2007-08-10, mRNA sequence
Length = 553

Score = 77.8 bits (39), Expect = 3e-10

Identities = 69/79 (87%)

Strand = Plus / Minus

Query: 706 gtgcaatctgccatatctaaggagaccgcattgggtgcttctctccttcgcttgttcttc 765

|||||

Sbjct: 427 gtgcaatctgctatcaataaggaaactcgaatgggtgcttctcttcttcgcctattcttc 368

Query: 766 cagcattgctttgtcaatg 784

|||||

Sbjct: 367 cagcattgctttgtcaatg 349

Score = 75.8 bits (38), Expect = 1e-09

Identities = 110/134 (82%)

Strand = Plus / Minus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552

||||||| ||| | ||||||||| || ||||| || ||||||| ||||||| ||||| |
Sbjct: 142 tggaatgtaaaattgggaagaagagatgcaagaacagcaagccaagctgctgcaaacagt 83

Query: 1553 ggcattccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612

|||| ||| |||| | | |||||||| | |||||||| | | | | ||| ||||
Sbjct: 82 agcattcctccacctacgtctaaccttaatcgactcatctctagtttcagtgtgttggc 23

Query: 1613 ctttcaccaagga 1626

|||||||||||
Sbjct: 22 ctttcaccaagga 9

Score = 54.0 bits (27), Expect = 0.004
Identities = 60/71 (84%)
Strand = Plus / Minus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291

||||| | |||| | | |||||||||||||||| | | ||||||||||| |
Sbjct: 274 tctgctaggagatttgaagtcattgacaacattaaatctgctgtagagaaagtgtgccct 215

Query: 1292 ggagttgtttc 1302

|| |||||||
Sbjct: 214 ggtgttgtttc 204

>emb|FN019008.1| FN019008 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0005I02_F.ab1 2007-08-10, mRNA sequence
Length = 588

Score = 77.8 bits (39), Expect = 3e-10
Identities = 69/79 (87%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttc 765

|||||||||| | ||||| | | ||||||||||||| ||||| | |||||||
Sbjct: 202 gtgcaatctgctatatcaataaggaaactcgaatgggtgcttctcttcttcgcctattcttc 261

Query: 766 cacgattgctttgtcaatg 784

|||||||||||||||
Sbjct: 262 cacgattgctttgtcaatg 280

Score = 54.0 bits (27), Expect = 0.004
Identities = 60/71 (84%)
Strand = Plus / Plus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
||||| | |||| | | ||||||||||||||| | | ||||||||||| |
Sbjct: 355 tctgctagaggatttgaagtcattgacaacattaaatctgctgtagagaaagtgtgcct 414

Query: 1292 ggagttgtttc 1302
|| |||||||
Sbjct: 415 ggtgttgtttc 425

Score = 52.0 bits (26), Expect = 0.016
Identities = 82/101 (81%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||| | ||||||||||| | |||| | ||||| ||||||| |||| |
Sbjct: 487 tggaatgtaaaattgggaagaagagatgcaagaacagcaagccaagctgctgcaaacagt 546

Query: 1553 ggcattccctgcaccacttcaaaccttaaccaactcatctc 1593
|||| ||| |||| | | |||||| | |||||||
Sbjct: 547 agcattctccacctacgtctaaccttantcgactcatctc 587

>emb|FN021689.1| FN021689 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0009N11_R.ab1 2007-08-10, mRNA sequence
Length = 556

Score = 77.8 bits (39), Expect = 3e-10
Identities = 117/143 (81%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| |||||||||||| | |||||| ||||||||||||| | | |||||||
Sbjct: 84 tcaggttcaggggacaacaacttagcaccacctgatcttcaaactcctacaaactttgac 143

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactg 2022

||||| ||| ||||||||||||| ||| | | ||||||||| ||| ||| ||||||||| |||||
Sbjct: 144 aacagttatttcaagaaccttgtaacagaaaggtctgcttcattctgatcaacaactc 203

Query: 2023 ttcaacggtgggtccaccgactc 2045

|| || ||||| ||||| |||||

Sbjct: 204 tttaatggtggatccactgactc 226

>emb|FN021688.1| FN021688 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0009N11_F.ab1 2007-08-10, mRNA sequence
Length = 526

Score = 77.8 bits (39), Expect = 3e-10

Identities = 117/143 (81%)

Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962

||||| ||||||||||||||| | ||||||| ||||||||||||||| || | |||||||

Sbjct: 502 tcagggtcaggggacaacaacttagcaccacctgatcttcaaactcctacaaactttgac 443

Query: 1963 aactactacttcaagaacctcggttcagaagaaggtctcctccactctgatcagcaactg 2022

||| || ||||||||||||| ||| | | ||||||||| || | ||||||||| |||||

Sbjct: 442 aacagttatttcaagaaccttgtaacagaaaggtctgcttcattctgatcaacaactc 383

Query: 2023 ttcaacggtgggtccaccgactc 2045

|| || ||||| ||||| |||||

Sbjct: 382 tttaatggtggatccactgactc 360

>emb|FN034858.1| FN034858 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs13P0012A19_R.ab1 2007-08-10, mRNA sequence
Length = 697

Score = 77.8 bits (39), Expect = 3e-10

Identities = 51/55 (92%)

Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784

||||| ||||||||||||||||||| | ||||||||||||||||| |||||||

Sbjct: 214 acccgaatgggtgcttctctccttcgccttttcttccacgattgcttcgtcaatg 268

Score = 71.9 bits (36), Expect = 2e-08
Identities = 54/60 (90%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||||||||||||||||| |||| | |||| |||||||||||||
Sbjct: 630 tcacactattggacaagcaaggtgcacaaagtttcagggcacgcatttacaacgagaccaa 689

>emb|FN019751.1| FN019751 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0006L16_F.ab1 2007-08-10, mRNA sequence
Length = 604

Score = 77.8 bits (39), Expect = 3e-10
Identities = 51/55 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctccttcgcttgttcttcacgattgctttgtcaatg 784
||||| ||||||||||||||||||| | ||||||||||||||||| |||||
Sbjct: 211 acccgaatgggtgcttctctccttcgccttttcttcacgattgcttcgtcaatg 265

>gb|FC869557.1| C31102G05EF AbioticR1 Citrus reshni cDNA clone C31102G05, mRNA
sequence
Length = 706

Score = 77.8 bits (39), Expect = 3e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttgttcttc 765
||||||| || || || || | ||||| || |||||||||||||||||
Sbjct: 200 gtgcaatctgctatttcaaaagagctcgcatgggcgcctctctccttcgcttgttcttc 259

Query: 766 cacgattgctt 776
|||||||
Sbjct: 260 cacgattgctt 270

Score = 56.0 bits (28), Expect = 0.001
Identities = 122/151 (80%), Gaps = 2/151 (1%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| | | | | | | | | | | | | | | | | | | |
Sbjct: 470 cttggaggcccaagctggcaagtaaaactcgggaaggagagatgctagaactgcaagccta 529

Query: 1538 tctgctgctaacaatggcatccctgcacc-cacttcaaaccttaaccaactcatctcaag 1596
||||||| | | | | | | | | | | | | | | | | | | |
Sbjct: 530 tctgctgctaataagcggcattcctgctcctnacctc-aacttgaatcaactcatctctag 588

Query: 1597 atttagcgctcttggactttccaccaaggac 1627
| | | | | | | | | | | | | | | | | | | |
Sbjct: 589 gttcaacgctctcggactttccaacaaggac 619

Score = 46.1 bits (23), Expect = 1.0
Identities = 101/127 (79%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| | | | | | | | | | | | | | | | | | | |
Sbjct: 278 ggatgcgatggatcagttctactggacgacacatcatctttcactggagagaaaaatgcg 337

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
| | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 338 aatgccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 397

Query: 1277 gagaaag 1283
|||||||
Sbjct: 398 gagaaag 404

>gb|FC870159.1| C31109C09EF AbioticR1 Citrus reshni cDNA clone C31109C09, mRNA
sequence
Length = 735

Score = 77.8 bits (39), Expect = 3e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttc 765
||||||| | | | | | | | | | | | | | | | | | | |

Sbjct: 206 gtgcaatctgctattttcaaaagaggctcgcatgggcgcctctctccttcgcttgttcttc 265

Query: 766 cacgattgctt 776

|||||||||

Sbjct: 266 cacgattgctt 276

Score = 50.1 bits (25), Expect = 0.065

Identities = 91/113 (80%)

Strand = Plus / Plus

Query: 1154 cagggatgtagtggttcaattctattggatgacacatcaagcttcaccggagagaagaac 1213

||||||| |||| | || |||| | || ||||||| || |||| | ||||||| ||

Sbjct: 561 cagggatgcatggatcagttctactggacgacacatcatctttcactggagagaaaaat 620

Query: 1214 gcaaaccceaacaggaactctgctcgttgattcgaggttattgacaacattaa 1266

|| || |||| | |||| | || || ||||||||| || |||||||||

Sbjct: 621 gcgaatgccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaa 673

>gb|FC924498.1| C31806G11EF StrCleopN Citrus reshni cDNA clone C31806G11, mRNA
sequence

Length = 699

Score = 77.8 bits (39), Expect = 3e-10

Identities = 63/71 (88%)

Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagacccgcgcatgggtgcttctctccttcgcttgttcttc 765

||||||||| || || || || | ||||||| || |||||||||||||||||||

Sbjct: 211 gtgcaatctgctattttcaaaagaggctcgcatgggcgcctctctccttcgcttgttcttc 270

Query: 766 cacgattgctt 776

|||||||||

Sbjct: 271 cacgattgctt 281

Score = 52.0 bits (26), Expect = 0.016

Identities = 104/130 (80%)

Strand = Plus / Plus

Query: 1598 tttagcgctcttggactttccac 1620
|| | ||||| |||||
Sbjct: 593 ttcaacgctctcggactttccac 615

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||| ||||| ||||| || |||
Sbjct: 281 ggatgcgatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 340

Query: 1217 aaccccaacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| || || |||
Sbjct: 341 gtccccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 400

Query: 1277 gagaaag 1283
|||||
Sbjct: 401 gagaaag 407

>gb|FC921479.1| C32105D10EF RVDevelopN Citrus clementina cDNA clone C32105D10, mRNA
sequence
Length = 690

Score = 77.8 bits (39), Expect = 3e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttc 765
||||||| || || || ||| | ||||| || ||||| ||||| |||||
Sbjct: 206 gtgcaatctgctatttcaaaagagctcgcatgggcgcctctctccttcgcttgttcttc 265

Query: 766 cacgattgctt 776
|||||||
Sbjct: 266 cacgattgctt 276

Score = 67.9 bits (34), Expect = 3e-07
Identities = 115/142 (80%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | | | | | | | | | | | | | | | |

Sbjct: 476 cttggaggcccaagctggcaagtaaaactcggaaggagagatgctagaactgcaagccta 535

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| | | | | | | | | | | | | | | | |

Sbjct: 536 tctgctgctaataagcggcattccagctcctacctcaaacttgaatcaactcatctctagg 595

Query: 1598 tttagcgctcttggactttcca 1619
| | | | | | | | | |

Sbjct: 596 ttcaacgctctcggactttcca 617

>gb|FC875071.1| C31503H10EF CEVdCidrol Citrus medica cDNA clone C31503H10, mRNA
sequence
Length = 739

Score = 77.8 bits (39), Expect = 3e-10

Identities = 63/71 (88%)

Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttc 765
||||||| | | | | | | | | | | | | | | | |

Sbjct: 203 gtgcaatctgctatttcgaaagaggctcgcatgggcgcctctctccttcgcttgttcttc 262

Query: 766 cacgattgctt 776
|||||||

Sbjct: 263 cacgattgctt 273

Score = 67.9 bits (34), Expect = 3e-07

Identities = 121/150 (80%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | | | | | | | | | | | | | | | |

Sbjct: 473 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 532

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

|||||
Sbjct: 533 tctgctgctaatagcggcattcctcctcctacctaacttgaatcaactcacctctagg 592

Query: 1598 tttagcgctcttggactttccaccaaggac 1627

|||
Sbjct: 593 ttcaacgctctcggactttccaacaaggac 622

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||
Sbjct: 281 ggatgcgatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||
Sbjct: 341 gtccccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 400

Query: 1277 gagaaag 1283

|||||
Sbjct: 401 gagaaag 407

>gb|EY867689.1| CL06-C4-500-007-B02-CT.F Rangpur lime root, greenhouse plant Citrus
limonia cDNA, mRNA sequence
Length = 827

Score = 77.8 bits (39), Expect = 3e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttc 765

|||||
Sbjct: 166 gtgcaatctgctatttcgaaagaggctcgcatgggcgcctctctccttcgcttggttcttc 225

Query: 766 cacgattgctt 776

|||||
Sbjct: 226 cacgattgctt 236

Score = 67.9 bits (34), Expect = 3e-07
Identities = 121/150 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | ||| | | |||| | | ||||| |||||
Sbjct: 436 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 495

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| | |||| | | | | | |||| | | ||||| ||| |
Sbjct: 496 tctgctgctaataagcggcattcctcctcctacctcaaactgaaatcaactcacctctagg 555

Query: 1598 tttagcgctcttggactttccaccaaggac 1627
|| | ||||| ||||| |||||
Sbjct: 556 ttcaacgctctcggactttccaacaaggac 585

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| || |||| | | ||||| ||||| ||||| |||
Sbjct: 244 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 303

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | |||| | | ||||| || ||||| ||| |
Sbjct: 304 gtcccaatcgtaactccgccgcggattcgaggtcatcgacaacattaagtcgcagtt 363

Query: 1277 gagaaag 1283
|||||
Sbjct: 364 gagaaag 370

>gb|FC325468.1| P00462_C7-H9_M13-F_A09_079.ab1 Onu-Ua-pathc Ulmus americana cDNA,
mRNA sequence
Length = 330

Score = 77.8 bits (39), Expect = 3e-10
Identities = 147/183 (80%)
Strand = Plus / Plus

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggc 2058
||||||| ||||| ||||| || ||||| || || ||||| ||
Sbjct: 30 ctctccactccgatcagcagctgttcaacggcgatccactgattcgctggtgcgcagc 89

Query: 2059 tacagcaccaacccgggcaccttctctctgatttcgccgcccatgatcaagatggga 2118
||||| || | ||| |||| | || ||||| || || ||||| |||||
Sbjct: 90 tacagcaacagcgaaggcagcttcacttccgatttcgtggcgcgatgatcaggatggga 149

Query: 2119 gacattagtcctctcactgggtccaatggagaaatcaggaagaattgtagaaggattaac 2178
|| || | ||||| || ||||| ||||| ||||| || ||||| ||
Sbjct: 150 gatatcaaacctctcactggaaacaatggagaaattaggaagaattgcaggaggatcaac 209

Query: 2179 taa 2181
|||
Sbjct: 210 taa 212

>gb|EG985866.1| GLE049_D04_013 Cyamopsis tetragonoloba (L.) Taub seeds at early
developmental stage Cyamopsis tetragonoloba cDNA, mRNA
sequence
Length = 686

Score = 77.8 bits (39), Expect = 3e-10
Identities = 54/59 (91%)
Strand = Plus / Plus

Query: 1151 atgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaa 1209
||||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 610 atgcagggatgtgatggttcgattctactagatgacacatcaagtttcagcgagagaa 668

Score = 65.9 bits (33), Expect = 1e-06
Identities = 51/57 (89%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctcttcgcttgttcttccacgattgctttgtcaatgtaatt 789
||||||| || || ||||| ||||| ||||| |||||
Sbjct: 229 cgcattgggtgcttctctgttgcgattgttcttccacgattgtttgttaatgtaatt 285

>gb|EG356679.1| P00462_C7-H9_M13-F_A09_079 Onu-Ua-pathc Ulmus americana cDNA, mRNA

sequence
Length = 479

Score = 77.8 bits (39), Expect = 3e-10
Identities = 147/183 (80%)
Strand = Plus / Plus

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggc 2058
||||| ||||| ||||| || ||||| || || ||||| ||
Sbjct: 52 ctctccactccgatcagcagctgttcaacggcgatccactgattcgctggtgcgcagc 111

Query: 2059 tacagcaccaacccgggcaccttctctctgatttcgccgccgcatgatcaagatggga 2118
||||| || | ||| |||| | || ||||| || || ||||| |||||
Sbjct: 112 tacagcaacagcgaaggcagcttcacttccgatttcgtggcgcgatgatcaggatggga 171

Query: 2119 gacattagtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaac 2178
|| || | ||||| || ||||| ||||| || ||||| ||
Sbjct: 172 gatatcaaacctctcactggaacaatggagaaattaggaagaattgcaggaggatcaac 231

Query: 2179 taa 2181
|||
Sbjct: 232 taa 234

>emb|FN034857.1| FN034857 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs13P0012A19_F.ab1 2007-08-10, mRNA sequence
Length = 633

Score = 75.8 bits (38), Expect = 1e-09
Identities = 113/138 (81%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||| ||||| ||||| ||||| ||||| || |||||
Sbjct: 319 ctgcccaagaacctcaggttcaggggacaacaacttggcacctcttgatctccagactcc 260

Query: 1950 aaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctcctccactc 2009
|| ||||| || || |||| || || || || ||||| |||||
Sbjct: 259 tacatactttgacaaccattatttcataaatcttgtaacaaaaagggtctgctccactc 200

Query: 2010 tgatcagcaactgttcaa 2027

||||| || |||||
Sbjct: 199 tgatcagcagctcttcaa 182

Score = 71.9 bits (36), Expect = 2e-08
Identities = 54/60 (90%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||||||||||||| ||||| || ||||| |||||||||||||||
Sbjct: 418 tcacactattggacaagcaaggtgcacaagtttcagggcacgcatttacaacgagaccaa 359

Score = 50.1 bits (25), Expect = 0.065
Identities = 67/81 (82%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||| ||||||| ||| || ||||| || ||||| || ||||||| |||
Sbjct: 105 atgattaagatgggagactttcgtccccttactggatctaattggcgagatcaggaagaac 46

Query: 2164 tgtagaaggattaactaattt 2184
|| || ||||| |||||||
Sbjct: 45 tgcaggaggatcaactaattt 25

>emb|FN045147.1| FN045147 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs21P0009020_F.ab1 2007-08-10, mRNA sequence
Length = 489

Score = 75.8 bits (38), Expect = 1e-09
Identities = 113/138 (81%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||| ||||||||||||||| ||||||| ||||||| || |||||
Sbjct: 318 ctgccaagaacctcaggttcaggggacaacaacttggcacctcttgatctccagactcc 259

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactc 2009
|| ||||||||| || ||||| || || ||| || ||||||| |||||||
Sbjct: 258 tacatactttgacaaccattatttcataaatcttgtaacaaaaagggtctgctccactc 199

Query: 2010 tgatcagcaactgttcaa 2027

||||||| || |||||

Sbjct: 198 tgatcagcagctcttcaa 181

Score = 71.9 bits (36), Expect = 2e-08

Identities = 54/60 (90%)

Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853

||||| ||||||||||||||||||| ||||| || ||||| |||||||||||||

Sbjct: 417 tcacactattggacaagcaaggtgcacaagtttcagggcacgcatttacaacgagaccaa 358

Score = 50.1 bits (25), Expect = 0.065

Identities = 67/81 (82%)

Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163

||||| ||||||| ||| || ||||| || ||||| || ||||| || |||||||||

Sbjct: 104 atgattaagatgggcgacttttcgtcccttactggatctaattggcgagatcaggaagaac 45

Query: 2164 tgtagaaggattaactaattt 2184

|| || ||||| |||||||||

Sbjct: 44 tgcaggaggatcaactaattt 24

>emb|FN019752.1| FN019752 Petunia axillaris subsp. axillaris pool of root and petal

tissue Petunia axillaris subsp. axillaris cDNA clone

drs31P0006L16_R.ab1 2007-08-10, mRNA sequence

Length = 590

Score = 75.8 bits (38), Expect = 1e-09

Identities = 113/138 (81%)

Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949

||||| ||||| ||||| ||||||||||||| ||||||| ||||||| || |||||

Sbjct: 301 ctgccaagaacctcaggttcaggggacaacaacttggcacctcttgatctccagactcc 242

```
Query: 2010  tgatcagcaactgttcaa 2027
          |||||
Sbjct: 181   tgatcagcagctcttcaa 164
```

```
Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||||| ||||| ||||| ||| ||||| ||||| ||||| |||||
Sbjct: 400 tcacactattggacaagcaaggtgcgcaagtttcagggcacgcatttacaacgagaccaa 341
```

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
 ||||| ||||| ||| || ||||| || ||||| || ||||| |||||
 Sbjct: 87 atgattaagatgggcgactttcgtcccttactggatctaattggcgagatcaggaagaac 28

Query: 2164 tgtagaaggattaactaattt 2184
 || || |||| |||||
 Sbjct: 27 tgcaggaggatcaactaattt 7

Score = 75.8 bits (38), Expect = 1e-09
Identities = 110/134 (82%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

Sbjct: 441 tcaggagataacaatttggtccacttgaccttcaaaccctacttctttcgacaacaac 500

Query: 1969 tacttcaagaacctcggttcagaagaagggtctctccactctgatcagcaactgttcaac 2028
||||||| ||||| | ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 501 tacttcaaaaacctaataccagaataaagggtctctccactctgaccagcagctcttcaat 560

Query: 2029 ggtgggtccaccga 2042
||||| |||||

Sbjct: 561 ggtggttccaccga 574

Score = 63.9 bits (32), Expect = 4e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1798 acaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||| ||||||||| ||||| ||||| |||||||||
Sbjct: 330 acaattgggcaagcaaggtgcacatcattcagaccccgcatatacaacgagaccaa 385

Score = 50.1 bits (25), Expect = 0.065
Identities = 100/125 (80%)
Strand = Plus / Plus

Query: 1508 ggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccctgcaccc 1567
||||||||||| || ||||| ||||| | ||||||||| ||||| | ||
Sbjct: 186 ggaagaagagacgcaaggactgcaagccaagccgctgctaacaacaacatccccctcca 245

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
|| ||||| ||||| ||||||| | ||| || || || ||||| ||||||||| |||
Sbjct: 246 acccgaaacctaaaccagctcatctctacattcagtgctgttggtctttccaccagagac 305

Query: 1628 ttggt 1632
|||||
Sbjct: 306 ttggt 310

>gb|EV227910.1| VV_Pe016c06.b1 Vitis vinifera cv. perlette LibA Vitis vinifera cDNA,
mRNA sequence
Length = 1149

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 284 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 343

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 344 tactacaagaacct 357

>gb|EH047301.1| AS2RM4P1E10.ab1 Roots inoculated with Meloidogyne arenaria (RM)
Arachis stenosperma cDNA 5', mRNA sequence
Length = 725

Score = 75.8 bits (38), Expect = 1e-09
Identities = 164/206 (79%)
Strand = Plus / Plus

Query: 1960 gacaactactacttcaagaacctcggttcagaagaagggtctctccactctgatcagcaa 2019
||||| ||||||| ||||||| | ||| || | ||||||| || || |||||
Sbjct: 80 gacaaccactacttcaacaacctcgtcgaccggaaaggccccctccattccgaccagcaa 139

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcacc 2079
|| ||||||| || || || ||||||| || ||||||| | ||||| || |
Sbjct: 140 ctettcaacggaggatctactgactccattgttcgcggtacagctcaaaccctagctct 199

Query: 2080 ttctcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactggc 2139
|| | | ||||| ||| ||||||| ||||||| || ||| |||||||
Sbjct: 200 ttttcgccgattttgccagtgccatgatcaagatgggagacataaatccctcactgga 259

Query: 2140 tccaatggagaaatcaggaagaattg 2165
||||| ||||| || || |||||||
Sbjct: 260 tccaagggagagattagaaagaattg 285

>gb|EC991497.1| WIN1142.C21_L14 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1142_L14 3', mRNA sequence
Length = 465

Score = 75.8 bits (38), Expect = 1e-09

Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||||||
Sbjct: 449 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 390

Query: 1969 tacttcaagaacct 1982
|||| |||||||||
Sbjct: 389 tactacaagaacct 376

>gb|EC987303.1| WIN1130.C21_E15 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1130_E15 3', mRNA sequence
Length = 851

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||||||
Sbjct: 694 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 753

Query: 1969 tacttcaagaacct 1982
|||| |||||||||
Sbjct: 754 tactacaagaacct 767

>gb|EC985323.1| WIN1124.C21_I01 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1124_I01 3', mRNA sequence
Length = 906

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||||||
Sbjct: 478 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 537

Query: 1969 tacttcaagaacct 1982
|||| |||||||||

Sbjet: 538 tactacaagaacct 551

>gb|CV861937.1| gonad_EST09518 Embryonic gonad cDNA Library Gallus gallus cDNA 5',
mRNA sequence
Length = 1288

Score = 75.8 bits (38), Expect = 1e-09
Identities = 59/66 (89%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||| ||||| || ||| ||||| ||||| |||||
Sbjet: 348 ttgacaccattaaagaagccgtggagagagagtgccaggagttgtttcctgtgcagata 407

Query: 1314 tccttg 1319
|||||
Sbjet: 408 tccttg 413

>gb|CX309187.1| C18022D10Rv Drought2 Citrus reshni cDNA clone C18022D10, mRNA
sequence
Length = 712

Score = 75.8 bits (38), Expect = 1e-09
Identities = 122/150 (81%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||| || ||| ||||| ||||| ||||| ||||| |||||
Sbjet: 516 cttggaggcccaagctggcaagtaaaactcgggaaggagagatgctagaactgcaagccta 457

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||| ||| ||||| || ||| ||||| || ||| ||||| ||
Sbjet: 456 tctgctgctaatagcggcattcctgctcctacctcaaacttgaatcaaccatctctagg 397

Query: 1598 tttagcgctcttggaactttccaccaaggac 1627
|| | ||||| ||||| |||||
Sbjet: 396 ttcaacgctctcggactttccaacaaggac 367

Score = 60.0 bits (30), Expect = 7e-05
Identities = 105/130 (80%)

Strand = Plus / Minus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||||| ||||||| ||||||| ||||||| ||||||| || || ||||||| ||

Sbjct: 230 caggcgacaacaacttggcaccgcttgatctgcaaactcctacttgttttgacaacaatt 171

Query: 1970 acttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
||||| ||||||| || || || ||||||| || ||||||| ||

Sbjct: 170 acttcaggaacctggtcaacagaaagggttgcttcactctgatcaacagctgttcaatg 111

Query: 2030 gtgggtccac 2039
|||||

Sbjct: 110 gtgggtccac 101

Score = 46.1 bits (23), Expect = 1.0

Identities = 101/127 (79%)

Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| |||||| ||| |||||| |||| ||||||| || |||| ||||||| || ||

Sbjct: 708 ggatgcgatggatcagttctactggacgacacatcatctttcactggagagaaaaatgcg 649

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||| | |||||| || || ||||||| || ||||||| || || ||

Sbjct: 648 aatgccaatcgtaactccgcccgcggattcgaggtcatcgacaacattaagtccgcagtt 589

Query: 1277 gagaaag 1283
|||||

Sbjct: 588 gagaaag 582

>gb|CA105303.1| SCJFHR1C05E10.g HR1 Saccharum officinarum cDNA clone SCJFHR1C05E10
5', mRNA sequence
Length = 857

Score = 75.8 bits (38), Expect = 1e-09

Identities = 80/94 (85%)

Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948

|||||
Sbjct: 402 gctgccctagaacctcaggttcaggtgacaacaatttggcgcctctggaccttcaaacc 461

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982

|||||
Sbjct: 462 caaccgtctttgagaacaactactacaagaacct 495

Score = 44.1 bits (22), Expect = 4.0
Identities = 40/46 (86%)
Strand = Plus / Plus

Query: 2137 ggctccaatggagaaatcaggaagaattgtagaaggattaactaat 2182

|||||
Sbjct: 650 ggctccaatgggcagatcaggaagaactgcagaagggttaactaat 695

>gb|CA102350.1| SCBGHR1058E08.g HR1 Saccharum officinarum cDNA clone SCBGHR1058E08
5', mRNA sequence
Length = 664

Score = 75.8 bits (38), Expect = 1e-09
Identities = 80/94 (85%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948

|||||
Sbjct: 402 gctgccctagaacctcaggttcaggtgacaacaatttggcgcctctggaccttcaaacc 461

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982

|||||
Sbjct: 462 caaccgtctttgagaacaactactacaagaacct 495

>gb|CF205258.1| RR890915I0004_IVa_Ra_B09 Vitis sp. RR890915I Vitis hybrid cultivar
cDNA clone RR890915I0004_IVa_Ra_B09 3', mRNA sequence
Length = 746

Score = 75.8 bits (38), Expect = 1e-09
Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 330 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 271

Query: 1969 tacttcaagaacct 1982

||||| |||||||
Sbjct: 270 tactacaagaacct 257

>dbj|FS421608.1| FS421608 normalized full-length tobacco cDNA library Nicotiana
tabacum cDNA clone TBK02GR0057_4_D10 5', mRNA sequence
Length = 547

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaat 783
||||| ||||| ||||||| ||||||| | ||||||| |||||||
Sbjct: 281 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 340

Query: 784 g 784
|
Sbjct: 341 g 341

>dbj|FS420315.1| FS420315 normalized full-length tobacco cDNA library Nicotiana
tabacum cDNA clone TBK02GR0054_1_H07 5', mRNA sequence
Length = 572

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaat 783
||||| ||||| ||||||| ||||||| | ||||||| |||||||
Sbjct: 205 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 264

Query: 784 g 784
|
Sbjct: 265 g 265

>gb|ES441310.1| TSH_EST01528 Theobroma cacao-Moniliophthora pernicioso incompatible
interaction library Theobroma cacao cDNA clone RT-052B08

5' similar to class III peroxidase [Gossypium hirsutum]
Length = 320, mRNA sequence
Length = 337

Score = 73.8 bits (37), Expect = 4e-09
Identities = 49/53 (92%)
Strand = Plus / Plus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 117 ccgcatgggtgcttctctcgttcgcttgttcttccatgactgtttgtcaatg 169

>emb|CU488677.1| CU488677 DROUGHTLS_KZOACAF Theobroma cacao cDNA clone
KZOACAF8YE10FM1, mRNA sequence
Length = 501

Score = 73.8 bits (37), Expect = 4e-09
Identities = 49/53 (92%)
Strand = Plus / Plus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 269 ccgcatgggtgcttctctcgttcgcttgttcttccatgactgtttgtcaatg 321

>gb|FG154278.1| AGN_RNC104xj04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 798

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
|||||
Sbjct: 174 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 233

Query: 784 g 784
|
Sbjct: 234 g 234

Score = 73.8 bits (37), Expect = 4e-09

Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| |||| | ||| ||| |||| |||| |||| |||| ||||
Sbjct: 426 cttggagggcctaattgggatgtaaaactcggaagaagagatgccagaacagcaagccaa 485

```
Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
          ||| | ||| | ||| ||| | || ||| ||| ||| ||| ||| ||| |||
Sbjct: 486 gctgccgcaaacagtagcattctctctccaacttctaaccttaaccggctcatctctagc 545
```

```
Query: 1598 tttagcgctcttggactttccaccaagga 1626
          || || ||| ||| ||||| ||||| |||
Sbjct: 546  ttcagtgtgttggcctttccaccaagga 574
```

Score = 48.1 bits (24), Expect = 0.26
Identities = 52/60 (86%), Gaps = 1/60 (1%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
 ||||| ||||| ||||| | |||| | |||| ||||| |||||
 Sbjct: 596 tcacaccattggacaagcaaagtgactagtttcag-gcacgatatacaacgagaccaa 654

>gb|FG173223.1| AGN_RNC126xi04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 829

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

```

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
          ||||| ||||| ||||||| ||||||| | ||||||| ||||||| |||||||
Sbjct: 182 aaggaaaccgatatgggtgcttccctccttcgctattcttccacgattgcttcgtcaat 241

```

Query: 784 g 784
Sbjct: 242 g 242

Query: 784 g 784
Sbjct: 434 g 434

Score = 58.0 bits (29), Expect = 3e-04
Identities = 120/149 (80%), Gaps = 1/149 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 625 cttggagggcctaattgggatgtaaaactcggaagaagagatgccaga-cagcaagccaa 683

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
 ||| | ||| | ||| ||| | || ||||| ||||| ||| ||| |||
 Sbjct: 684 gctgccgcaaacagtagcattctctccaacttctaaccttaaccggctcatctctagc 743

```
Query: 1598 tttagcgctcttggactttccaccaagga 1626
          || || ||| ||| ||||| ||||| |||
Sbjct: 744  ttcagtgtgttggcctttccaccaagga 772
```

>gb|FG157638.1| AGN_RNC025xk16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 907

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

```
Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 201 aaggaaaccgatatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 260
```

Query: 784 g 784
Sbjct: 261 g 261

Score = 73.8 bits (37), Expect = 4e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537

Sbjct: 453 cttggaggggcctaattgggatgtaaaactcgaagaagagatgccagaacagcaagccaa 512

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

Sbjct: 513 gctgccgcgaacagtagcattctctctccaacttctaaccttaaccggtcatctctagc 572

Query: 1598 tttagcgctcttggactttccaccaagga 1626

Sbjct: 573 ||| ||| |||| | ||||| ||||| ||||| 601
ttcagtgtgctgttggcctttccaccaagga

Score = 56.0 bits (28), Expect = 0.001
Identities = 52/60 (86%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853

[illegible]

```
>dbj|DB920515.1| DB920515 full-length enriched cassava cDNA library Manihot esculenta
cDNA clone CAS01_002_E19 5', mRNA sequence
Length = 556
```

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 1497 atgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556

Sbjct: 480 atgttaaacttggagaagagatgctagaactgcaagcctttctgctgcaaataatggca 539

Query: 1557 t 1557

Sbjct: 540 t 540

Score = 65.9 bits (33), Expect = 1e-06
Identities = 45/49 (91%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||||| ||| ||||||||||||||| ||||||||| |||
Sbjct: 221 atgggtgcttccctcgcttcgcttggttcttccatgattgctttgttaatg 269

Score = 56.0 bits (28), Expect = 0.001
Identities = 70/84 (83%)
Strand = Plus / Plus

Query: 1256 gacaacattaaatcagccgtggagaaagtgtgtccaggagtgtttcctgcgcagatatac 1315
||||| || ||||| || || ||||||| ||||| ||||| || || || || |||||
Sbjct: 368 gacaatataaaatccgcagttgagaaagcttgctcctggagtagtctcatgtgctgatatac 427

Query: 1316 cttgccatcgctgccagagactct 1339
||||||||||||| |||||||||
Sbjct: 428 cttgccatcgctgctagagactct 451

>gb|EB450877.1| KT7C.108P16F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108P16,
mRNA sequence
Length = 785

Score = 73.8 bits (37), Expect = 4e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaat 783
||||| ||||| ||||||||||| ||||||||| | ||||||||||||||||| |||||
Sbjct: 194 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 253

Query: 784 g 784
|
Sbjct: 254 g 254

Score = 73.8 bits (37), Expect = 4e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| |||| ||| |||| ||||| ||||||||||| || ||||| || |||||

Sbjct: 446 cttggagggcctaattgggatgtaaaactaggaagaagagatgccagaacagcaagccaa 505

Query: 1598 tttagcgctcttggactttccaccaagga 1626
 ||| ||| ||| ||| ||| ||| ||| ||| |||
 Sbjct: 566 ttcactgctgttggcctttccaccaagga 594

```
Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 616 tcacaccattggacaagcaaggtgcacaaagtttcagggcacgcataatacaacgagaccaa 675
```

Score = 73.8 bits (37), Expect = 4e-09
Identities = 73/85 (85%)
Strand = Plus / Minus

```
Query: 2138 gctccaatggagaaatcaggaagaa 2162
          |||||
Sbjct: 121 gctccaatggcgagattaggaagaa 97
```

Score = 73.8 bits (37), Expect = 4e-09
Identities = 70/81 (86%)

Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||||

Sbjct: 263 gccatgatcaagatgggtgacatcaaacctctcaccggctctaattggagaaattcgcaag 322

Query: 2161 aattgtagaaggattaactaa 2181
|||||||

Sbjct: 323 aattgtagaaagatcaactaa 343

Score = 71.9 bits (36), Expect = 2e-08

Identities = 87/104 (83%)

Strand = Plus / Plus

Query: 1939 cttcaaactccaaccagctttgacaactactacttcaagaacctcggttcagaagaagggt 1998
|||||||

Sbjct: 101 cttcaaaccccaacggcctttgacaacaagtatttcaagaacctgattaacaagaagggc 160

Query: 1999 ctctccactctgatcagcaactgttcaacggtgggtccaccga 2042
|| |||||

Sbjct: 161 ctctccactctgatcagcagctcttcaatggtgggtccgccga 204

>gb|CN782128.1| EST00224 cqseed Chenopodium quinoa cDNA clone S02D05 5' similar to
peroxidase, putative At5g05340, mRNA sequence
Length = 803

Score = 73.8 bits (37), Expect = 4e-09

Identities = 46/49 (93%)

Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
|||||||

Sbjct: 238 atgggtgcttctctcctacgttggttcttccacgattgcttcgtcaatg 286

Score = 46.1 bits (23), Expect = 1.0

Identities = 68/83 (81%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| || || ||||| || || || || ||||| ||||| || |||||
Sbjct: 478 cttggaggaccaacttggaacgtaaagctaggtagaagagatgctaggacagctagccaa 537

Query: 1538 tctgctgctaacaatggcatccc 1560
|| |||| ||||| |||||
Sbjct: 538 tccactgcaaacaatgacatccc 560

>gb|FC869818.1| C31105F02EF AbioticR1 Citrus reshni cDNA clone C31105F02, mRNA
sequence
Length = 630

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctt 776
||||||| || |||||||||||||||||||||||||||||
Sbjct: 51 cgcatgggcctctctccttcgcttgttcttccacgattgctt 94

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||||||| ||||||||||||| || |||
Sbjct: 102 ggatgcatgatgcatcttctactagacgacacatcatctttcaccggagagaaaaatgca 161

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||| | ||||| || || |||||||||||| || |||||||||||| || || ||
Sbjct: 162 gtccccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 221

Query: 1277 gagaaag 1283
|||||||
Sbjct: 222 gagaaag 228

Score = 54.0 bits (27), Expect = 0.004
Identities = 87/107 (81%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcacccacttcaaacctta 1580
||||||| ||||||||| | ||| | || | || ||||| |
Sbjct: 337 ctagaactgcaagccaatctgctgctaataagcggcgttcctcctctacctaacttga 396

Query: 1581 accaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
| ||||| ||| || | ||||| ||||||| |||||
Sbjct: 397 atcaactcacctctaggttcaacgctctcggactttccaacaaggac 443

>gb|FC874065.1| C31202A05EF BiotPhyR1 Citrus aurantium cDNA clone C31202A05, mRNA
sequence
Length = 689

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttggttcttccacgattgctt 776
||||||| || ||||||||| ||||||||| |||||
Sbjct: 228 cgcatgggcgctctctccttcgcttggttcttccacgattgctt 271

Score = 56.0 bits (28), Expect = 0.001
Identities = 82/100 (82%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcacccacttcaaacctta 1580
||||||| ||||||||| ||||| ||| | || ||||| |
Sbjct: 514 ctagaactgcaagccaatctgctgctaataagcgattcctcctcctacctaacttga 573

Query: 1581 accaactcatctcaagatttagcgctcttggactttccac 1620
| ||||| ||| || | ||||| |||||||
Sbjct: 574 atcaactcacctctaggttcaacgctctcggactttccac 613

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

Query: 2085 ctctgatttcgccgccgatgatcaagatgggagacattagtcctctcactgggtccaa 2144
||||||| || ||||| ||||||||||||| || ||||||| || ||||| |||||
Sbjct: 33 ctctgattttgctgccgcgatgatcaagatgggtgatattagtcctcttactgggtccaa 92

Query: 2145 tggagaaatcaggaag 2160
||| ||||| |||||
Sbjct: 93 tggcgaaataaggaag 108

>gb|EY845171.1| CA26-C1-002-040-C02-CT.F Sour orange leaf, field plant Citrus
aurantium cDNA, mRNA sequence
Length = 812

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtcttctctccttcgcttgttcttccacgattgctt 776
||||||| || |||||||||||||||||||||||||||||||
Sbjct: 267 cgcattgggcctctctccttcgcttgttcttccacgattgctt 310

Score = 60.0 bits (30), Expect = 7e-05
Identities = 120/150 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| || ||| || || ||||| || || ||||| ||||||||| |||||
Sbjct: 510 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 569

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaactcatctcaaga 1597
||||||| || ||||| ||| || || || ||||| || || ||||| ||| ||
Sbjct: 570 tctgctgctaataagcggcattcctcctcctacctcaaacttgaatcaactcacctctagg 629

Query: 1598 tttagcgctcttggactttccaccaaggac 1627
| | ||||| ||||||||| |||||
Sbjct: 630 tccaacgctctcggactttccaacaaggac 659

Score = 54.0 bits (27), Expect = 0.004

Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||||| ||||| ||||| |||||
Sbjct: 318 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 377

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 378 gtccccaatcgtaactccgccgcggattcgaggtcatcgacaacattaagtccgcagtt 437

Query: 1277 gagaaag 1283
|||||
Sbjct: 438 gagaaag 444

>gb|EY794850.1| CR05-C3-701-027-F03-CT.F Mandarin fruit, development stadium (2 of
3) Citrus reticulata cDNA, mRNA sequence
Length = 850

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctt 776
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 235 cgcattgggccttctctccttcgcttgttcttccacgattgctt 278

Score = 61.9 bits (31), Expect = 2e-05
Identities = 88/107 (82%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcacccacttcaaactta 1580
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 521 ctagaactgcaagccaatctgctgctaataagcgcatcctcctcctacactcaaactga 580

Query: 1581 accaactcatctcaagatttagcgctcttgactttccaccaaggac 1627
| ||||| ||| || || || ||||| ||||| ||||| |||||
Sbjct: 581 atcaactcacctctaggttcaacgctctcgactttccaacaaggac 627

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||| ||||| ||||| ||| |||
Sbjct: 286 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 345

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || ||| |||
Sbjct: 346 gtccccaatcgtaactccgccgcggattcgaggtcatcgacaacattaagtccgcagtt 405

Query: 1277 gagaaag 1283
|||||||
Sbjct: 406 gagaaag 412

>gb|EY776217.1| CR05-C1-103-015-D05-CT.F Mandarin leaf, infected with Xylella
fastidiosa (stage 2 of 2) Citrus reticulata cDNA, mRNA
sequence
Length = 968

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctctcttcgcttgttcttccacgattgctt 776
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 225 cgcatgggcctctctctcttcgcttgttcttccacgattgctt 268

Score = 54.0 bits (27), Expect = 0.004
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||| ||||| ||||| ||| |||
Sbjct: 276 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 335

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || ||| |||

Sbjct: 336 gtccccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtcgcagtt 395

Query: 1277 gagaaag 1283

|||||||

Sbjct: 396 gagaaag 402

>gb|EY725128.1| CS00-C3-703-086-B09-CT.F Sweet orange fruit, development stadium (4
of 6) Citrus sinensis cDNA, mRNA sequence
Length = 840

Score = 71.9 bits (36), Expect = 2e-08

Identities = 42/44 (95%)

Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctt 776

||||||| || |||||||||||||||||||||||||||||||

Sbjct: 210 cgcattgggcctctctccttcgcttgttcttccacgattgctt 253

Score = 67.9 bits (34), Expect = 3e-07

Identities = 121/150 (80%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

||||||||||| | ||| | || ||||| || || ||||| ||||||||||| |||||

Sbjct: 453 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 512

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597

||||||||||| | ||||| ||| | || || ||||| | || ||||||| ||| ||

Sbjct: 513 tctgctgctaatacggcattcctcctctacctcaaacttgaatcaactcacctctagg 572

Query: 1598 tttagcgctcttggactttccaccaaggac 1627

|| | ||||| ||||||||| |||||

Sbjct: 573 ttcaacgctctcggactttccaacaaggac 602

Score = 54.0 bits (27), Expect = 0.004

Identities = 102/127 (80%)

Strand = Plus / Plus

>gb|CX670039.1| UCRCP01_048_E06_T7 Swingle citrumelo nematode-challenged root cDNA
library - UCRCP01 Citrus x paradisi x Poncirus trifoliata

cDNA clone UCRCP01_048_T7_E06, mRNA sequence
Length = 848

Score = 71.9 bits (36), Expect = 2e-08
Identities = 111/136 (81%)
Strand = Plus / Plus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||||| ||||| ||||| ||||| ||||| || || ||||| ||
Sbjct: 286 caggcgacaacaacttgccaccgcttgatctgcaaactcctacttgttttgacaacaatt 345

Query: 1970 acttcaagaacctcggtcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
||||| ||||| || || || ||||| || || ||||| || ||||| ||
Sbjct: 346 acttcaagaacctggtcaacagaaagggttgcttcactctgatcaacagctgttcaatg 405

Query: 2030 gtgggtccaccgactc 2045
||||| |||||
Sbjct: 406 gtgggtccactgactc 421

Score = 56.0 bits (28), Expect = 0.001
Identities = 88/108 (81%)
Strand = Plus / Plus

Query: 1520 gctagaactgctagccaatctgctgctaacaatggcatccctgcaccacacttcaaactt 1579
||||| ||||| ||||| ||||| || || ||||| || || ||||| ||
Sbjct: 42 gctagaactgcaagcctatctgctgctaatacgcgcatcctgctcctacctcaaacttg 101

Query: 1580 aaccaactcatctcaagatttagcgctcttgactttccaccaaggac 1627
|| || |||| || || || || ||||| ||||| ||||| |||||
Sbjct: 102 aatcagctcacctctaggttcaacgctctcggactttccaacaaggac 149

>gb|CX050341.1| UCRC09_31H06_b Ruby Orange Developing Seed cDNA Library UCRC09
Citrus sinensis cDNA clone UCRC09-31H06-P12-1-4.b, mRNA
sequence
Length = 888

Score = 71.9 bits (36), Expect = 2e-08
Identities = 42/44 (95%)
Strand = Plus / Minus

Query: 733 cgcatgggtgcttctctccttcgcttggttcttccacgattgctt 776
||||||| || ||||||||||||||||||||||||||||
Sbjct: 512 cgcatgggcgcctctctccttcgcttggttcttccacgattgctt 469

Score = 60.0 bits (30), Expect = 7e-05
Identities = 105/130 (80%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaac 1213
||||||| ||||| ||| ||||| | || ||||||||| ||||||||||||| ||
Sbjct: 175 cagggatgcgatggatcagttctactagacgacacatcatctttcaccggagagaaaaat 116

Query: 1214 gcaaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagcc 1273
||| ||||| | ||||| || || ||||||||||| || ||||||||||| || ||
Sbjct: 115 gcagtcaccaatcgtaactccgccgcggattcgaggtcatcgacaacattaagtccgca 56

Query: 1274 gtggagaaag 1283
|| |||||
Sbjct: 55 gttgagaaag 46

>gb|CV717574.1| UCRCS08_0009D08_f Parent Washington Navel Orange Callus cDNA Library
UCRCS08-1 Citrus sinensis cDNA clone CS_AEa0009D08, mRNA
sequence
Length = 694

Score = 71.9 bits (36), Expect = 2e-08
Identities = 123/152 (80%)
Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535
||||||||||| | ||| | || ||||| || || ||||| ||||||||| |||||
Sbjct: 120 agcttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagcc 179

Query: 1536 aatctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaa 1595
||||||||||| | ||||| ||| || || ||||||| || ||||||| |||||
Sbjct: 180 aatctgctgctaatagcggcatctctcctcctacctcaaacttgaatcaactcacctcta 239

Query: 1596 gatttagcgctcttggactttccaccaaggac 1627
| || | ||||| ||||||||| |||||
Sbjct: 240 ggttcaacgctctcggactttccaacaaggac 271

Score = 46.1 bits (23), Expect = 1.0
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 2005 cactctgatcagcaactgttcaacgggtgggtccac 2039
||||||| || ||||| |||||
Sbjct: 626 cactctgatcaacagctgttcaatgggtgggtccac 660

>gb|CV093292.1| FAMU_USDA_FP_1315 Vitis shuttleworthii L., grape Vitis shuttleworthii
cDNA clone JLVs077_F09 5', mRNA sequence
Length = 666

Score = 71.9 bits (36), Expect = 2e-08
Identities = 101/120 (84%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
||||||| ||| || ||||| ||||| || ||||| || |||
Sbjct: 230 tcaggggacaacaacttggccctctggatcttcaaactcctac-agcttttgagaaca 288

Query: 1968 ctacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaa 2027
|||| | ||||| | ||||| || ||||| ||||| |||||
Sbjct: 289 ctactacaagaacctgatcaagaagaaggacttctccactctgatcagcagctgttcaa 348

Score = 60.0 bits (30), Expect = 7e-05
Identities = 54/62 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 116 cacacaattgggcaagcaaggtgcacatccttcagggtcgcatatacaatgagacaaac 175

Query: 1855 at 1856
||
Sbjct: 176 at 177

Score = 50.1 bits (25), Expect = 0.065
Identities = 58/69 (84%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
|||||
Sbjct: 426 atgatcaagatgggagatatcagccactcactggatcaaacggagagattaggaagaac 485

Query: 2164 tgtagaagg 2172
||
Sbjct: 486 tgcagaagg 494

Score = 48.1 bits (24), Expect = 0.26
Identities = 81/100 (81%)
Strand = Plus / Plus

Query: 1539 ctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagat 1598
|||||
Sbjct: 6 ctgctgcaaacaacagcatccctcctccaacttcaaacctgaaccaactaatctctagtt 65

Query: 1599 ttagcgctcttggactttccaccaaggacttggctgcctt 1638
|
Sbjct: 66 tccaagctcttggcctctcaaccaggacttgggtgcctt 105

>gb|C0866271.1| Mdfrt3046b02.y1 Mdfrt Malus x domestica cDNA clone Mdfrt3046b02 5'
similar to TR:Q41326 Q41326 PEROXIDASE ;, mRNA sequence
Length = 509

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 277 gccatgatcaagatgggagacatcaaacctctcactggatccagtggggagattaggaag 336

Query: 2161 aattgtag 2168
|||||
Sbjct: 337 aattgtag 344

Score = 46.1 bits (23), Expect = 1.0
Identities = 90/111 (81%), Gaps = 1/111 (0%)
Strand = Plus / Plus

Query: 1918 aacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaag 1977
||||| |||| ||||||| ||||||| || || || ||||||| |||||||||
Sbjct: 92 aacaatttggctccacttgaccttcaaaccctacttctttcgacaacaactacttcaa 151

Query: 1978 aacctcgttcagaagaagg-gtctcctccactctgatcagcaactgttcaa 2027
||||| | ||||| || | ||||||||| ||||||| || |||||
Sbjct: 152 aacctaatccagaataaagagtctcctccactctgaccagcagctcttcaa 202

>gb|C0417575.1| Mdfrt3031k23.y1 Mdfrt Malus x domestica cDNA clone Mdfrt3031k23 5'
similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;, mRNA sequence
Length = 363

Score = 71.9 bits (36), Expect = 2e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||||| ||||||| || || ||||||| |||| || || || |||||
Sbjct: 129 gccatgatcaagatgggagacatcaaacctctcactggatccagtggggagattaggaag 188

Query: 2161 aattgtag 2168
|||||||
Sbjct: 189 aattgtag 196

>gb|C0070833.1| GR_Ea28B05.r GR_Ea Gossypium raimondii cDNA clone GR_Ea28B05 3',
mRNA sequence
Length = 857

Score = 71.9 bits (36), Expect = 2e-08
Identities = 48/52 (92%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| ||||||| || || ||||||| |||||
Sbjct: 227 cgcatgggtgcttctctcgtccgcttgttcttccatgactgctttgtcaatg 278

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 633 tcacacaattggactagcaaggtgcaca 660

>emb|CU505430.1| CU505430 PODMEUPA_KZOACAB Theobroma cacao cDNA clone KZOACAB5YF04FM1,
 mRNA sequence
 Length = 769

Score = 69.9 bits (35), Expect = 7e-08
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 |||||
Sbjct: 455 cttggaggcccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 514

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
 |||||
Sbjct: 515 gctgctgccaacaacagcattcctcctccaacttctaacttgacagactcatttctaga 574

Query: 1598 tttagcgctcttggactttccaccaaggacttggt 1632
 |||
Sbjct: 575 ttcaatgctcttggactttccaccaggacatggt 609

Score = 48.1 bits (24), Expect = 0.26
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 625 tcacacaattggactagcaaggtgcaca 652

>emb|CU478688.1| CU478688 COPHAS_KZOAAAL Theobroma cacao cDNA clone KZOAAAL11YB20FM1,
 mRNA sequence
 Length = 642

Score = 69.9 bits (35), Expect = 7e-08
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 458 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 517

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||| ||||| ||| | | ||||| ||| | ||| ||||| || |||
Sbjct: 518 gctgctgccaacaacagcattcctcctccaacttctaacttgaacagactcatttctaga 577

Query: 1598 tttagcgctcttggactttccaccaaggacttggt 1632
|| | ||||||||||||||||||| ||||| |||||
Sbjct: 578 ttcaatgctcttggactttccaccaggacatggt 612

>emb|CU478933.1| CU478933 COPHAS_KZ0AAL Theobroma cacao cDNA clone KZ0AAL12YN22FM1,
mRNA sequence
Length = 744

Score = 69.9 bits (35), Expect = 7e-08
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 458 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 517

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||| ||||| ||| | | ||||| ||| | ||| ||||| || |||
Sbjct: 518 gctgctgccaacaacagcattcctcctccaacttctaacttgaacagactcatttctaga 577

Query: 1598 tttagcgctcttggactttccaccaaggacttggt 1632
|| | ||||||||||||||||||| ||||| |||||
Sbjct: 578 ttcaatgctcttggactttccaccaggacatggt 612

Score = 48.1 bits (24), Expect = 0.26
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
||||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 628 tcacacaattggactagcaaggtgcaca 655

>emb|CU480774.1| CU480774 CORTEXS_KZ0AAT Theobroma cacao cDNA clone KZ0AAT11YE09FM1,
mRNA sequence
Length = 703

Score = 69.9 bits (35), Expect = 7e-08
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 455 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 514

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 515 gctgctgccaacaacagcattcctcctccaacttctaactgaacagactcatttctaga 574

Query: 1598 tttagcgctcttggactttccaccaaggacttggt 1632
|||
Sbjct: 575 ttcaatgctcttggactttccaccaggacatggt 609

Score = 48.1 bits (24), Expect = 0.26
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
|||||
Sbjct: 625 tcacacaattggactagcaaggtgcaca 652

>dbj|DC895850.1| DC895850 PCC Citrus unshiu cDNA clone PCC0206 5', mRNA sequence
Length = 338

Score = 69.9 bits (35), Expect = 7e-08
Identities = 167/211 (79%)
Strand = Plus / Minus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
|||||
Sbjct: 289 caggcgacaacaacttgccaccgcttgatctgcaaactcctacttgttttgacaacaatt 230

Query: 1970 acttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
 ||||| ||||| || | |||| | || ||||| |||||
 Sbjct: 229 acttcaggaacctgggtcaacagaaagggtgcttcactctgatcaacagctgttcaatg 170

```
Query: 2030 gtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctg 2089
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 169 gtgggtccacagattcacagtcgcacgtacagtaacaaccggagcaccttcagctctg 110
```

```
Query: 2090 atttcgccgcccatgatcaagatgggaga 2120
      ||| | |||| ||||| ||||| |||||
Sbjct: 109 attttgccgcccatgatcaagatgggaga 79
```

>gb|EX266960.1| 1447232_5_A14_063 PY06 Carica papaya cDNA, mRNA sequence
Length = 1047

Score = 69.9 bits (35), Expect = 7e-08
Identities = 53/59 (89%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
 ||||| ||||||| ||||| || ||||| || ||||||| |||||
 Sbjct: 684 cacacgattggacaagcaaggtgcacgaatttcagggtcgcataatacaacgagaccaa 742

>gb|EX289762.1| 1577761_5_L07_022 PY06 Carica papaya cDNA, mRNA sequence
Length = 1029

Score = 69.9 bits (35), Expect = 7e-08
Identities = 53/59 (89%)
Strand = Plus / Plus

```
Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||||| ||||||||||||||||| || ||||| || ||||| |||||||||||||
Sbjct: 180  cacacgattggacaagcaaggtgcacgaatttcagggtcgcataatacaacgagaccaa 238
```

>gb|EX272151.1| 1452845_5_K11_038 PY06 Carica papaya cDNA, mRNA sequence
Length = 1098

Score = 69.9 bits (35), Expect = 7e-08
Identities = 53/59 (89%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||||||||||||| || ||||| || ||||||| |||||||
Sbjct: 686 cacacgattggacaagcaaggtgcacgaatttcagggtcgcataataacgagaccaa 744

>gb|EB110403.1| 000430AFBC008068HT (AFBC) Royal Gala pre-opened floral bud Malus x
domestica cDNA clone AFBC008068, mRNA sequence
Length = 481

Score = 69.9 bits (35), Expect = 7e-08
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||||||||||||| ||||| ||||||| ||||| || |||||||
Sbjct: 217 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcataataacgagaccaa 276

Query: 1854 cat 1856
|||
Sbjct: 277 cat 279

>gb|DW157696.1| CLVX9795.b1_E02.ab1 CLV(XYZ) lettuce virosa Lactuca virosa cDNA clone
CLVX9795, mRNA sequence
Length = 440

Score = 69.9 bits (35), Expect = 7e-08
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 2088 tgatttcgccgccgccatgatcaagatgggagacattagtcctctcactggtccaatgg 2147
||||| || ||||||||||||||||||| ||||| || ||| ||||| ||||||| ||||| ||
Sbjct: 198 tgattttgcggccgccatgatcaacatgggtgatattcgtccctcactggtccaacgg 257

Query: 2148 agaaatcaggaagaa 2162
|| |||||||
Sbjct: 258 cgagatcaggaagaa 272

>gb|DW145800.1| CLVX10900.b1_H13.ab1 CLV(XYZ) lettuce virosa Lactuca virosa cDNA
clone CLVX10900, mRNA sequence
Length = 453

|||
Sbjct: 153 cat 155

>gb|CN880015.1| 010418AASA009843HT (AASA) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASA009843, mRNA sequence
Length = 687

Score = 69.9 bits (35), Expect = 7e-08
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 710 aatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttccacg 769
||||||| |||| ||||| | ||||||||||||||||||||| | |||||
Sbjct: 168 aatctgccgtatcaaaggaaaagcgcatgggtgcttctctccttcgctccatttccacg 227

Query: 770 attgctttgtcaatg 784
|||||||||||||||
Sbjct: 228 attgctttgtcaatg 242

Score = 67.9 bits (34), Expect = 3e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||||||||||||||| |||| || ||||||||||||| |||||||||
Sbjct: 608 cacacaataggacaagcaaggtgcaccgtcttccgaaccgcgcatctacaccgagaccaac 667

Query: 1855 at 1856
||
Sbjct: 668 at 669

>gb|GR871114.1| Pq_F_00457 American ginseng Flower cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 519

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 354 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 413

Query: 1314 tccttg 1319

|||||
Sbjct: 414 tccttg 419

>gb|GR875194.1| Pq_R_02677 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 453

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 354 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 413

Query: 1314 tccttg 1319

|||||
Sbjct: 414 tccttg 419

>gb|GR873483.1| Pq_R_00966 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 494

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 292 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 351

Query: 1314 tccttg 1319

|||||
Sbjct: 352 tccttg 357

>gb|GR873276.1| Pq_R_00759 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence

Length = 557

Score = 67.9 bits (34), Expect = 3e-07

Identities = 58/66 (87%)

Strand = Plus / Plus

```
Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
          ||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 341 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 400
```

Query: 1314 tccttg 1319

|||||

Sbjct: 401 tccttg 406

>gb|GR871777.1| Pq_F_01120 American ginseng Flower cDNA Library Panax quinquefolius

cDNA 5', mRNA sequence

Length = 435

Score = 67.9 bits (34), Expect = 3e-07

Identities = 58/66 (87%)

Strand = Plus / Plus

```
Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
          ||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 293 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 352
```

Query: 1314 tccttg 1319

|||||

Sbjct: 353 tccttg 358

>gb|GR874357.1| Pq_R_01840 American ginseng Root cDNA Library Panax quinquefolius

cDNA 5', mRNA sequence

Length = 397

Score = 67.9 bits (34), Expect = 3e-07

Identities = 58/66 (87%)

Strand = Plus / Plus

```
Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
          ||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 315 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 374
```

Query: 1314 tccttg 1319
|||||
Sbjct: 375 tccttg 380

>gb|GR874227.1| Pq_R_01710 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 415

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||||| || ||||||| || || ||||||| ||||||| |||||||
Sbjct: 67 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 126

Query: 1314 tccttg 1319
|||||
Sbjct: 127 tccttg 132

>emb|CU507988.1| CU507988 PODSSHWB1Sb_KZOACD Theobroma cacao cDNA clone
KZOACD3YE10FM1, mRNA sequence
Length = 336

Score = 67.9 bits (34), Expect = 3e-07
Identities = 61/70 (87%)
Strand = Plus / Minus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| ||||||| || || ||||||| ||||||| |||||||
Sbjct: 328 catgatcaagatgggagacatcagtcacctcactggatcaaggggagagatcaggaagaa 269

Query: 2163 ttgtagaagg 2172
|| |||||||
Sbjct: 268 ctgcagaagg 259

>gb|EY664481.1| CS00-C1-101-067-A09-CT.F Sweet orange leaf, infected with Xylella
fastidiosa (stage 1 of 2) Citrus sinensis cDNA, mRNA
sequence
Length = 677

Score = 67.9 bits (34), Expect = 3e-07
Identities = 214/274 (78%)
Strand = Plus / Plus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 206 cagggcacaacaacttggcaccgcttgatctgcaaactcctacttcttttgacaacaatt 265

Query: 1970 acttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 266 acttcaagaacctggtcaacagaaagggtggttcactctgatcaacagctgttcaatg 325

Query: 2030 gtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctctg 2089
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 326 gtgggtccactgattcacaagtcgcgacgtacagtaacaacccgagcaccttcagctctg 385

Query: 2090 atttcgccgccgccatgatcaagatgggagacattagtcctctcactggctccaatggag 2149
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 386 attttgttgctggcatgatcaagatgggagatatcagcccactcactggatcccgcggtg 445

Query: 2150 aaatcaggaagaattgtagaaggattaactaatt 2183
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 446 aaattaggaagaattgcaggaggatcaattaatt 479

>gb|EW712042.1| Ginseng-Feq Contig4 Ginseng F. equiseti subtraction library Panax
quinquefolius cDNA, mRNA sequence
Length = 1030

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 410 ttgacaccattaaagaagctgtggagagagagtgtccaggagttgtttcctgtgcagata 469

Query: 1314 tccttg 1319
|||||
Sbjct: 470 tccttg 475

>gb|EL366609.1| CCES2712.b1_005.ab1 CCE(LMS) endive Cichorium endivia cDNA clone
CCES2712, mRNA sequence
Length = 465

Score = 67.9 bits (34), Expect = 3e-07
Identities = 64/74 (86%)
Strand = Plus / Plus

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||||||||||||| ||||| || ||| ||||| ||||||| ||||| ||
Sbjct: 267 gatttcgccgccgcatgatcaatatgggtgatattcgtcccctcaccggctccaacggc 326

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||
Sbjct: 327 gagatcaggaagaa 340

>gb|EH664510.1| 11.2E05 Transformed tobacco Lambda Zap II library Nicotiana tabacum
cDNA 5', mRNA sequence
Length = 1034

Score = 67.9 bits (34), Expect = 3e-07
Identities = 54/61 (88%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttggttcttcacgattgctttgtcaat 783
||||| ||||| ||||||||||| ||||||||| | ||||| ||||||||| |||||
Sbjct: 206 aaggaaaccgcatgggtgcttccctccttcgcctattcttcnagattgcttcgtcaat 265

Query: 784 g 784
|
Sbjct: 266 g 266

>gb|EC600006.1| PNSSH3G-1469 panax notoginseng subtracted cDNA libraries Panax
notoginseng cDNA 5' similar to secretory peroxidase, mRNA
sequence
Length = 454

Score = 67.9 bits (34), Expect = 3e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 30 ttgacaccattaaagaagctgtggagagagagtcccaggagttgttcctgtgcagata 89

Query: 1314 tccttg 1319

|||||
Sbjct: 90 tccttg 95

Database: /usr/local/blast/db/blastlibs/est_others

Posted date: Feb 13, 2010 7:48 AM

Number of letters in database: 29,218,461,503

Number of sequences in database: 51,680,690

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 51680690

Number of Hits to DB: 860,649,786

Number of extensions: 51423138

Number of successful extensions: 14543517

Number of sequences better than 10.0: 2195

Number of HSP's gapped: 14543355

Number of HSP's successfully gapped: 2740

Length of query: 2730

Length of database: 29,218,461,503

Length adjustment: 24

Effective length of query: 2706

Effective length of database: 27,978,124,943

Effective search space: 75708806095758

Effective search space used: 75708806095758

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 50 (99.1 bits)

S1: 12 (24.3 bits)

S2: 22 (44.1 bits)

BLASTx Output of the 5' Border Sequence Flanking the Insert in Soybean Event DAS-68416-4 against GenBank Non-redundant Protein Sequences (nr)

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 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.

Query= 68416_5_border
(2730 letters)

Database: /usr/local/blast/db/blastlibs/nr
10,432,217 sequences; 3,559,509,877 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
gb ACU17608.1	unknown [Glycine max]	249	2e-63
gb ACU17865.1	unknown [Glycine max]	242	2e-61
gb AAP76387.1	class III peroxidase [Gossypium hirsutum]	218	2e-54
gb AB077632.1	peroxidase [Medicago truncatula]	217	7e-54
dbj BAA82306.1	peroxidase [Nicotiana tabacum]	212	2e-52
ref XP_002278996.1	PREDICTED: hypothetical protein [Vitis vinif...	211	5e-52
gb AAX44001.2	putative secretory peroxidase [Catharanthus roseus]	209	1e-51
gb AAP42508.1	anionic peroxidase swpb3 [Ipomoea batatas]	209	1e-51
gb ABR23054.1	basic peroxidase swpb4 [Ipomoea batatas]	209	1e-51
gb ACU23245.1	unknown [Glycine max]	208	2e-51
gb ACM47317.1	peroxidase [Capsicum annuum]	205	3e-50
ref XP_002328991.1	predicted protein [Populus trichocarpa] >gi ...	204	4e-50
ref XP_002269918.1	PREDICTED: hypothetical protein [Vitis vinif...	204	4e-50
emb CAD67479.1	peroxidase [Asparagus officinalis]	203	1e-49
ref NP_196153.1	peroxidase, putative [Arabidopsis thaliana] >gi ...	202	2e-49
dbj BAF27413.2	Os11g0112400 [Oryza sativa Japonica Group]	201	5e-49
ref NP_001065568.1	Os11g0112400 [Oryza sativa (japonica cultiva...	201	5e-49
gb EAY79693.1	hypothetical protein OsI_34840 [Oryza sativa Indi...	199	1e-48
ref NP_001065971.1	Os12g0112000 [Oryza sativa (japonica cultiva...	199	1e-48
ref XP_002450132.1	hypothetical protein SORBIDRAFT_05g001000 [S...	199	2e-48
gb ACT35473.1	peroxidase 52 [Brassica rapa]	197	7e-48
ref XP_002441703.1	hypothetical protein SORBIDRAFT_08g000990 [S...	196	1e-47
ref XP_002450133.1	hypothetical protein SORBIDRAFT_05g001010 [S...	196	1e-47
gb ABV24960.2	putative secretory peroxidase [Catharanthus roseus]	196	1e-47
sp P00434.3	PERP7_BRARA RecName: Full=Peroxidase P7; AltName: Fu...	196	1e-47

gb AAD37423.1 AF149281_1 peroxidase 6 [Phaseolus vulgaris]	195	3e-47
ref XP_002520835.1 Peroxidase 52 precursor, putative [Ricinus c...	194	4e-47
ref XP_002319968.1 predicted protein [Populus trichocarpa] >gi ...	193	8e-47
ref NP_001151940.1 peroxidase 52 [Zea mays] >gi 195651251 gb AC...	191	3e-46
ref XP_002489046.1 hypothetical protein SORBIDRAFT_0246s002010 ...	190	7e-46
ref XP_002441702.1 hypothetical protein SORBIDRAFT_08g000980 [S...	190	7e-46
gb AAA96137.1 peroxidase [Stylosanthes humilis]	190	7e-46
gb AAL93151.1 AF485265_1 class III peroxidase [Gossypium hirsutum]	189	2e-45
emb CAD67478.1 peroxidase [Asparagus officinalis]	188	3e-45
gb AAR31108.1 peroxidase precursor [Quercus suber]	188	3e-45
gb AAR31106.1 peroxidase precursor [Quercus suber]	187	8e-45
ref NP_001131000.1 hypothetical protein LOC100192105 [Zea mays]...	186	1e-44
gb AAD43561.1 AF155124_1 bacterial-induced peroxidase precursor ...	185	2e-44
gb ACN33662.1 unknown [Zea mays]	184	4e-44
emb CBI25393.1 unnamed protein product [Vitis vinifera]	184	7e-44
gb ACU23223.1 unknown [Glycine max]	182	2e-43
emb CAA71491.1 peroxidase [Spinacia oleracea]	182	2e-43
gb ABK21858.1 unknown [Picea sitchensis]	180	7e-43
emb CAD67477.1 peroxidase [Asparagus officinalis]	179	1e-42
emb CAA62597.1 korean-radish isoperoxidase [Raphanus sativus]	179	1e-42
gb AC090366.1 peroxidase precursor [Triticum aestivum]	179	2e-42
gb ACN34270.1 unknown [Zea mays]	179	2e-42
gb ACU24215.1 unknown [Glycine max]	178	4e-42
gb AAB48184.1 peroxidase precursor [Linum usitatissimum]	178	4e-42
emb CBI27506.1 unnamed protein product [Vitis vinifera]	177	5e-42
ref XP_002274550.1 PREDICTED: hypothetical protein [Vitis vinif...	177	5e-42
gb ACN42168.1 peroxidase 1 [Sesuvium portulacastrum]	177	6e-42
ref XP_002269058.1 PREDICTED: hypothetical protein [Vitis vinif...	177	8e-42
emb CBI27505.1 unnamed protein product [Vitis vinifera]	177	8e-42
emb CAL25300.1 properoxidase [Picea abies]	176	1e-41
ref XP_002269145.1 PREDICTED: hypothetical protein [Vitis vinif...	175	2e-41
gb ACJ85500.1 unknown [Medicago truncatula]	174	5e-41
emb CAN80097.1 hypothetical protein [Vitis vinifera]	173	1e-40
emb CBI27503.1 unnamed protein product [Vitis vinifera]	172	2e-40
emb CBI27502.1 unnamed protein product [Vitis vinifera]	172	2e-40
ref XP_002269169.1 PREDICTED: hypothetical protein [Vitis vinif...	172	2e-40
gb AA013838.1 AF405326_1 peroxidase 2 [Lupinus albus]	172	2e-40
gb ABA96220.1 Cationic peroxidase 1 precursor, putative, expres...	172	2e-40
tpe CAH69378.1 TPA: class III peroxidase 136 precursor [Oryza s...	172	2e-40
ref XP_002269216.1 PREDICTED: hypothetical protein [Vitis vinif...	172	2e-40
emb CAH10839.1 peroxidase [Picea abies]	172	2e-40
ref XP_002266365.1 PREDICTED: hypothetical protein [Vitis vinif...	172	3e-40
ref NP_001106040.1 plasma membrane-bound peroxidase 2b precurs...	172	3e-40
gb EAY82023.1 hypothetical protein OsI_37207 [Oryza sativa Indi...	171	3e-40
gb ABA91154.1 Cationic peroxidase 1 precursor, putative, expres...	171	3e-40
ref NP_001065566.1 Os11g0112200 [Oryza sativa (japonica cultiva...	171	3e-40
gb EEE67815.1 hypothetical protein OsJ_25569 [Oryza sativa Japo...	171	4e-40
ref NP_001060628.1 Os07g0677200 [Oryza sativa (japonica cultiva...	171	4e-40
tpe CAH69353.1 TPA: class III peroxidase 111 precursor [Oryza s...	171	4e-40

emb	CBI27501.1	unnamed protein product [Vitis vinifera]	170	7e-40
ref	XP_002269266.1	PREDICTED: hypothetical protein [Vitis vinif...	170	7e-40
ref	XP_002509730.1	Lignin-forming anionic peroxidase precursor,...	170	7e-40
emb	CBI18066.1	unnamed protein product [Vitis vinifera]	170	1e-39
ref	XP_002268259.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
ref	XP_002299006.1	predicted protein [Populus trichocarpa] >gi ...	170	1e-39
ref	XP_002333334.1	predicted protein [Populus trichocarpa] >gi ...	170	1e-39
ref	XP_002285723.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
emb	CAA46916.1	peroxidase [Oryza sativa (japonica cultivar-grou...	170	1e-39
ref	XP_002319967.1	predicted protein [Populus trichocarpa] >gi ...	169	1e-39
gb	ABK24123.1	unknown [Picea sitchensis]	169	2e-39
gb	AAA20473.1	peroxidase [Cenchrus ciliaris]	169	2e-39
gb	ABK23423.1	unknown [Picea sitchensis]	168	3e-39
ref	NP_001060629.1	Os07g0677300 [Oryza sativa (japonica cultiva...	168	3e-39
gb	ACJ11762.1	class III peroxidase [Gossypium hirsutum]	168	4e-39
gb	ABK25962.1	unknown [Picea sitchensis]	168	4e-39
gb	EAZ05133.1	hypothetical protein OsI_27326 [Oryza sativa Indi...	168	4e-39
ref	NP_001046400.1	Os02g0240100 [Oryza sativa (japonica cultiva...	168	4e-39
gb	AAC49818.1	peroxidase [Oryza sativa Indica Group]	168	4e-39
dbj	BAD28869.1	putative bacterial-induced peroxidase precursor ...	168	4e-39
ref	XP_002274693.1	PREDICTED: hypothetical protein [Vitis vinif...	167	5e-39
gb	EEC82680.1	hypothetical protein OsI_27324 [Oryza sativa Indi...	167	5e-39
ref	NP_001060626.1	Os07g0676900 [Oryza sativa (japonica cultiva...	167	5e-39
emb	CAH10840.1	peroxidase [Picea abies]	167	5e-39
dbj	BAC83101.1	putative peroxidase precursor [Oryza sativa Japo...	167	5e-39
tpe	CAH69351.1	TPA: class III peroxidase 109 precursor [Oryza s...	167	5e-39
ref	XP_002451848.1	hypothetical protein SORBIDRAFT_04g008620 [S...	167	6e-39
gb	ACN33811.1	unknown [Zea mays]	167	6e-39
gb	ABR18139.1	unknown [Picea sitchensis]	167	6e-39
sp	A2YPX3.2	PER2_ORYSI RecName: Full=Peroxidase 2; Flags: Precu...	167	8e-39
ref	XP_002461208.1	hypothetical protein SORBIDRAFT_02g042850 [S...	166	1e-38
ref	XP_002320417.1	predicted protein [Populus trichocarpa] >gi ...	166	1e-38
ref	NP_001130666.1	hypothetical protein LOC100191769 [Zea mays]...	166	1e-38
ref	NP_200648.1	peroxidase, putative [Arabidopsis thaliana] >gi...	166	1e-38
ref	XP_002338628.1	predicted protein [Populus trichocarpa] >gi ...	166	1e-38
ref	XP_002336344.1	predicted protein [Populus trichocarpa] >gi ...	166	1e-38
emb	CAA71493.1	peroxidase [Spinacia oleracea]	166	1e-38
gb	AAX53172.1	peroxidase [Populus alba x Populus tremula var. g...	166	1e-38
ref	XP_002509738.1	Lignin-forming anionic peroxidase precursor,...	166	2e-38
ref	XP_002453592.1	hypothetical protein SORBIDRAFT_04g008630 [S...	165	2e-38
gb	ACN60163.1	class III peroxidase [Tamarix hispida]	164	5e-38
ref	XP_002450134.1	hypothetical protein SORBIDRAFT_05g001030 [S...	163	9e-38
gb	AAC05277.1	peroxidase FLXPER4 [Linum usitatissimum]	163	9e-38
ref	XP_002269343.1	PREDICTED: hypothetical protein [Vitis vinif...	163	1e-37
gb	EAY85148.1	hypothetical protein OsI_06503 [Oryza sativa Indi...	163	1e-37
ref	XP_002269301.1	PREDICTED: hypothetical protein [Vitis vinif...	162	2e-37
gb	AAD37428.1	AF149278_1 peroxidase 3 precursor [Phaseolus vulga...	162	2e-37
ref	XP_002334243.1	predicted protein [Populus trichocarpa] >gi ...	162	2e-37
ref	XP_002438530.1	hypothetical protein SORBIDRAFT_10g021630 [S...	162	3e-37

ref XP_002281755.1	PREDICTED: hypothetical protein [Vitis vinif...	162	3e-37
ref XP_002437128.1	hypothetical protein SORBIDRAFT_10g021610 [S...	161	3e-37
ref XP_002517727.1	Cationic peroxidase 1 precursor, putative [R...	160	6e-37
ref NP_001057822.1	Os06g0547400 [Oryza sativa (japonica cultiva...	160	6e-37
ref XP_002285724.1	PREDICTED: hypothetical protein [Vitis vinif...	160	8e-37
ref XP_002521867.1	Lignin-forming anionic peroxidase precursor,...	160	8e-37
emb CAH10841.1	peroxidase [Picea abies]	160	8e-37
gb EEE67814.1	hypothetical protein OsJ_25568 [Oryza sativa Japo...	160	1e-36
tpe CAH69352.1	TPA: class III peroxidase 110 precursor [Oryza s...	160	1e-36
ref NP_001060627.1	Os07g0677100 [Oryza sativa (japonica cultiva...	160	1e-36
gb ABD66594.1	peroxidase [Litchi chinensis]	159	1e-36
emb CBI19219.1	unnamed protein product [Vitis vinifera]	159	1e-36
ref XP_002334317.1	predicted protein [Populus trichocarpa] >gi ...	159	1e-36
emb CAN73051.1	hypothetical protein [Vitis vinifera]	159	1e-36
gb EEE67818.1	hypothetical protein OsJ_25573 [Oryza sativa Japo...	159	2e-36
gb EEE56633.1	hypothetical protein OsJ_06032 [Oryza sativa Japo...	159	2e-36
ref XP_002281731.1	PREDICTED: hypothetical protein [Vitis vinif...	159	2e-36
gb EAO5136.1	hypothetical protein OsI_27329 [Oryza sativa Indi...	159	2e-36
ref NP_001046402.1	Os02g0240500 [Oryza sativa (japonica cultiva...	159	2e-36
ref NP_001060630.1	Os07g0677400 [Oryza sativa (japonica cultiva...	159	2e-36
emb CAA59487.1	peroxidase [Triticum aestivum] >gi 193074375 gb ...	159	2e-36
gb AAB02554.1	cationic peroxidase [Stylosanthes humilis]	159	2e-36
sp P16147.2	PERX_LUPPO RecName: Full=Peroxidase >gi 1345541 emb ...	159	2e-36
dbj BAA77389.1	peroxidase 3 [Scutellaria baicalensis]	159	2e-36
ref XP_002461207.1	hypothetical protein SORBIDRAFT_02g042840 [S...	158	3e-36
gb EEC82684.1	hypothetical protein OsI_27330 [Oryza sativa Indi...	158	3e-36
gb AAW52720.1	peroxidase 6 [Triticum monococcum]	158	3e-36
gb AAQ55292.1	class III peroxidase GvPx2b [Vitis vinifera]	158	3e-36
gb AAF65464.2	AF247700_1 peroxidase POC1 [Oryza sativa Indica Gr...	158	3e-36
ref XP_002311022.1	predicted protein [Populus trichocarpa] >gi ...	158	4e-36
gb EEE67819.1	hypothetical protein OsJ_25574 [Oryza sativa Japo...	158	4e-36
ref NP_001147216.1	LOC100280824 [Zea mays] >gi 195608630 gb ACG...	158	4e-36
ref NP_001060631.1	Os07g0677500 [Oryza sativa (japonica cultiva...	158	4e-36
pdb 1SCH A Chain A, Peanut Peroxidase >gi 1633131 pdb 1SCH B Cha...		158	4e-36
sp P22195.2	PER1_ARAHY RecName: Full=Cationic peroxidase 1; AltN...	158	4e-36
gb ACU22965.1	unknown [Glycine max]	157	5e-36
ref XP_002311955.1	predicted protein [Populus trichocarpa] >gi ...	157	5e-36
gb AAM61588.1	peroxidase [Arabidopsis thaliana]	157	5e-36
ref NP_200647.1	peroxidase, putative [Arabidopsis thaliana] >gi...	157	5e-36
ref XP_002460939.1	hypothetical protein SORBIDRAFT_02g037840 [S...	157	7e-36
ref XP_002334018.1	predicted protein [Populus trichocarpa] >gi ...	157	7e-36
gb EAY85151.1	hypothetical protein OsI_06506 [Oryza sativa Indi...	157	7e-36
emb CAH10842.1	peroxidase [Picea abies]	157	7e-36
emb CBI22007.1	unnamed protein product [Vitis vinifera]	157	9e-36
ref XP_002283995.1	PREDICTED: hypothetical protein [Vitis vinif...	157	9e-36
emb CAN81400.1	hypothetical protein [Vitis vinifera]	157	9e-36
emb CAN63655.1	hypothetical protein [Vitis vinifera]	157	9e-36
gb AAA20472.1	peroxidase [Cenchrus ciliaris]	156	1e-35
gb ACF08096.1	class III peroxidase [Triticum aestivum]	156	1e-35

ref XP_002461211.1	hypothetical protein SORBIDRAFT_02g042870 [S...	156	1e-35
sp Q02200.1 PERX_NICSY	RecName: Full=Lignin-forming anionic pero...	156	1e-35
ref XP_002437129.1	hypothetical protein SORBIDRAFT_10g021620 [S...	155	2e-35
gb AAW52718.1	peroxidase 4 [Triticum monococcum]	155	2e-35
gb ACI03401.1	peroxidase 1 [Litchi chinensis]	155	2e-35
ref XP_002284007.1	PREDICTED: hypothetical protein [Vitis vinif...	155	2e-35
ref XP_002323054.1	predicted protein [Populus trichocarpa] >gi ...	155	2e-35
gb EEC82681.1	hypothetical protein OsI_27325 [Oryza sativa Indi...	155	2e-35
gb EAZ01280.1	hypothetical protein OsI_23303 [Oryza sativa Indi...	155	2e-35
gb AAV89058.1	class III peroxidase [Phelipanche ramosa]	155	2e-35
gb AAW52719.1	peroxidase 5 [Triticum monococcum]	155	2e-35
gb AAC49819.1	peroxidase [Oryza sativa Indica Group]	155	2e-35
dbj BAD97435.1	peroxidase [Pisum sativum]	155	2e-35
ref NP_001057821.1	Os06g0547100 [Oryza sativa (japonica cultiva...	155	2e-35
emb CBI19220.1	unnamed protein product [Vitis vinifera]	155	3e-35
gb ACN30737.1	unknown [Zea mays]	155	3e-35
gb ACG40622.1	peroxidase 2 precursor [Zea mays]	155	3e-35
emb CAN83972.1	hypothetical protein [Vitis vinifera]	154	4e-35
ref XP_002509737.1	Lignin-forming anionic peroxidase precursor,...	154	6e-35
ref XP_002268412.1	PREDICTED: hypothetical protein [Vitis vinif...	154	6e-35
dbj BAD36900.1	peroxidase [Lotus japonicus]	154	6e-35
gb ACN26131.1	unknown [Zea mays]	154	7e-35
gb ACF08094.1	class III peroxidase [Triticum aestivum]	153	9e-35
ref XP_002509733.1	Lignin-forming anionic peroxidase precursor,...	153	9e-35
ref XP_002319407.1	predicted protein [Populus trichocarpa] >gi ...	153	9e-35
dbj BAA77388.1	peroxidase 2 [Scutellaria baicalensis]	153	9e-35
gb ACF08095.1	class III peroxidase [Triticum aestivum]	153	1e-34
gb EAZ01279.1	hypothetical protein OsI_23302 [Oryza sativa Indi...	153	1e-34
ref NP_001046392.1	Os02g0236600 [Oryza sativa (japonica cultiva...	152	2e-34
gb EAZ37287.1	hypothetical protein OsJ_21626 [Oryza sativa Japo...	152	2e-34
gb ABD47726.1	peroxidase [Eucalyptus globulus subsp. globulus]	152	2e-34
ref NP_001057820.1	Os06g0546500 [Oryza sativa (japonica cultiva...	152	2e-34
ref XP_002438534.1	hypothetical protein SORBIDRAFT_10g021650 [S...	152	2e-34
ref NP_001140437.1	hypothetical protein LOC100272496 [Zea mays]...	152	2e-34
gb ACF82414.1	unknown [Zea mays]	152	2e-34
dbj BAF19735.2	Os06g0547100 [Oryza sativa Japonica Group]	152	3e-34
ref XP_002438533.1	hypothetical protein SORBIDRAFT_10g021640 [S...	151	4e-34
gb ACE00594.1	lignin biosynthetic peroxidase [Leucaena leucocep...	151	4e-34
emb CBI19221.1	unnamed protein product [Vitis vinifera]	151	5e-34
ref XP_002451846.1	hypothetical protein SORBIDRAFT_04g008590 [S...	151	5e-34
emb CAL25299.1	properoxidase [Picea abies]	151	5e-34
emb CBI15847.1	unnamed protein product [Vitis vinifera]	150	6e-34
ref XP_002451850.1	hypothetical protein SORBIDRAFT_04g008650 [S...	150	6e-34
ref XP_002276796.1	PREDICTED: hypothetical protein [Vitis vinif...	150	6e-34
gb EAZ22364.1	hypothetical protein OsJ_06022 [Oryza sativa Japo...	150	6e-34
gb EAY85141.1	hypothetical protein OsI_06496 [Oryza sativa Indi...	150	6e-34
tpe CAH69268.1	TPA: class III peroxidase 26 precursor [Oryza sa...	150	6e-34
ref NP_001046393.1	Os02g0236800 [Oryza sativa (japonica cultiva...	150	6e-34
gb ABK22680.1	unknown [Picea sitchensis]	150	8e-34

emb CAN61440.1	hypothetical protein [Vitis vinifera]	150	8e-34
gb AAC31550.1	peroxidase PXC2 precursor [Avena sativa]	150	8e-34
gb AAC31551.1	peroxidase PXC6 precursor [Avena sativa]	150	8e-34
emb CAA71492.1	peroxidase [Spinacia oleracea]	149	2e-33
ref NP_001054096.1	Os04g0651000 [Oryza sativa (japonica cultiva...	149	2e-33
ref XP_002308244.1	predicted protein [Populus trichocarpa] >gi ...	149	2e-33
emb CBI19222.1	unnamed protein product [Vitis vinifera]	148	3e-33
ref XP_002467656.1	hypothetical protein SORBIDRAFT_01g031740 [S...	148	3e-33
gb EEE61812.1	hypothetical protein OsJ_16433 [Oryza sativa Japo...	148	3e-33
gb EEC78144.1	hypothetical protein OsI_17703 [Oryza sativa Indi...	148	3e-33
emb CAJ86184.1	H0212B02.16 [Oryza sativa (indica cultivar-group...	148	3e-33
gb EAZ22372.1	hypothetical protein OsJ_06030 [Oryza sativa Japo...	148	3e-33
ref NP_001046401.1	Os02g0240300 [Oryza sativa (japonica cultiva...	148	3e-33
gb ABK21983.1	unknown [Picea sitchensis]	148	4e-33
ref XP_002461210.1	hypothetical protein SORBIDRAFT_02g042860 [S...	148	4e-33
emb CBI18065.1	unnamed protein product [Vitis vinifera]	147	5e-33
gb ACF08091.1	class III peroxidase [Triticum aestivum]	147	5e-33
gb EAY85149.1	hypothetical protein OsI_06504 [Oryza sativa Indi...	147	5e-33
gb AAW52716.1	peroxidase 2 [Triticum monococcum]	147	5e-33
gb AAA32972.1	peroxidase [Hordeum vulgare]	147	5e-33
emb CBI22008.1	unnamed protein product [Vitis vinifera]	147	7e-33
gb ACD70388.1	class III peroxidase [Triticum aestivum]	147	7e-33
gb ABF48527.1	cell wall peroxidase [Capsicum annuum] >gi 110348...	147	9e-33
gb ACF08092.1	class III peroxidase [Triticum aestivum]	146	1e-32
gb ACN37032.1	unknown [Zea mays]	146	1e-32
sp P27337.1	PER1_HORVU RecName: Full=Peroxidase 1; Flags: Precur...	146	1e-32
gb ABV24961.1	peroxidase [Catharanthus roseus]	146	2e-32
emb CAL25298.1	properoxidase [Picea abies]	146	2e-32
gb ACF08089.1	class III peroxidase [Triticum aestivum]	146	2e-32
ref XP_002467893.1	hypothetical protein SORBIDRAFT_01g036000 [S...	145	2e-32
gb EEC75221.1	hypothetical protein OsI_11488 [Oryza sativa Indi...	145	2e-32
gb ABF95843.1	Peroxidase 52 precursor, putative, expressed [Ory...	145	2e-32
tpe CAH69282.1	TPA: class III peroxidase 40 precursor [Oryza sa...	145	2e-32
ref XP_002531319.1	Peroxidase 2 precursor, putative [Ricinus co...	145	2e-32
ref NP_001147254.1	peroxidase 52 [Zea mays] >gi 195609124 gb AC...	145	2e-32
ref XP_002465306.1	hypothetical protein SORBIDRAFT_01g035990 [S...	145	3e-32
emb CAA39486.1	peroxidase [Triticum aestivum]	145	3e-32
gb ACR36744.1	unknown [Zea mays]	145	3e-32
ref XP_002323056.1	predicted protein [Populus trichocarpa] >gi ...	145	3e-32
gb ACF88317.1	unknown [Zea mays]	145	3e-32
gb AAZ42168.1	lignin peroxidase-like [Cucumis sativus]	145	3e-32
gb AAB48986.1	peroxidase precursor [Medicago truncatula]	144	4e-32
ref XP_002521852.1	Lignin-forming anionic peroxidase precursor,...	144	4e-32
ref NP_001106020.1	plasma membrane-bound peroxidase 3-2 precurs...	144	4e-32
ref XP_002521866.1	Lignin-forming anionic peroxidase precursor,...	144	6e-32
ref XP_002521851.1	Lignin-forming anionic peroxidase precursor,...	144	6e-32
gb EEC75545.1	hypothetical protein OsI_12177 [Oryza sativa Indi...	144	6e-32
ref NP_001050435.1	Os03g0434800 [Oryza sativa (japonica cultiva...	144	6e-32
gb AAU89207.1	peroxidase, putative [Oryza sativa Japonica Group...	144	6e-32

gb ACU21160.1	unknown [Glycine max]	144	6e-32
gb ACF08090.1	class III peroxidase [Triticum aestivum]	144	7e-32
emb CAA59484.1	pox1 [Triticum aestivum]	144	7e-32
gb AAW52715.1	peroxidase 1 [Triticum monococcum]	143	1e-31
ref NP_001042342.1	Os01g0205900 [Oryza sativa (japonica cultiva...	143	1e-31
tpe CAH69245.1	TPA: class III peroxidase 2 precursor [Oryza sat...	143	1e-31
gb ACU20213.1	unknown [Glycine max]	143	1e-31
gb EEC75220.1	hypothetical protein OsI_11487 [Oryza sativa Indi...	143	1e-31
emb CAB99487.1	peroxidase [Hordeum vulgare subsp. vulgare]	143	1e-31
ref NP_001050059.1	Os03g0339300 [Oryza sativa (japonica cultiva...	143	1e-31
emb CAD92857.1	peroxidase [Picea abies]	142	2e-31
gb ACF08086.1	class III peroxidase [Triticum aestivum]	142	2e-31
emb CAN80096.1	hypothetical protein [Vitis vinifera]	142	2e-31
gb AAB97854.1	ferriprotein porphyrin-containing peroxidase [Str...	142	2e-31
emb CAC81821.1	peroxidase [Beta vulgaris]	142	2e-31
gb ACF08083.1	class III peroxidase [Triticum aestivum]	142	2e-31
ref NP_001106019.1	LOC100101533 precursor [Zea mays] >gi 221272...	142	2e-31
ref NP_172906.1	anionic peroxidase, putative [Arabidopsis thali...	142	2e-31
gb ACF70708.1	root peroxidase [Triticum aestivum]	142	3e-31
gb ACF70706.1	root peroxidase [Triticum aestivum]	142	3e-31
ref NP_001050434.1	Os03g0434500 [Oryza sativa (japonica cultiva...	142	3e-31
gb AAU89205.1	peroxidase, putative [Oryza sativa Japonica Group...	142	3e-31
gb EEC70139.1	hypothetical protein OsI_00829 [Oryza sativa Indi...	141	4e-31
ref XP_002319422.1	predicted protein [Populus trichocarpa] >gi ...	141	5e-31
gb ACF70710.1	root peroxidase [Triticum aestivum]	140	6e-31
gb ACF70709.1	root peroxidase [Triticum aestivum]	140	6e-31
gb ACF70705.1	root peroxidase [Triticum aestivum] >gi 194425605...	140	6e-31
gb ACF70701.1	root peroxidase [Triticum aestivum]	140	6e-31
gb AAM76682.1	AF387866_1 peroxidase [Triticum aestivum]	140	6e-31
ref XP_002448660.1	hypothetical protein SORBIDRAFT_06g030940 [S...	140	8e-31
gb AAM65211.1	peroxidase [Arabidopsis thaliana] >gi 42494611 gb...	140	8e-31
gb ACF08087.1	class III peroxidase [Triticum aestivum]	140	8e-31
ref XP_002270068.1	PREDICTED: hypothetical protein [Vitis vinif...	140	8e-31
ref XP_002323055.1	predicted protein [Populus trichocarpa] >gi ...	140	8e-31
gb AAF43956.1	AC012188_33 Strong similarity to an Anionic Peroxi...	140	8e-31
gb AAF63165.1	AC010657_1 T5E21.5 [Arabidopsis thaliana]	140	8e-31
ref NP_172907.1	anionic peroxidase, putative [Arabidopsis thali...	140	8e-31
ref NP_001147443.1	peroxidase 52 [Zea mays] >gi 195611432 gb AC...	140	1e-30
gb ACF08085.1	class III peroxidase [Aegilops ventricosa]	140	1e-30
gb ACF70703.1	root peroxidase [Triticum aestivum]	140	1e-30
gb ACT78791.1	putative peroxidase [Cucumis sativus]	139	1e-30
gb ACD87898.1	class III peroxidase [Aegilops ventricosa]	139	1e-30
gb ACF70707.1	root peroxidase [Triticum aestivum]	139	1e-30
emb CAN61439.1	hypothetical protein [Vitis vinifera]	139	1e-30
gb AAW52717.1	peroxidase 3 [Triticum monococcum] >gi 193074352 ...	139	1e-30
sp Q05855.1	PER1_WHEAT RecName: Full=Peroxidase; AltName: Full=W...	139	1e-30
gb ACF08084.1	class III peroxidase [Triticum aestivum]	139	2e-30
ref XP_002521868.1	Lignin-forming anionic peroxidase precursor,...	139	2e-30
gb ACF70702.1	root peroxidase [Triticum aestivum]	139	2e-30

ref XP_002327780.1 predicted protein [Populus trichocarpa] >gi ...	139	2e-30
gb EEE54081.1 hypothetical protein OsJ_00811 [Oryza sativa Japo...	139	2e-30
gb AAQ55233.1 peroxidase [Orobancha cernua var. cumana]	138	3e-30
emb CAN80051.1 hypothetical protein [Vitis vinifera]	138	4e-30
ref XP_002521850.1 Peroxidase 30 precursor, putative [Ricinus c...	138	4e-30
gb ABR13314.1 putative peroxidase class III [Prunus dulcis]	138	4e-30
ref XP_002530724.1 Peroxidase 53 precursor, putative [Ricinus c...	137	5e-30
emb CAA59485.1 peroxidase [Triticum aestivum]	137	5e-30
gb ABK59095.1 peroxidase 1 [Sesbania rostrata]	137	9e-30
gb AAP42504.1 anionic peroxidase swpa5 [Ipomoea batatas]	137	9e-30
emb CBI27504.1 unnamed protein product [Vitis vinifera]	136	1e-29
emb CBI17443.1 unnamed protein product [Vitis vinifera]	136	1e-29
gb ACU23405.1 unknown [Glycine max]	136	1e-29
ref XP_002521512.1 Peroxidase 72 precursor, putative [Ricinus c...	136	1e-29
ref XP_002275309.1 PREDICTED: hypothetical protein [Vitis vinif...	136	1e-29
ref XP_002531320.1 Cationic peroxidase 1 precursor, putative [R...	136	1e-29
gb ABG49114.1 peroxidase [Dimocarpus longan]	136	2e-29
gb AAP42506.1 anionic peroxidase swpb1 [Ipomoea batatas]	136	2e-29
gb ACU24350.1 unknown [Glycine max]	135	2e-29
gb ACU21179.1 unknown [Glycine max]	135	2e-29
ref XP_002310274.1 predicted protein [Populus trichocarpa] >gi ...	135	2e-29
gb ABR17414.1 unknown [Picea sitchensis]	135	2e-29
gb AAB97853.1 ferriprotein porphyrin-containing peroxidase [Str...	135	2e-29
ref XP_002322726.1 predicted protein [Populus trichocarpa] >gi ...	135	3e-29
gb ACI22425.1 pericarp peroxidase 3 [Litchi chinensis]	134	5e-29
ref XP_002304885.1 predicted protein [Populus trichocarpa] >gi ...	134	6e-29
gb ABR17480.1 unknown [Picea sitchensis]	134	6e-29
gb ABZ80408.1 class III peroxidase [Casuarina glauca]	134	6e-29
gb AAK52085.1 peroxidase [Nicotiana tabacum]	134	6e-29
ref XP_002455406.1 hypothetical protein SORBIDRAFT_03g010250 [S...	134	8e-29
ref XP_002455405.1 hypothetical protein SORBIDRAFT_03g010240 [S...	134	8e-29
gb ACG44598.1 peroxidase 72 precursor [Zea mays]	134	8e-29
ref NP_001136736.1 hypothetical protein LOC100216875 [Zea mays]...	134	8e-29
ref NP_195361.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	134	8e-29
gb ABR23055.1 basic peroxidase swpb5 [Ipomoea batatas]	133	1e-28
gb EAY85142.1 hypothetical protein OsI_06497 [Oryza sativa Indi...	133	1e-28
gb AAC49822.1 peroxidase [Oryza sativa Indica Group]	133	1e-28
gb ACU21377.1 unknown [Glycine max]	133	1e-28
ref NP_001148509.1 peroxidase 72 [Zea mays] >gi 195619908 gb AC...	132	2e-28
gb ABK26974.1 unknown [Picea sitchensis]	132	2e-28
gb AAF63025.1 AF244922_1 peroxidase prx13 precursor [Spinacia ol...	132	2e-28
gb AAM61616.1 putative peroxidase [Arabidopsis thaliana]	132	2e-28
ref NP_179407.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	132	2e-28
emb CBI27500.1 unnamed protein product [Vitis vinifera]	132	2e-28
gb AAP42507.1 anionic peroxidase swpb2 [Ipomoea batatas]	132	2e-28
gb ABV26013.1 peroxidase [Musa acuminata]	132	3e-28
sp Q9LEH3.1 PER15_IPOBA RecName: Full=Peroxidase 15; Short=Prx15...	132	3e-28
ref XP_002300745.1 predicted protein [Populus trichocarpa] >gi ...	131	4e-28
gb ABC60345.1 putative peroxidase [Musa acuminata AAA Group]	131	4e-28

emb CAA66964.1	peroxidase [Arabidopsis thaliana] >gi 1429215 em...	131	4e-28
gb AAR15704.3	peroxidase [Brassica napus]	131	5e-28
gb AAM63684.1	peroxidase, putative [Arabidopsis thaliana]	131	5e-28
ref NP_175117.1	peroxidase, putative [Arabidopsis thaliana] >gi...	131	5e-28
ref NP_001050060.1	Os03g0339400 [Oryza sativa (japonica cultiva...	131	5e-28
sp Q4W1I8.1 PER1_ZINEL	RecName: Full=Basic peroxidase; AltName: ...	131	5e-28
sp Q4W1I9.1 PER2_ZINEL	RecName: Full=Basic peroxidase; AltName: ...	131	5e-28
gb AAF63026.1 AF244923_1	peroxidase prx14 precursor [Spinacia ol...	130	7e-28
ref NP_001046394.1	Os02g0237000 [Oryza sativa (japonica cultiva...	130	9e-28
dbj BAD27600.1	putative bacterial-induced peroxidase precursor ...	130	9e-28
ref NP_201440.1	peroxidase 72 (PER72) (P72) (PRXR8) [Arabidopsi...	130	9e-28
gb ABB45838.1	hypothetical protein [Thellungiella halophila]	130	1e-27
gb AAS00456.1	acid isoperoxidase [Brassica napus]	129	1e-27
emb CBI25854.1	unnamed protein product [Vitis vinifera]	129	2e-27
ref XP_002281048.1	PREDICTED: hypothetical protein [Vitis vinif...	129	2e-27
ref XP_002263033.1	PREDICTED: hypothetical protein [Vitis vinif...	129	2e-27
ref XP_002510443.1	Peroxidase 9 precursor, putative [Ricinus co...	129	2e-27
emb CBI15846.1	unnamed protein product [Vitis vinifera]	128	3e-27
ref XP_002457158.1	hypothetical protein SORBIDRAFT_03g002370 [S...	128	3e-27
ref XP_002455760.1	hypothetical protein SORBIDRAFT_03g024460 [S...	128	3e-27
ref XP_002438468.1	hypothetical protein SORBIDRAFT_10g020100 [S...	128	3e-27
gb ABI37011.1	peroxidase [Oryza sativa]	128	4e-27
emb CBI16459.1	unnamed protein product [Vitis vinifera]	127	6e-27
ref XP_002285642.1	PREDICTED: hypothetical protein [Vitis vinif...	127	6e-27
gb EAY73397.1	hypothetical protein OsI_01277 [Oryza sativa Indi...	127	6e-27
ref NP_001042657.1	Os01g0263300 [Oryza sativa (japonica cultiva...	127	6e-27
emb CBI16466.1	unnamed protein product [Vitis vinifera]	127	7e-27
ref XP_002463385.1	hypothetical protein SORBIDRAFT_02g042880 [S...	127	7e-27
ref XP_002285649.1	PREDICTED: hypothetical protein [Vitis vinif...	127	7e-27
gb ABI97032.1	peroxidase [Solanum tuberosum]	127	7e-27
gb AAU04440.2	secreted peroxidase [Phelipanche ramosa]	127	7e-27
dbj BAG55221.1	peroxidase 2 [Sesbania rostrata]	127	7e-27
ref NP_001151639.1	peroxidase 68 [Zea mays] >gi 195648284 gb AC...	127	9e-27
gb EAY74439.1	hypothetical protein OsI_02330 [Oryza sativa Indi...	127	9e-27
ref XP_002269425.1	PREDICTED: hypothetical protein [Vitis vinif...	126	2e-26
ref NP_001043276.1	Os01g0543100 [Oryza sativa (japonica cultiva...	126	2e-26
dbj BAB89258.1	putative peroxidase ATP6a [Oryza sativa Japonica...	126	2e-26
dbj BAA94962.1	peroxidase [Asparagus officinalis]	125	2e-26
ref NP_179406.1	peroxidase, putative [Arabidopsis thaliana] >gi...	125	4e-26
emb CBI27497.1	unnamed protein product [Vitis vinifera]	124	5e-26
gb AAM28296.1	peroxidase [Ananas comosus]	124	5e-26
gb ABD47725.1	peroxidase [Eucalyptus globulus subsp. globulus]	124	5e-26
gb ACF88307.1	unknown [Zea mays]	124	6e-26
gb EAZ22365.1	hypothetical protein OsJ_06023 [Oryza sativa Japo...	123	1e-25
ref NP_564948.1	peroxidase, putative [Arabidopsis thaliana] >gi...	122	2e-25
emb CAH69540.1	putative peroxidase [Zinnia elegans]	122	3e-25
ref XP_002312356.1	predicted protein [Populus trichocarpa] >gi ...	121	4e-25
dbj BAD43011.1	peroxidase ATP23a [Arabidopsis thaliana]	121	4e-25
emb CAH69535.1	putative peroxidase [Zinnia elegans]	121	5e-25

gb AA013837.1 AF403735_1	extensin peroxidase [Lupinus albus]	121	5e-25
ref XP_002457609.1	hypothetical protein SORBIDRAFT_03g010230 [S...	120	7e-25
emb CAB65334.1	SPI2 protein [Picea abies]	120	9e-25
gb ACF22712.1	peroxidase precursor [Brachypodium distachyon]	120	1e-24
ref XP_002315983.1	predicted protein [Populus trichocarpa] >gi ...	120	1e-24
emb CAM31942.1	hypothetical protein [Lolium perenne]	120	1e-24
ref XP_002438233.1	hypothetical protein SORBIDRAFT_10g010040 [S...	119	2e-24
ref XP_002451847.1	hypothetical protein SORBIDRAFT_04g008600 [S...	119	2e-24
ref NP_190668.2	electron carrier/ heme binding / peroxidase [Ar...	119	2e-24
emb CAB62621.1	peroxidase-like protein [Arabidopsis thaliana] >...	119	2e-24
gb EAO5138.1	hypothetical protein OsI_27331 [Oryza sativa Indi...	119	2e-24
ref NP_001060632.1	Os07g0677600 [Oryza sativa (japonica cultiva...	119	2e-24
emb CBI27438.1	unnamed protein product [Vitis vinifera]	119	3e-24
ref XP_002270660.1	PREDICTED: hypothetical protein [Vitis vinif...	119	3e-24
emb CAN65777.1	hypothetical protein [Vitis vinifera]	119	3e-24
gb EAY89162.1	hypothetical protein OsI_10658 [Oryza sativa Indi...	118	3e-24
ref NP_001042655.1	Os01g0263000 [Oryza sativa (japonica cultiva...	118	3e-24
ref NP_001049480.1	Os03g0234500 [Oryza sativa (japonica cultiva...	118	3e-24
ref XP_002509732.1	Lignin-forming anionic peroxidase precursor,...	118	3e-24
ref XP_002509731.1	Lignin-forming anionic peroxidase precursor,...	118	3e-24
gb EEC70836.1	hypothetical protein OsI_02331 [Oryza sativa Indi...	118	4e-24
emb CAH55694.1	putative peroxidase [Lolium perenne]	117	6e-24
emb CAH55692.1	putative peroxidase [Festuca pratensis]	117	6e-24
ref NP_001057377.1	Os06g0274800 [Oryza sativa (japonica cultiva...	117	7e-24
ref XP_002509735.1	Lignin-forming anionic peroxidase precursor,...	117	1e-23
gb ACF08088.1	class III peroxidase [Aegilops ventricosa]	116	1e-23
gb ACG43658.1	hypothetical protein [Zea mays]	116	1e-23
gb ACF80021.1	unknown [Zea mays]	116	1e-23
ref NP_001130123.1	hypothetical protein LOC100191217 [Zea mays]...	116	1e-23
ref XP_002304020.1	predicted protein [Populus trichocarpa] >gi ...	115	2e-23
ref XP_002306459.1	predicted protein [Populus trichocarpa] >gi ...	115	3e-23
gb ABF95842.1	Peroxidase 2 precursor, putative, expressed [Oryz...	115	3e-23
emb CAA59486.1	peroxidase [Triticum aestivum]	115	4e-23
dbj BAA01992.1	peroxidase [Nicotiana tabacum]	114	6e-23
ref XP_002529736.1	Peroxidase 27 precursor, putative [Ricinus c...	114	8e-23
gb ACJ84393.1	unknown [Medicago truncatula]	114	8e-23
gb ACU23010.1	unknown [Glycine max]	113	1e-22
ref XP_001751508.1	predicted protein [Physcomitrella patens sub...	112	2e-22
gb AA013839.1 AF405327_1	peroxidase 1 [Lupinus albus]	112	3e-22
gb AAL58444.1 AF455807_1	anionic peroxidase [Nicotiana tomentososi...	112	3e-22
ref XP_002464560.1	hypothetical protein SORBIDRAFT_01g020830 [S...	111	4e-22
gb ACF70704.1	root peroxidase [Triticum aestivum]	111	4e-22
dbj BAD97439.1	peroxidase [Pisum sativum]	111	4e-22
gb AAQ67366.1	POD9 precursor [Gossypium hirsutum]	111	4e-22
ref XP_002309830.1	predicted protein [Populus trichocarpa] >gi ...	111	5e-22
gb EEE59027.1	hypothetical protein OsJ_10774 [Oryza sativa Japo...	111	5e-22
gb AAA34101.1	peroxidase [Nicotiana tabacum]	110	7e-22
sp P11965.1 PERX_TOBAC	RecName: Full=Lignin-forming anionic pero...	110	7e-22
emb CBI28955.1	unnamed protein product [Vitis vinifera]	110	9e-22

ref XP_002274157.1	PREDICTED: hypothetical protein [Vitis vinif...	110	9e-22
sp P15003.1 PER1_SOLLC	RecName: Full=Suberization-associated ani...	110	9e-22
gb EAZ22371.1	hypothetical protein OsJ_06029 [Oryza sativa Japo...	110	1e-21
gb ABK22032.1	unknown [Picea sitchensis]	109	2e-21
ref XP_001783974.1	predicted protein [Physcomitrella patens sub...	108	3e-21
gb EAZ37178.1	hypothetical protein OsJ_21519 [Oryza sativa Japo...	108	3e-21
emb CBI28956.1	unnamed protein product [Vitis vinifera]	108	3e-21
gb ACJ11761.1	class III peroxidase [Gossypium hirsutum]	108	3e-21
dbj BAF08306.2	Os02g0236600 [Oryza sativa Japonica Group]	108	3e-21
gb EAZ01154.1	hypothetical protein OsI_23183 [Oryza sativa Indi...	108	3e-21
tpe CAH69331.1	TPA: class III peroxidase 89 precursor [Oryza sa...	108	3e-21
ref NP_001058379.1	Os06g0681600 [Oryza sativa (japonica cultiva...	108	3e-21
dbj BAD45811.1	putative bacterial-induced peroxidase precursor ...	108	3e-21
ref NP_001057744.1	Os06g0521200 [Oryza sativa (japonica cultiva...	108	3e-21
gb EAZ01158.1	hypothetical protein OsI_23186 [Oryza sativa Indi...	108	5e-21
gb ACJ11766.1	class III peroxidase [Gossypium hirsutum]	108	5e-21
ref XP_002443277.1	hypothetical protein SORBIDRAFT_08g016840 [S...	107	8e-21
emb CAA50597.1	peroxidase [Solanum lycopersicum]	107	8e-21
emb CAB67121.1	peroxidase [Solanum lycopersicum]	107	8e-21
ref XP_002465968.1	hypothetical protein SORBIDRAFT_01g049140 [S...	107	8e-21
gb ACU20287.1	unknown [Glycine max]	107	1e-20
gb EEE65802.1	hypothetical protein OsJ_21515 [Oryza sativa Japo...	107	1e-20
sp P12437.2 PERX_SOLTU	RecName: Full=Suberization-associated ani...	107	1e-20
dbj BAD98313.2	peroxidase [Nicotiana tabacum]	107	1e-20
dbj BAD98314.1	peroxidase [Nicotiana tabacum]	107	1e-20
ref NP_001057745.1	Os06g0521400 [Oryza sativa (japonica cultiva...	107	1e-20
sp P15004.1 PER2_SOLLC	RecName: Full=Suberization-associated ani...	107	1e-20
gb AAA33837.1	anionic peroxidase [Solanum tuberosum] >gi 228610...	107	1e-20
ref XP_002336172.1	predicted protein [Populus trichocarpa] >gi ...	107	1e-20
ref NP_001136722.1	hypothetical protein LOC100216859 [Zea mays]...	107	1e-20
ref XP_002516846.1	Peroxidase 24 precursor, putative [Ricinus c...	106	1e-20
ref NP_001140982.1	hypothetical protein LOC100273061 [Zea mays]...	106	1e-20
gb ABU63712.1	lignin peroxidase [Garcinia mangostana]	106	1e-20
emb CBI25927.1	unnamed protein product [Vitis vinifera]	106	2e-20

>gb|ACU17608.1| unknown [Glycine max]

Length = 320

Score = 249 bits (635), Expect = 2e-63

Identities = 120/124 (96%), Positives = 121/124 (97%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCTNFRARIYNETNI TAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV

Sbjct: 197 QARCTNFRARIYNETNIGTAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

QKKG LHSDQQLFNGGSTDSIVRGYSTNPGTF SDFAAAMIKMGDISPLTGSNGE+RKNC

Sbjct: 257 QKKGFLHSDQQLFNGGSTDSIVRGYSTNPGTFPSDFAAAMIKMGDISPLTGSNGEVRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 213 bits (543), Expect = 8e-53
Identities = 118/165 (71%), Positives = 120/165 (72%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI
Sbjct: 70 VNGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ G PTWNVKLG
Sbjct: 130 RDSVQILGG-----PTWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG
Sbjct: 147 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 191

Score = 145 bits (365), Expect = 3e-32
Identities = 70/71 (98%), Positives = 70/71 (98%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKS VQSAISKETRMGASL
Sbjct: 1 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKS VQSAISKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>gb|ACU17865.1| unknown [Glycine max]
Length = 320

Score = 242 bits (618), Expect = 2e-61
Identities = 117/124 (94%), Positives = 120/124 (96%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRARIYNE+NI+TAFAR RQQSCPRTSGSGDNNLA LDLQTPT FDNYFKNLV
Sbjct: 197 QARCTNFRARIYNESNIDTAFARARQQSCPRTSGSGDNNLATLDLQTPTF DNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKGLLHSDQQLFNGGSTDSIVRGYSTNP +FSSDFAAAMIKMGDISPLTGSNGEIRKNC
Sbjct: 257 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPSSFSSDFAAAMIKMGDISPLTGSNGEIRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 208 bits (530), Expect = 2e-51
Identities = 114/165 (69%), Positives = 119/165 (72%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARG+EVIDNIKSAVEK CPGVVSCADILAI
Sbjct: 70 VNGCDGSILLDDTSSFTGEKNANPNRNSARGYEVIDNIKSAVEKACPGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ GGP+WNVK+G
Sbjct: 130 RDSVQIL-----GGPSWNVKVG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANNGIP PTSNLNQLISRFSALGLSTKDLVALSG
Sbjct: 147 RRDARTASQSAANNGIPPPTSNLNQLISRFSALGLSTKDLVALSG 191

Score = 138 bits (347), Expect = 4e-30
Identities = 68/71 (95%), Positives = 69/71 (97%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MASFCSRLTICLALFVLI GSANAQLSTNFYYHSCP NLF+VKSTVQSAISKETRMGASL
Sbjct: 1 MASFCSRLTICLALFVLILGSANAQLSTNFYYHSCP NLFSTVKSTVQSAISKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LR FFHDCFVN
Sbjct: 61 LRPFFHDCFVN 71

>gb|AAP76387.1| class III peroxidase [Gossypium hirsutum]
Length = 330

Score = 218 bits (556), Expect = 2e-54
Identities = 100/124 (80%), Positives = 116/124 (93%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT+FRARIYNE+NI+ +FA+TRQ++CPRT+GSGDNNLAPLD+QTPTSFDN YFKNL+
Sbjct: 207 QARCTSFARIYNESNIDASFAQTRQRNCPRTTGSGDNNLAPLDIQTPTSFDNNYFKNLI 266

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQQLFNGGSTDSIVRGY +P +F+SDF AAMIKMGDISPLTGS GEIRKNC

Sbjct: 267 SQRGLLHSDQQLFNGGSTDSIVRGYGNPSSFNDFVAAMIKMGDISPLTGSRGEIRKNC 326

Query: 2167 RRIN 2178

RR+N

Sbjct: 327 RRVN 330

Score = 196 bits (499), Expect = 1e-47
Identities = 107/169 (63%), Positives = 117/169 (69%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKPCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNANPNRNS+RGF+V+DNIKSAVE VCPGVVSCADILAIAA

Sbjct: 80 VNGCDGSVLLDDTSSFTGEKNANPNRNSRGRFVDVVDNIKSAVENVCPGVVSCADILAIAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W VKLG

Sbjct: 140 RDSVEI-----LGGPKWAVKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDAR+ASQSAANNGIP PTSNLN+L SRF+ALGLST+DLVALSG I

Sbjct: 157 RRDARSASQSAANNGIPPPTSNLNRLTSRFNALGLSTRDLVALSGAHTI 205

Score = 100 bits (248), Expect = 1e-18
Identities = 51/75 (68%), Positives = 58/75 (77%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRM 738
+K+ AS S+ + L L V + GS NAQLSTNFY SCPNL S+VKSTV SAI+KE RM

Sbjct: 7 TKMGSASSFSKFCLTLLLLVDVLGSTNAQLSTNFYSKCPNLLSTVKSTVTSAINKEARM 66

Query: 739 GASLLRLFFHDCFVN 783

GASLLRLFFHDCFVN

Sbjct: 67 GASLLRLFFHDCFVN 81

>gb|AB077632.1| peroxidase [Medicago truncatula]
Length = 322

Score = 217 bits (552), Expect = 7e-54
Identities = 104/124 (83%), Positives = 112/124 (90%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNETNI A A TRQ +CP+ SGSGDNNLAPLDLQTP+SFDN YFKNLV

Sbjct: 199 QARCTNFRARIYNETNINAAXASTRQSNCPKASGSGDNNLAPLDLQTPSSFDNYYFKNLV 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGBISPLTGSNGEIRKNC 2166
Q KGLLHSDQQLFNGGST+SIV GYST+P +FSSDFAAAMIKMGI PLTGSNGEIRKNC

Sbjct: 259 QNKGLLHSDQQLFNGGSTNSIVSGYSTSPSSFSSDFAAAMIKMGNIKPLTGSNGEIRKNC 318

Query: 2167 RRIN 2178

R+ N

Sbjct: 319 RKTN 322

Score = 188 bits (478), Expect = 3e-45

Identities = 105/169 (62%), Positives = 112/169 (66%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARGF+VIDNIK+AVE VCPGVVSCADILAI AA

Sbjct: 72 VNGCDGSILLDDTSSFTGEKNANPNRNSARGFDVIDNIKTAVENVCPGVVSCADILAI AA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
DSV I+ G PTWNVKLG

Sbjct: 132 ADSVAILGG-----PTWNVKLG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657

RRDA+TASQSAAN IPAPTSNLN L S FSA+GLS+KDLV LSG I

Sbjct: 149 RRDAKTASQSAANTAIPAPTSNLNTLTSMFSAVGLSSKDLVTLGAHTI 197

Score = 100 bits (249), Expect = 9e-19

Identities = 52/68 (76%), Positives = 58/68 (85%), Gaps = 1/68 (1%)

Frame = +1

Query: 583 CSRLT-ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
CSRLT I L L VLI GSANAQLSTNFY +CP L ++VKST+Q+AISKE RMGAS+LRL

Sbjct: 6 CSRLTMISLVLSVLIIGSANAQLSTNFYSKTCPKLSTTVKSTLQT AISKEARMGASILRL 65

Query: 760 FFHDCFVN 783

FFHDCFVN

Sbjct: 66 FFHDCFVN 73

>dbj|BAA82306.1| peroxidase [Nicotiana tabacum]

Length = 321

Score = 212 bits (540), Expect = 2e-52
Identities = 102/125 (81%), Positives = 110/125 (88%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT+FRARIYNETN ++ +FARTRQ +CPR+SGSGDNNLAPLDLQTP FDN YFKNL
Sbjct: 197 QARCTSFARIYNETNNLDASFARTRQSNCPRSSGSGDNNLAPLDLQTPNKFDNYYFKNL 256

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V KKGLLHSDQQLFNGGS DSIV YS NP +FSSDF AMIKMGDI PLTGSNGEIRKN
Sbjct: 257 VDKKGLLHSDQQLFNGGSADSIIVTSYNNPSSSFSSDFVTAMIKMGDIRPLTGSNGEIRKN 316

Query: 2164 CRRIN 2178
CRR+N
Sbjct: 317 CRRLN 321

Score = 187 bits (476), Expect = 5e-45
Identities = 105/169 (62%), Positives = 113/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEK A PN NSARGFEVIDNIKSAVEKVCPGVVSCADILA+ A
Sbjct: 70 VNGCDGSLLDDTSSFTGEKRAAPNVNSARGFEVIDNIKSAVEKVCPGVVSCADILAVTA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP WNVKLG
Sbjct: 130 RDSVVI-----LGGPNWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
RRD+RTASQSAAN+GIP TSNLN+LIS FSA+GLSTKD+VALSG I
Sbjct: 147 RRDSRTASQSAANS GIPPATSNLNLRISSFSAVGLSTKDMVALSGAHTI 195

Score = 91.3 bits (225), Expect = 6e-16
Identities = 46/71 (64%), Positives = 53/71 (74%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFS SVKSTVQSAISKETRMGASL 750
MAS + L L+ GS++AQLST FY SCP L+ +VKS VQSAI+KETRMGASL
Sbjct: 1 MASLKINAIVLFILVSLIGSSAQLSTGFYSKSCP KLYQTVKSAVQSAINKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>ref|XP_002278996.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 321

Score = 211 bits (536), Expect = 5e-52
Identities = 98/124 (79%), Positives = 112/124 (90%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI+ +FA+TRQ +CPR SGSGDNNLAPLDLQTPT+F+N Y+KNL+
Sbjct: 198 QARCTSFARIYNETNIDNSFAKTRQSNCPRASGSGDNNLAPLDLQTPTAFENNYKNLI 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQLFNGGSTDSIVR YS + F++ F A MIKMGDISPLTGSNGEIRKNC
Sbjct: 258 KKKGLLHSDQQLFNGGSTDSIVRKYSNSRSNFNAHFVAGMIKMGDISPLTGSNGEIRKNC 317

Query: 2167 RRIN 2178
RR+N
Sbjct: 318 RRVN 321

Score = 184 bits (466), Expect = 7e-44
Identities = 100/169 (59%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LLDDTSSF GEKNA PN NS RGF+V+D+IKS VE CPGVVSCAD+LAI AA
Sbjct: 71 VNGCDGSVLLDDTSSFIGEKNAAPNANSVRGFDVDDIKSKVETACPGVVSCADVLAI AA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGP+WNVKLG
Sbjct: 131 RDSVVIL-----GGPSWNVKLG 147

Query: 1511 RRDARTASQSAANN GIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF ALGLST+DLVAL+G+ I
Sbjct: 148 RRDARTASQAAANNSIPPPTSNLNQLISRFAQALGLSTRDLVALAGSHTI 196

Score = 90.1 bits (222), Expect = 1e-15
Identities = 46/72 (63%), Positives = 56/72 (77%), Gaps = 1/72 (1%)
Frame = +1

Query: 571 MASFCSRLTIC-LALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
MAS S + I +AL +L GS+ AQLST++Y SCP LF +VKS V+SA++KE RMGAS
Sbjct: 1 MASPSSYMAIVTMALLILFLGSSTAQLSTDYYSQSCP KLFPTVKS AVKSAVAKEARMGAS 60

Query: 748 LLRLFFHDCFVN 783

LLRLFFHDCFVN
Sbjct: 61 LLRLFFHDCFVN 72

>gb|AAx44001.2| putative secretory peroxidase [Catharanthus roseus]
Length = 318

Score = 209 bits (533), Expect = 1e-51
Identities = 101/125 (80%), Positives = 113/125 (90%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRARIYNETN ++ A A+TR+ +CPR SGS DNNLAPLDLQTP +FDN Y+KNL
Sbjct: 194 QARCTNFRARIYNETNNLDAALAQTRRSNCPRPSGSRDNNLAPLDLQTPRAFDNNYYKNL 253

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V ++GLLHSDQQLFNGGSTDSIVR YS NP +F+SDFAAAMIKMGDISPLTGSNG+IRKN
Sbjct: 254 VNRRGLLHSDQQLFNGGSTDSIVRSYSGNPASFASDFAAAMIKMGDISPLTGSNGQIRKN 313

Query: 2164 CRRIN 2178
CRRIN
Sbjct: 314 CRRIN 318

Score = 191 bits (484), Expect = 5e-46
Identities = 106/169 (62%), Positives = 114/169 (67%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEK A PN NSARGFEV+DNIKSAVE VCPGVVSCADILAIAA
Sbjct: 67 VNGCDGSILLDDTSSFTGEKRAAPNFNSARGFEVVDNIKSAVENVCPGVVSCADILAIAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ GGP+WNVKLG
Sbjct: 127 RDSVQIL-----GGPSWNVKLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA TASQ+AANN IP PTSNLN L+SRF+ALGLST DLVALSG+ I
Sbjct: 144 RRDATTASQAAANNSIPPPTSNLNALVSRFNALGLSTNDLVALSGSHTI 192

Score = 85.1 bits (209), Expect = 4e-14
Identities = 42/61 (68%), Positives = 52/61 (85%), Gaps = 1/61 (1%)
Frame = +1

Query: 604 LALFVL-IWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
L +F+L + GS++AQLST++Y SCPN+F++VKS V SAI KE RMGASLLRLFFHDCFV

Sbjct: 8 LGIFLLFLIGSSSAQLSTDYYSKSCPNVNTVKSQVHSAILKEARMGASLLRLFFHDCFV 67

Query: 781 N 783

N

Sbjct: 68 N 68

>gb|AAP42508.1| anionic peroxidase swpb3 [Ipomoea batatas]

Length = 320

Score = 209 bits (533), Expect = 1e-51

Identities = 100/124 (80%), Positives = 110/124 (88%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCTNFRARIYNE+NI+++FA++R+ +CPR SGSGDNNLAPLDLQTP FDN Y+ NLV

Sbjct: 197 QARCTNFRARIYNESNIDSSFAQSRKGNCPRASGSGDNNLAPLDLQTPIKFDNNYYVNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166

KKGLLHSDQQLFNG STDS VRGYSTNP F SDFAAAMIKMGGDI PLTG+NGEIRKNC

Sbjct: 257 NKKGLLHSDQQLFNGVSTDSTVRGYSTNPSKFKSDFAAAMIKMGGDIKPLTGNGEIRKNC 316

Query: 2167 RRIN 2178

RR N

Sbjct: 317 RRRN 320

Score = 184 bits (467), Expect = 5e-44

Identities = 103/169 (60%), Positives = 113/169 (66%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330

+ GCDGSILLDDTSSFTGEK A PN SARGFEVID IKSAREKVCPCGVVSCADILAI+

Sbjct: 70 VNGCDGSILLDDTSSFTGEKRAAPNFQSARGFEVIDQIKSAVEKVCPCGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDS ++ LGGP+WNVKLG

Sbjct: 130 RDS-----TVTLGGPSWNVKLG 146

Query: 1511 RRDARTASQAANNIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657

RRDARTASQ+AANN IPAPTSNLN+LIS FSA+GLST D+V LSG+ I

Sbjct: 147 RRDARTASQAAANSIPAPTSNLNRLISSFSAVGLSTNDMVVLGSHTI 195

Score = 82.8 bits (203), Expect = 2e-13

Identities = 42/71 (59%), Positives = 48/71 (67%)

Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MA LT L +++ G +AQLS FY SCP LF +V S V+SAI KE RMGASL
Sbjct: 1 MAVSVKALTAVLLCVLVLVGGCSAQLSPGFYSKSCPQLFQTVNSVVRSAIQKEARMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>gb|ABR23054.1| basic peroxidase swpb4 [Ipomoea batatas]
Length = 320

Score = 209 bits (532), Expect = 1e-51
Identities = 100/124 (80%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRARIYNE+NI+++FA++R+ +CPR SGSGDNNLAPLDLQTP FDN Y+ NLV
Sbjct: 197 QARCTNFRARIYNESNIDSSFAQSRKGNCPRASGSGDNNLAPLDLQTPIKFDNYYVNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS VRGYSTNP F SDFAAAMIKMGDI PLTG+NGEIRKNC
Sbjct: 257 NKKGLLHSDQQLFNGVSTDSTVRGYSTNPSKFRSDFAAAMIKMGIKPLTGNGEIRKNC 316

Query: 2167 RRIN 2178
RR N
Sbjct: 317 RRRN 320

Score = 182 bits (462), Expect = 2e-43
Identities = 102/169 (60%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEK A PN SARGFEVID IKSAREKVCPGVVSCADILAIA+
Sbjct: 70 VNGCDGSILLDDTSSFTGEKRAAPNFQSARGFEVIDQIKSAVEKVCPGVVSCADILAIAS 129

Query: 1331 RDSVQIVSGGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP+WNVKLG
Sbjct: 130 RDS-----TVTLGGPSWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRDAR ASQ+AANN IPAPTSNLN+LIS FSA+GLST D+V LSG+ I
Sbjct: 147 RRDARAASQAAANNSIPAPTSNLNRLISSFSAVGLSTNDMVVLGSHTI 195

Score = 80.5 bits (197), Expect = 1e-12
Identities = 40/62 (64%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRFFHDCF 777
+ L + VL+ G +AQLS FY SCP LF +V S V+SAI KE RMGASLLRFFHDCF
Sbjct: 11 VLLCVLVLV-GGCSAQLSPGFYSKSCPRLFQTVNSVVRSAIQKEARMGASLLRFFHDCF 69

Query: 778 VN 783
VN
Sbjct: 70 VN 71

>gb|ACU23245.1| unknown [Glycine max]
Length = 326

Score = 208 bits (530), Expect = 2e-51
Identities = 95/124 (76%), Positives = 111/124 (89%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FRARIYNE+NI+++FAR RQ CPRTSGSGDNNLAP+D TPT FDN+YFKNL+
Sbjct: 203 QARCTTFRARIYNESNIDSSFARMRQSRCPRTSGSGDNNLAPIDFATPTFFDNHYFKNLI 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
QKKG +HSDQ+LFNGGSTDS+V YSTNP +F +DF+AAMI+MGDISPLTGS GEIR+NC
Sbjct: 263 QKKGFIHSDQELFNGGSTDSLVTYSTNPASFFADFSAAIRMGDISPLTGSRGIRENC 322

Query: 2167 RRIN 2178
RR+N
Sbjct: 323 RRVN 326

Score = 200 bits (509), Expect = 7e-49
Identities = 111/165 (67%), Positives = 116/165 (70%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNA PNRNSARGFEVID IKSAREKVCPGVVSCADILAI
Sbjct: 76 VNGCDGSILLDDTSSFTGEKNAGPNRNSARGFEVIDQIKSAVEKVCPGVVSCADILAI 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I L GPTW+VKLG
Sbjct: 136 RDSVEI-----LRGPTWDVKLG 152

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+RTASQSAANNIP PTSNLNLISRF+ LGLSTKDLVALSG
Sbjct: 153 RRDSRTASQSAANNIPRPTSNLNLISRFNTLGLSTKDLVALSG 197

Score = 100 bits (248), Expect = 1e-18
Identities = 53/77 (68%), Positives = 57/77 (74%), Gaps = 6/77 (7%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS-----ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKET 732
MAS CS I LAL VL+ G+ AN L TNFYY SCP LF +VK TV+SAISKET
Sbjct: 1 MASSCSSSMITLALLVLVLGTNTSSANANPTLHTNFYSSCPKLFDTVKRTVESAIKET 60

Query: 733 RMGASLLRLFFHDCFVN 783
RMGASLLRLFFHDCFVN
Sbjct: 61 RMGASLLRLFFHDCFVN 77

>gb|ACM47317.1| peroxidase [Capsicum annuum]
Length = 324

Score = 205 bits (521), Expect = 3e-50
Identities = 100/125 (80%), Positives = 108/125 (86%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT+FRARIYNETN I+++FA TRQ++CPR SGSGDNNLAPLDLQTPT FDN YFKNL
Sbjct: 200 QARCTSFARIYNETNNIDSSFATTRQRNCPRNSGSGDNNLAPLDLQTPTKFDNNYFKNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V K+GLLHSDQQLFNGGS DSIV YS NP +FSSDF AMIKMGD PLTGSNGEIRKN
Sbjct: 260 VSKRGLLHSDQQLFNGGSADSIVTSYSNNPSSFSSDFVTAMIKMGDNRP L TGSNGEIRKN 319

Query: 2164 CRRIN 2178
CR N
Sbjct: 320 CRTRN 324

Score = 184 bits (468), Expect = 4e-44
Identities = 104/169 (61%), Positives = 109/169 (64%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEK A PN NS RGFEVIDNIKSAVEK CPGVVSCADILAI A
Sbjct: 73 VNGCDGSLLDDTSSFTGEKRAAPNVNSVRGFEVIDNIKSAVEKACPGVVSCADILAITA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP WNVKLG
Sbjct: 133 RDSVVI-----LGGPNWNVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ AAN+ IP PTSNLNQLIS FSA+GLST D+VALSG I
Sbjct: 150 RRDARTASQGAANSSIPPTSNLNQLISSFSAVGLSTTDMVALSGAHTI 198

Score = 89.4 bits (220), Expect = 2e-15
Identities = 44/60 (73%), Positives = 51/60 (85%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
L + L+ S++AQLSTNFY SCP LF +VKSTVQSAI++ETRMGASLLRLFFHDCFVN
Sbjct: 15 LVVVNLLIVSSSAQLSTNFYSKSCPFLFQTVKSTVQSAINRETRMGASLLRLFFHDCFVN 74

>ref|XP_002328991.1| predicted protein [Populus trichocarpa]
gb|EEE77576.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 204 bits (520), Expect = 4e-50
Identities = 96/124 (77%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNET I+++ A+TR+ +CPRTSGSGDNNLAPLDLQTPT F+N Y+KNL+
Sbjct: 199 QARCTNFRARIYNETTIDSSLAQTRRSNCPRTSGSGDNNLAPLDLQTPTRFENNYKNLI 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQQLFNGGSTDSIV YS+N TF SDF A MIKMGDI PLTGS GEIR NC
Sbjct: 259 NRRGLLHSDQQLFNGGSTDSIVSTYSSNENTFRSDFVAGMIKMGDIRPLTGSRGEIRNNC 318

Query: 2167 RRIN 2178
RRIN
Sbjct: 319 RRIN 322

Score = 194 bits (493), Expect = 5e-47
Identities = 107/169 (63%), Positives = 116/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNA PN+NSARGFEVIDNIKSAVEK CPGVVSCADILAIAA
Sbjct: 72 VNGCDGSLLDDTSSFTGEKNAAPKNNSARGFEVIDNIKSAVEKACPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP W+VKLG
Sbjct: 132 RDSTVI-----LGGPEWDVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF+ALGLST+D+VALSG+ I
Sbjct: 149 RRDARTASQAAANNSIPRPTSNLNLISRFNALGLSTRDMVALSGSHTI 197

Score = 87.8 bits (216), Expect = 6e-15
Identities = 43/70 (61%), Positives = 52/70 (74%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
+SF + L +L GS+NAQLS +FY SCP+L S+VK VQSAI+KE RMGAS+L
Sbjct: 4 SSFSKAIVTLAILVMSMGSSNAQLSIDFYKSCPHLLSTVKPVVQSAINKEARMGASIL 63

Query: 754 RLFFHDCFVN 783
RLFFHDCFVN
Sbjct: 64 RLFFHDCFVN 73

>ref|XP_002269918.1| PREDICTED: hypothetical protein [Vitis vinifera]
sp|A7NY33.1|PER4_VITVI RecName: Full=Peroxidase 4; Flags: Precursor
emb|CBI15844.1| unnamed protein product [Vitis vinifera]
Length = 321

Score = 204 bits (520), Expect = 4e-50
Identities = 94/124 (75%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FRARIYNETNI+++FA+TRQ SCP SGSGDNNLAPLDLQTPT+FDNYY+KNL+
Sbjct: 198 QARCTSFARIYNETNIDSSFAKTRQASCPSASGSGDNNLAPLDLQTPTTFDNYYYKNLI 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L+NGGSTDS V+ Y NP TF+SDF A MIKMGGDI+PLTGS GEIRK+C
Sbjct: 258 NQKGLLHSDQVLYNGGSTDSTVKTYVNNPKTFTSDFVAGMIKMGDITPLTGSEGEIRKSC 317

Query: 2167 RRIN 2178
++N
Sbjct: 318 GKVN 321

Score = 165 bits (417), Expect = 3e-38
Identities = 92/169 (54%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD S+LLDDTSSFTGE+ A PN+NS RG VIDNIKS VE VCPGVVSCADI+AIAA
Sbjct: 71 VNGCDASVLLDDTSSFTGEQTAVPNKNSIRGLNVIDNIKSQVESVCPGVVSCADIIAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG
Sbjct: 131 RDSVVI-----LGGPDWDVKLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD++TAS S ANN IP PTS+L+ LIS+F A GLST+D+VALSG I
Sbjct: 148 RRDSKTASLSGANNIPPTSSLSNLISKFQAQGLSTRDMVALSGAHTI 196

Score = 90.5 bits (223), Expect = 1e-15
Identities = 44/70 (62%), Positives = 54/70 (77%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLL 753
+S S + + L + L GS++AQLSTNFY +CP +F +VKS VQSA+SKE RMGASLL
Sbjct: 3 SSSFSIVVVALGVLALFAGSSSAQLSTNFYSKTCPKVFDTVKSGVQSAVSKERRMGASLL 62

Query: 754 RLFFHDCFVN 783
RLFFHDCFVN
Sbjct: 63 RLFFHDCFVN 72

>emb|CAD67479.1| peroxidase [Asparagus officinalis]
Length = 320

Score = 203 bits (516), Expect = 1e-49
Identities = 95/124 (76%), Positives = 109/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA +YN+T+I+ FA+TRQ +CP TSGSGDNNLAPLDLQTP +FDN YFKNLV
Sbjct: 197 QARCTNFRAHVYNDTIDATFAKTRQSNCPSTSGSGDNNLAPLDLQTPVAFDNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQ+F+GGST+S V YST+P T+SSDF AAMIKMGDISPLTG +GEIRKNC
Sbjct: 257 SKKGLLHSDQQVFSGGSTNSQVSTYSTSPSTWSSDFVAAAMIKMGDISPLTGKSGEIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKTN 320

Score = 169 bits (427), Expect = 2e-39
Identities = 92/169 (54%), Positives = 107/169 (63%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDTSSFTGEKNA PN+ S RGF+VID IK+AVE+ CPGVVSCADILA+ A
Sbjct: 70 VNGCDGSLLDDTSSFTGEKNAIPNKGSVRGFDVIDKIKTAVEQACPGVVSCADILAVTA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV ++ G PTWNVKLG
Sbjct: 130 RDSVLLGG-----PTWNVKLG 146

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTASQS ANN IP PTS+L+ LIS+FSA GLS K++VAL G I
Sbjct: 147 RRDSRTASQSGANNIPPTSSLSNLISKFSAQGLSAKEMVALVGAHTI 195

Score = 80.1 bits (196), Expect = 1e-12
Identities = 42/73 (57%), Positives = 52/73 (71%)
Frame = +1

Query: 565 LTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGA 744
+ +SF S I L + + +++AQL+ NFY SCP LF ++KS VQSAIS E RMGA
Sbjct: 1 MASSSFKSLAPISLVSYPV--RASSAQLTPNFYSSSCPTLFPTIKSVVQSAISSEKRMGA 58

Query: 745 SLLRLFFHDCFVN 783
SLLRLFFHDCFVN
Sbjct: 59 SLLRLFFHDCFVN 71

>ref|NP_196153.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9FLC0.1|PER52_ATH RecName: Full=Peroxidase 52; Short=Atperox P52; AltName: Full=ATP49;
Flags: Precursor
dbj|BAB09977.1| peroxidase [Arabidopsis thaliana]
gb|AAL38746.1| putative peroxidase [Arabidopsis thaliana]
Length = 324

Score = 202 bits (513), Expect = 2e-49
Identities = 97/124 (78%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFRARIYNETNI AFA TRQ++CPR SGSGD NLAPLD+ T SFDN YFKNL+
Sbjct: 201 QSRCTNFRARIYNETNINAAFATTRQRTCPRASGSGDGNLAPLDVTTAASFDNYYFKNLM 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNGGSTDSIVRGYS NP +F+SDF AAMIKMGDISPLTGS+GEIRK C
Sbjct: 261 TQRGLLHSDQQLFNGGSTDSIVRGYSNPNSSFNSDFTAAMIKMGDISPLTGSNGEIRKVC 320

Query: 2167 RRIN 2178
R N
Sbjct: 321 GRTN 324

Score = 187 bits (476), Expect = 5e-45
Identities = 104/169 (61%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGE+NA PNRNSARGF VIDNIKSAVEK CPGVVSCADILAI
Sbjct: 74 VNGCDGSILLDDTSSFTGEQNAAPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAI 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 134 RDSV-----VALGGPNWNVKVG 150

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AA+ IPAPTS+L+QLIS FSA+GLST+D+VALSG I
Sbjct: 151 RRDARTASQAANSNIPAPTSLSQLISSFSAVGLSTRDMVALSGAHTI 199

Score = 78.2 bits (191), Expect = 5e-12
Identities = 38/66 (57%), Positives = 50/66 (75%), Gaps = 4/66 (6%)
Frame = +1

Query: 598 ICLALFVLIWGSAN----AQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
+ L + +L+ G N AQL+TNFY SCPNL S+V++ V+SA++ E RMGAS+LRLFF
Sbjct: 10 LVLVVTLLLQGDNNYVVEAQLTTFYSTSCP NLSTVQTAVKSAVNSEARMGASILRLFF 69

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 70 HDCFVN 75

>dbj|BAF27413.2| Os11g0112400 [Oryza sativa Japonica Group]
Length = 136

Score = 201 bits (510), Expect = 5e-49
Identities = 93/124 (75%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA +RQ CPR+SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 13 QARCTNFRAHIYNETNIDSGFAMSRQSGCPRSSGSGDNNLAPLDLQTPTVFENNYKLV 72

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 73 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 132

Query: 2167 RRIN 2178
RRIN
Sbjct: 133 RRIN 136

>ref|NP_001065568.1| Os11g0112400 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69372.1| TPA: class III peroxidase 130 precursor [Oryza sativa (japonica
cultivar-group)]
gb|ABA91159.1| Peroxidase 52 precursor, putative, expressed [Oryza sativa (japonica
cultivar-group)]
gb|EAZ00524.1| hypothetical protein OsI_22542 [Oryza sativa Indica Group]
gb|EAZ17186.1| hypothetical protein OsJ_32693 [Oryza sativa Japonica Group]
dbj|BAH01350.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 324

Score = 201 bits (510), Expect = 5e-49
Identities = 93/124 (75%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA +RQ CPR+SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 201 QARCTNFRAHIYNETNIDSGFAMSRQSGCPRSSGSGDNNLAPLDLQTPTVFENNYKNLV 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 261 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 320

Query: 2167 RRIN 2178
RRIN
Sbjct: 321 RRIN 324

Score = 166 bits (419), Expect = 2e-38
Identities = 94/169 (55%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID IKSAVE +CPGVVSCADILAI AA
Sbjct: 74 VQGCDASLLDDTASFTGEKMANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAI AA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 134 RDSVAI-----LGGPSWDVKVG 150

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG+ I
Sbjct: 151 RRDRTASLSGANNIPPTSGLANLTSFAAQGLSQKDMVALSGSHTI 199

Score = 75.5 bits (184), Expect = 3e-11
Identities = 35/75 (46%), Positives = 56/75 (74%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETR 735
+++ T ++ CS L + + + + + G ++AQLS +FY +SCP +F +VK +QSAI+ E R
Sbjct: 1 MAQPTSSARCS-LVVMVVVLAVAGGSSAQLSPSFYSYSCPGVFDVAVKCGMQSAIANEKR 59

Query: 736 MGASLLRLFFHDCFV 780
+GAS++RLFFHDCFV
Sbjct: 60 IGASIVRLFFHDCFV 74

>gb|EAY79693.1| hypothetical protein OsI_34840 [Oryza sativa Indica Group]
Length = 329

Score = 199 bits (507), Expect = 1e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA RQ CPR SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 206 QARCTNFRAHIYNETNIDSGFAMRRQSGCPRNSGSGDNNLAPLDLQTPTVFENNYKLV 265

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 266 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 325

Query: 2167 RRIN 2178
RRIN
Sbjct: 326 RRIN 329

Score = 166 bits (421), Expect = 1e-38
Identities = 94/169 (55%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID IKSVE +CPGVVSCADILAIAA
Sbjct: 79 VQGCDASLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 139 RDSVAI-----LGGPSWDVKVG 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG+ I
Sbjct: 156 RRDSRTASLSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGSHTI 204

Score = 70.1 bits (170), Expect = 1e-09
Identities = 31/61 (50%), Positives = 47/61 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCF 777
+ + + + + G + AQLS +FY SCP +F++VK +QSAI++E R+GAS++RLFFHDCF
Sbjct: 19 VVVVVVLAVAGGSWAQLSPSFYSFSCPGVFNAVKRGMQSAIAREKRIGASIVRLFFHDCF 78

Query: 778 V 780
V
Sbjct: 79 V 79

>ref|NP_001065971.1| Os12g0112000 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69377.1| TPA: class III peroxidase 135 precursor [Oryza sativa (japonica
cultivar-group)]
gb|ABA96259.1| Peroxidase 52 precursor, putative, expressed [Oryza sativa (japonica
cultivar-group)]
dbj|BAF28990.1| Os12g0112000 [Oryza sativa Japonica Group]
gb|EAZ19424.1| hypothetical protein OsJ_34981 [Oryza sativa Japonica Group]
dbj|BAG91443.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 327

Score = 199 bits (507), Expect = 1e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA RQ CPR SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 204 QARCTNFRAHIYNETNIDSGFAMRRQSGCPRNSGSGDNNLAPLDLQTPTVFENNYKLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 264 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 323

Query: 2167 RRIN 2178
RRIN
Sbjct: 324 RRIN 327

Score = 164 bits (415), Expect = 5e-38
Identities = 93/169 (55%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID I KSAVE +CPGVVSCADILAI AA
Sbjct: 77 VQGCDASLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVE TICPGVVSCADILAI AA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 137 RDSVAI-----LGGPSWDVKVG 153

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A LS KD+VALSG+ I
Sbjct: 154 RRDSRTASLSGANNIPPTSGLANLTSLFAAQALSQKDMVALSGSHTI 202

Score = 72.8 bits (177), Expect = 2e-10
Identities = 32/63 (50%), Positives = 49/63 (77%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L + + + + G + AQLS +FY +SCP +F++VK +QSAI++E R+GAS++RLFFHD
Sbjct: 15 LVVMVVVLAVAGGSWAQLSPSFYSYSCPGVFNAVKRGMQSAIAREKRIGASIVRLFFHD 74

Query: 772 CFV 780
CFV
Sbjct: 75 CFV 77

>ref|XP_002450132.1| hypothetical protein SORBIDRAFT_05g001000 [Sorghum bicolor]
gb|EES09120.1| hypothetical protein SORBIDRAFT_05g001000 [Sorghum bicolor]
Length = 331

Score = 199 bits (505), Expect = 2e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRA +YN+TNI+ FARTRQ CPRTSGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 208 QARCTNFRAHVYNDTNIDGTFARTRQSGCPRTSGSGDNNLAPLDLQTPTVFENNYFKNLV 267

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD+ V+ Y ++ TF SDF MIKMGDI+PLTGSNG+IRKNC
Sbjct: 268 CKKGLLHSDQELFNGGATDAQVQSYISSQSTFFSDFVTGMIKMGDITPLTGSNGQIRKNC 327

Query: 2167 RRIN 2178
R IN
Sbjct: 328 RMIN 331

Score = 160 bits (404), Expect = 1e-36
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDT+SF GEK A PN S RGFVID +KSAVEKVCPGVVSCADILAIAA
Sbjct: 81 VQGCASLLDDTASFQGEKMATPNNGSVRGFEVIDAVKSAVEKVCPGVVSCADILAIAA 140

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 141 RDSVVI-----LGGPSWDVKVG 157

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 158 RRDSTTASFSGANNNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 206

Score = 82.8 bits (203), Expect = 2e-13
Identities = 39/74 (52%), Positives = 55/74 (74%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRM 738
+K + + S L + L L ++ G+++AQLST+FY SCP ++ SVKS +QSAI+ E RM
Sbjct: 8 TKSSSSCASGLALLLLVLMAGTSSAQLSTSFYSSSCPGVYDSVKSAIQSAIATEQRM 67

Query: 739 GASLLRLFFHDCFV 780
GAS++RLFFHDCFV
Sbjct: 68 GASIVRLFFHDCFV 81

>gb|ACT35473.1| peroxidase 52 [Brassica rapa]
Length = 306

Score = 197 bits (500), Expect = 7e-48
Identities = 93/124 (75%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFR R+YNETNI AFA RQ+SCPR +GSGD NLAPLD+ + +FDN YFKNLV
Sbjct: 183 QSRCTNFRTRVYNETNINAAAFATLRQRSCPRAGSGDGNLAPLDVNSANTFDNSYFKNLV 242

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGSTDSIV GYS NP +FSSDF AAMIKMGDISPLTGS+GEIRK C
Sbjct: 243 AQRGLLHSDQQLFNGGSTDSIVTGYSNNPSSFSSDFTAAMIKMGDISPLTGSSGEIRKVC 302

Query: 2167 RRIN 2178
R N

Sbjct: 303 GRTN 306

Score = 189 bits (481), Expect = 1e-45
Identities = 104/169 (61%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGE+NANPNRNSARGF VIDNIK+AVE CPGVVSCADILAIAA
Sbjct: 56 VNGCDGSILLDDTSSFTGEQNANPNRNSARGFNVIDNIKTAVEAACPGVVSCADILAIAA 115

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 116 RDSVVL-----LGGPNWNVKVG 132

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IPAPTS+L+QLIS FSA+GLST+D+VALSG I
Sbjct: 133 RRDARTASQAAANNIPAPTSSLSQLISSFSAVGLSTRDMVALSGAHTI 181

Score = 75.9 bits (185), Expect = 3e-11
Identities = 34/48 (70%), Positives = 41/48 (85%)
Frame = +1

Query: 640 AQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
AQL+TNFY SCPNL S+V+STV+SA+ + R GAS+LRLFFHDCFVN
Sbjct: 10 AQLTTFYSTSCP NLSTVRSTVKS AVDSQPRTGASILRLFFHDCFVN 57

>ref|XP_002441703.1| hypothetical protein SORBIDRAFT_08g000990 [Sorghum bicolor]
gb|EES15541.1| hypothetical protein SORBIDRAFT_08g000990 [Sorghum bicolor]
Length = 328

Score = 196 bits (498), Expect = 1e-47
Identities = 92/123 (74%), Positives = 105/123 (85%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFRA IYN+TNI+ +FAR+RQ CPRTSGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 206 ARCTNFRAHIYNDTNIDGSFARSRSVCPRTS GSGDNNLAPLDLQTPTVFENNYK NLVY 265

Query: 1990 KKGLLHSDQQLFN GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKG+LHSDQ+LFN GGSTD+ V+ Y ++ F +DF MIKMGDI PLTGSNGEIRKNCR
Sbjct: 266 KKGILHSDQELFN GGSTDAQVQSYVSSQSAFFADFVTGMIKMGDIMPLTGSNGEIRKNCR 325

Query: 2170 RIN 2178
RIN

Sbjct: 326 RIN 328

Score = 164 bits (415), Expect = 5e-38
Identities = 95/169 (56%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+QGCD S+LLDDT SF GEK ANPN SARGFEVID IKS AV+KVCPCGVVSCADILAI
Sbjct: 78 VQGCDASLLDDTPSFQGEKMANPNNGSARGFEVIDAIKSAVDKVCPCGVVSCADILAI 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 138 RDSVVI-----LGGPSWDVKVG 154

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 155 RRDSRTASFSGANNIPPTSGLVNLTSLFAAQGLSQKDMVALSGAHTI 203

Score = 77.4 bits (189), Expect = 9e-12
Identities = 36/61 (59%), Positives = 50/61 (81%), Gaps = 2/61 (3%)
Frame = +1

Query: 604 LALFVLI--WGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCF 777
L L VL+ G+++AQL T+FY HSCP ++ +V+S +Q+AI+++E RMGAS+LRLFFHDCF
Sbjct: 18 LLLLVLLAGTGTSSAQLCTSFYSHSCPGVYDAVRSVLQAAIAREQRMGASILRFFHDCF 77

Query: 778 V 780
V
Sbjct: 78 V 78

>ref|XP_002450133.1| hypothetical protein SORBIDRAFT_05g001010 [Sorghum bicolor]
gb|EES09121.1| hypothetical protein SORBIDRAFT_05g001010 [Sorghum bicolor]
Length = 328

Score = 196 bits (498), Expect = 1e-47
Identities = 89/124 (71%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYN+T+I +AFA+TRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNL+
Sbjct: 205 QARCTNFRAHIYNDTDINSAFAKTRQSGCPSTSGAGDNNLAPLDLQTPTVFENNYKNLL 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y + TF +DF MIKMGDI+PLTGSNG+IRKNC

Sbjct: 265 SKKGLLHSDQELFNGGATDTLVQSYVGSQSTFFTFVTGMIKMGDITPLTGSNGQIRKNC 324

Query: 2167 RRIN 2178
RR+N

Sbjct: 325 RRVN 328

Score = 159 bits (401), Expect = 2e-36
Identities = 91/169 (53%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDT++F GEK A PN S RGFEVID +KSAVEKVCPGVVSCADILAI
Sbjct: 78 VQGCDASLLDDTATFQGEKMATPNNGSVRGFEVIDAVKSAVEKVCPGVVSCADILAI 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 138 RDSVVI-----LGGPSWDVKVG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 155 RRDSTTASFSGANNIPPTSGLANLTS LFAAQGLSQKDMVALSGAHTI 203

Score = 77.4 bits (189), Expect = 9e-12
Identities = 38/70 (54%), Positives = 52/70 (74%), Gaps = 1/70 (1%)
Frame = +1

Query: 574 ASFC SRLTICLALFVL-IWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
AS S + L L L + G+++AQLST FY +SCP ++ +VKS ++SAI+ E RMGAS+
Sbjct: 9 ASSSSAAALLLLLLALAVAGTSSAQLSTGFYSYSCPGVYGAVKSVMSAIANEKRMGASI 68

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 69 VRLFFHDCFV 78

>gb|ABV24960.2| putative secretory peroxidase [Catharanthus roseus]
Length = 330

Score = 196 bits (498), Expect = 1e-47
Identities = 92/124 (74%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FRARIYNE+NIET+FARTRQ +CP +G+GDN+LAPLDLQ+P FD Y+KNL+
Sbjct: 207 QARCTVFRARIYNESNIETSFARTRQGNCLPTGNGDNSLAPLDLQSPNGFDINYYKNLI 266

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+L+NGGST+S+V YS + F SDFAAAMIKMGDISPLTGSNGE+RKNC
Sbjct: 267 NKKGLLHSDQELYNGGSTNSLVEAYSKDTKAFYSDFAAAMIKMGDISPLTGSNGEVRKNC 326

Query: 2167 RRIN 2178
RR+N
Sbjct: 327 RRVN 330

Score = 164 bits (414), Expect = 7e-38
Identities = 92/169 (54%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLDDTSS GEK A PN S RGF+V+DNIS VEVCPGVVSCADILAI
Sbjct: 80 VQGCDGSILLDDTSSLRGEKTAGPNVGSVRGFDVVDNIKSDVEKVCPGVVSCADILAI 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W VK+G
Sbjct: 140 RDSV-----VALGGPSWKVKVG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S AN+ IP PTSNL LIS F A+GLS KD+V LSG+ I
Sbjct: 157 RRDSKTASLSGANSRIPPPTSNLRLISSFQAVGLSAKDMVVLSGSHTI 205

Score = 72.4 bits (176), Expect = 3e-10
Identities = 37/77 (48%), Positives = 52/77 (67%), Gaps = 3/77 (3%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVL---IWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKE 729
S + +SF S I + + VL + S + QLS+ FY +CP ++++V+ V+SA+SKE
Sbjct: 4 SSSSSSSFSNFGIVIMVIVLSIIMRSCSGQLSSEFYSKTCPQVYNTVRKGVESAVSKE 63

Query: 730 TRMGASLLRLFFHDCFV 780
RMGASLLRL FHDCFV
Sbjct: 64 KRMGASLLRLHFHDCFV 80

>sp|P00434.3|PERP7_BRARA RecName: Full=Peroxidase P7; AltName: Full=TP7
Length = 296

Score = 196 bits (498), Expect = 1e-47
Identities = 93/124 (75%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC NFRAR+YNETNI AFA RQ+SCPR +GSGD NLAPLD+ + TSFDN YFKNL+
Sbjct: 173 QSRCVNFRRVYNETNINAAAFATLRQRCSPRAAGSGDANLAPLDINSATSFDNSYFKNLM 232

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNGGSTDSIVRGYS +P +F+SDFAAAMIKMGGDISPLTGS+GEIRK C
Sbjct: 233 AQRGLLHSDQVLFNGGSTDSIVRGYSNSPSSFNSDFAAAMIKMGGDISPLTGSSGEIRKVC 292

Query: 2167 RRIN 2178
+ N
Sbjct: 293 GKTN 296

Score = 179 bits (455), Expect = 1e-42
Identities = 99/169 (58%), Positives = 114/169 (67%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGE+NA PNRNSARGF VI++IKSAVEK CPGVVSCADILAI AA
Sbjct: 46 VNGCDGSILLDDTSSFTGEQ NAGPNRNSARGFTVINDIKSAVEKACPGVVSCADILAI AA 105

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 106 RDSV-----VQLGGPNWNVKVG 122

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA+TASQ+ AAN+ IPAP+ +L+QLIS FSA+GLST+D+VALSG I
Sbjct: 123 RRDARTASQAAANSNIPAPSM SLSQLISSFSAVGLSTRDMVALSGAHTI 171

Score = 76.6 bits (187), Expect = 1e-11
Identities = 35/47 (74%), Positives = 41/47 (87%)
Frame = +1

Query: 643 QLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
QL+TNFY SCPNL S+VKS V+SA+S + RMGAS+LRLFFHDCFVN
Sbjct: 1 QLTTNFYSTSCP NLLSTVKSGVKS AVSSQPRMGASILRLFFHDCFVN 47

>gb|AAD37423.1|AF149281_1 peroxidase 6 [Phaseolus vulgaris]
Length = 128

Score = 195 bits (495), Expect = 3e-47
Identities = 106/165 (64%), Positives = 116/165 (70%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330

+ GCDGSILLDDTSSFTGEKNA PN+NSARGF+VID IKSAVE+VCPGVVSCADILAI
 Sbjct: 7 VNGCDGSILLDDTSSFTGEKNARPNKNSARGFDVIDKIKSAVEEVCPGVVSCADILAI 66
 Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV I+ GGP+WNVKLG
 Sbjct: 67 RDSVHIL-----GGPSWNVKLG 83
 Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
 RRD+RTASQSAANNGIP PTSN+NQLISRF++LGLS KDLVALSG
 Sbjct: 84 RRDSRTASQSAANNGIPPPTSNVNLISRFSNLGLSPKDLVALSG 128

>ref|XP_002520835.1| Peroxidase 52 precursor, putative [Ricinus communis]
 gb|EEF41544.1| Peroxidase 52 precursor, putative [Ricinus communis]
 Length = 318

Score = 194 bits (494), Expect = 4e-47
 Identities = 109/169 (64%), Positives = 115/169 (68%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
 + GCDGSILLDDTSSFTGE+ A PNRNS RGFEVID+IKSAVEK CPGVVSCADILAI
 Sbjct: 70 VNGCDGSILLDDTSSFTGEQTAVPNRNSVRGFEVIDSIKSAVEKACPCGVVSCADILAI 129
 Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDS I+ GGP+WNVKLG
 Sbjct: 130 RDSTAIL-----GGPSWNVKLG 146
 Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 RRDARTAS SAANNGIPAPTSNLNQLISRFSALGLST+DLVALSG I
 Sbjct: 147 RRDARTASLSAANNGIPAPTSNLNQLISRFSALGLSTRDLVALSGAHTI 195

Score = 193 bits (490), Expect = 1e-46
 Identities = 93/124 (75%), Positives = 105/124 (84%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QARCTNFR RIYN+TNI+++FA+TR+ +CP T G DNNLAPLDLQTPTSFDN YFKNL+
 Sbjct: 197 QARCTNFRTRIYNDTNIDSSFAQTRRSNCPSTGG--DNNLAPLDLQTPTSFDNYYFKNLL 254
 Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
 +KGLLHSDQ+LFN GSTDSIVR YS TF SDF A MIKMGGDISPLTGS GEIRKNC
 Sbjct: 255 VQKGLLHSDQQLFNGGSTDSIVRTYSNGQSTFFSDFVAGMIKMGGDISPLTGSQGEIRKNC 314
 Query: 2167 RRIN 2178
 ++N
 Sbjct: 315 GKV 318

Score = 88.2 bits (217), Expect = 5e-15
Identities = 43/63 (68%), Positives = 50/63 (79%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
TI +L+ +NAQLSTNFY SCPNLFS+VK VQSAI++E RMGASL+RLFFHDC
Sbjct: 9 TIVTLSELLVVSISNAQLSTNFYSKSCPRLFSTVKPVVQSAINQEKRMGASLVRLFFHDC 68

Query: 775 FVN 783
FVN
Sbjct: 69 FVN 71

>ref|XP_002319968.1| predicted protein [Populus trichocarpa]
gb|EEE95891.1| predicted protein [Populus trichocarpa]
Length = 325

Score = 193 bits (491), Expect = 8e-47
Identities = 92/124 (74%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI+++FA TRQ++CP GDN LAPLD+QTPTSFDN Y+KNL+
Sbjct: 202 QARCTSFARIYNETNIDSSFATTRQKNCPFPKPKGDNKLAPLDVQTPTSFDNKYYKNLI 261

Query: 1987 QKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ LFNGGSTDS+VR YS+NP TFSSDF AMIKMGDI PLTGS GEIRK C
Sbjct: 262 SQKGLLHSDQVLFNGGSTDSLVRTYSSNPKTFSSDFVTAMIKMGDIDPLTGSQGEIRKIC 321

Query: 2167 RRIN 2178
+ N
Sbjct: 322 SKRN 325

Score = 160 bits (406), Expect = 6e-37
Identities = 91/170 (53%), Positives = 107/170 (62%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCDGSILL+DTSSFTGE+ A PN NS RGF V+ IKS VEKVCPG+VSCADI+AIAA
Sbjct: 74 VKGCDGSILLEDTSSTFTGEQTAGPNNSVRGFNVVAKIKSQVEKVCPGIVSCADIVAIAA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP WNVKLG
Sbjct: 134 RDSTVI-----LGGPFWNVKLG 150

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS SAAN+G IP PTS L+ LI+RF++ GLS KD+VALSG+ I
Sbjct: 151 RRDSKTASLSAANSVIPPTSTLSNLINRFNSKGLSVKDMVALSGSHTI 200

Score = 86.7 bits (213), Expect = 1e-14
Identities = 44/70 (62%), Positives = 55/70 (78%), Gaps = 1/70 (1%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGS-ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
+SF S + I F++I+ S ++AQLSTNFY SCP +F +VKS VQSA+SKE RMGASL
Sbjct: 5 SSFSSYMAIFTLAFLVIFTSHSSAQLSTNFYKSCPKVFGAVKSVVQSAVSKERRMGASL 64

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 65 VRLFFHDCFV 74

>ref|NP_001151940.1| peroxidase 52 [Zea mays]
gb|ACG45093.1| peroxidase 52 precursor [Zea mays]
Length = 334

Score = 191 bits (486), Expect = 3e-46
Identities = 89/126 (70%), Positives = 106/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG--SGDNNLAPLDLQTPTSFDNYYFKN 1980
QARCTNFRA +YN+TNI+ +FARTRQ CPR+S SGDNNLAPLDLQTPT FDN Y+KN
Sbjct: 209 QARCTNFRAHVYNDTNIDGSFARTRQSGCPRSSSGSSGDNNLAPLDLQTPTVFDNNYYKN 268

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
LV KKGLLHSDQ+LFNGG+TD++V+ Y++ F SDF M+KMGGDI+PLTGS G+IRK
Sbjct: 269 LVCKKGLLHSDQQLFNGGATDALVQSYASGQSEFFSDFVTGMVKMGDITPLTGSQQIRK 328

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 329 NCRRVN 334

Score = 162 bits (409), Expect = 3e-37
Identities = 93/169 (55%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEKVC PGVVSCADILAIAA
Sbjct: 82 VQGCDASLLDDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKVC PGVVSCADILAIAA 141

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G
Sbjct: 142 RDSVVIL-----GGPTWDVKVG 158

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSLGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 159 RRDSTTASFSGANNIPPTSGLANLTSFAAQGLSQKDMVALSGAHTI 207

Score = 79.0 bits (193), Expect = 3e-12
Identities = 36/59 (61%), Positives = 47/59 (79%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPNISSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
LAL + G+++AQLST FY SCP ++ +VKS VQSA++ E RMGAS++RLFFHDCFV
Sbjct: 24 LALLMAAAGTSSAQLSTGFYSSSCPGVYDAVKSVVQSAVASEQRMGASIVRLFFHDCFV 82

>ref|XP_002489046.1| hypothetical protein SORBIDRAFT_0246s002010 [Sorghum bicolor]
gb|EES20431.1| hypothetical protein SORBIDRAFT_0246s002010 [Sorghum bicolor]
Length = 320

Score = 190 bits (483), Expect = 7e-46
Identities = 88/124 (70%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR IYN+TN++ AFARTRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 197 QARCTNFRDHIYNDTNVDGAFARTRQSGCPSTSGTGDNNLAPLDLQTPTVFENDYYKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFNGG+TD++V+ Y ++ F +DF MIKMGDI+PLTGS GEIRKNC
Sbjct: 257 SNMGLLHSDQELFNGGATDALVQSYVSSQSAFFADFVTGMIKMGDITPLTGSAGEIRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 155 bits (392), Expect = 2e-35
Identities = 90/169 (53%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT++F GEK A PN S RGFEVID KSAVE VCPGVVSCADILAIAA
Sbjct: 70 VQGCDASLLDDTATFQGEKMATPNNGSVRGFEVIDAAKSAVENVCPGVVSCADILAIAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 130 RDSVVI-----LGGPSWDVKVG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 147 RRDSTTASFSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 195

Score = 73.9 bits (180), Expect = 1e-10
Identities = 38/70 (54%), Positives = 47/70 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ L + L G++ AQLST FY SCP L+S+VK VQSAI E R+GAS+
Sbjct: 1 MAAQSIALWLLTTTLMALQAGTSAQLSTGFYSSSCPGLYSAVKPVVQSAIDSEKRVGASI 60

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 61 VRLFFHDCFV 70

>ref|XP_002441702.1| hypothetical protein SORBIDRAFT_08g000980 [Sorghum bicolor]
gb|EES15540.1| hypothetical protein SORBIDRAFT_08g000980 [Sorghum bicolor]
Length = 131

Score = 190 bits (483), Expect = 7e-46
Identities = 88/124 (70%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR IYN+TN++ AFARTRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 8 QARCTNFRDHIYNDTNVDGAFARTRQSGCPSTSGTGDNNLAPLDLQTPTVFENDYYKNLV 67

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFNGG+TD++V+ Y ++ F +DF MIKMGDI+PLTGS GEIRKNC
Sbjct: 68 SNMGLLHSDQELFNGGATDALVQSYVSSQSAFFADFVTGMIKMGDITPLTGSAGEIRKNC 127

Query: 2167 RRIN 2178
RRIN
Sbjct: 128 RRIN 131

>gb|AAA96137.1| peroxidase [Stylosanthes humilis]
Length = 136

Score = 190 bits (483), Expect = 7e-46

Identities = 87/124 (70%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FR IYN+T+I+ +FA+ RQ++CPR SG+GD+NLAPLDLQTPT F+N Y+KNL+

Sbjct: 13 QARCTSFGRHIYNDTIDPSFAKLRRQKNCPRQSGTGDSNLAPLDLQTPHFENNYKNLI 72

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS+V+ YS N F+SDF MIKMGD+ PLTGS GEIRKNC

Sbjct: 73 NKKGLLHSDQELFNGGSTDSLVQTYSKNNKAFTSDFVPGMIKMGDLLPLTGSKEIRKNC 132

Query: 2167 RRIN 2178

RR+N

Sbjct: 133 RRMN 136

>gb|AAL93151.1|AF485265_1 class III peroxidase [Gossypium hirsutum]
Length = 320

Score = 189 bits (480), Expect = 2e-45
Identities = 91/124 (73%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
+ARC FR RIYN+T I+T+FA+TR+ SCPRT GSGDNNLAPLDL TP SFD+ YF+NL+

Sbjct: 197 KARCLVFRNRIYNDTIIDTSFAKTRRSSCPRTSGSGDNNLAPLDLATPNSFDSKYFENLL 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS+V+ YS+N F SDF AAMIKMGDI PLTGSNGEIRKNC

Sbjct: 257 NKKGLLHSDQELFNGGSTDSLVKTYSSNVKKFYSDFAAAMIKMGDIKPLTGSNGEIRKNC 316

Query: 2167 RRIN 2178

+ N

Sbjct: 317 GKPN 320

Score = 160 bits (404), Expect = 1e-36
Identities = 92/170 (54%), Positives = 106/170 (62%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGE+ A PN S RGFEV+D IK+ VEKVCPGVVSCADILAIAA

Sbjct: 69 VNGCDGSVLLDDTSSFTGEQTATPNNGSLRGFEVVDEIKAKVEKVCPGVVSCADILAIAA 128

Query: 1331 RDSVQIVSGQTTNKNLTN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP TWNVKLG 1510
RDSV I LGGP W+VKLG

Sbjct: 129 RDSVVI-----LGGPDWDVKLG 145

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S AN+G+ P ++NL+QLIS F A GLSTKD+VALSG I
Sbjct: 146 RRDSKTASFSDANSGVPLPGSANLSQLISLFQAQGLSTKDMVALSGAHTI 195

Score = 76.6 bits (187), Expect = 1e-11
Identities = 34/60 (56%), Positives = 48/60 (80%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+ +++++ + AQLSTNFY SCP + S+V+ V++A+SKE R+GASLLRLFFHDCFVN
Sbjct: 11 VGVWMMMGSGSYAQLSTNFYSKCPKVLSTVELVVETAVSKEQRLGASLLRLFFHDCFVN 70

>emb|CAD67478.1| peroxidase [Asparagus officinalis]
Length = 301

Score = 188 bits (478), Expect = 3e-45
Identities = 87/124 (70%), Positives = 104/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FR IYN+ +I+ +FA RQ+ CPR SGSGD NLAPLDLQTPT+FDN Y+KNL+
Sbjct: 178 QARCTSFRGHIYNDADIDASFASLRQKICPRKSGSGDTNLAPLDLQTPTAFDNYYKNLI 237

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFN G+TDS+V+ YS + G+F+SDF AMIKMGDISPLTGS GEIRK C
Sbjct: 238 NKKGLLHSDQELFNNGATDSLVSYSNSEGSFNSDFVKAMIKMGDISPLTGSKGEIRKIC 297

Query: 2167 RRIN 2178
+IN
Sbjct: 298 SKIN 301

Score = 161 bits (407), Expect = 5e-37
Identities = 90/169 (53%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILL DT++F GE++A PN S RGF+VID IK+AVE CPGVVSCADILA+AA
Sbjct: 51 VNGCDGSILLADTANFRGEQHAGPNNGSVRGFKVIDKIKTAVENACPGVVSCADILAVAA 110

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W VKLG
Sbjct: 111 RDSVVI-----LGGPDWKVKLG 127

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTAS + ANN IP PTS+L+ LIS+F+A GLSTKD+VALSG I
Sbjct: 128 RRDARTASATLANNIPPTSSLSNLISKFAAQLSTKDMVALSGAHTI 176

Score = 82.4 bits (202), Expect = 3e-13
Identities = 37/52 (71%), Positives = 45/52 (86%)
Frame = +1

Query: 628 GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
GS++A LSTNFY SCP +FS++K +QSAI+KE RMGAS+LRLFFHDCFVN
Sbjct: 1 GSSSAHLSTNFYSSSCP KVFSTIKPVLQSAIAKEKRMGASILRLFFHDCFVN 52

>gb|AAR31108.1| peroxidase precursor [Quercus suber]
Length = 330

Score = 188 bits (477), Expect = 3e-45
Identities = 88/125 (70%), Positives = 107/125 (85%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG-SGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR RIY + NI+++FA+TRQ CP+T+G GDN +APLDLQTPT+FDNYY+KNL
Sbjct: 205 QARCTVFRDRIYKDKNIDSSFAKTRQNKCPKTTGLPGDNKIAPLDLQTPTAFDNYYKLN 264

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQQLFNGGSTDS+V+ YS + TF SDF AMIKMGDI PLTGS+GEIRKN
Sbjct: 265 IKEKGLLRSDQQLFNGGSTDSLVKKYSQDTKTFYSDFVNAMIKMGDIQPLTGSSGEIRKN 324

Query: 2164 CRRIN 2178
CR++N
Sbjct: 325 CRKVN 329

Score = 162 bits (409), Expect = 3e-37
Identities = 93/166 (56%), Positives = 103/166 (62%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDT +FTGEK A PN S R FEV+D IKS VEK CPGVVSCADILAIAA
Sbjct: 77 VNGCDGSILLDDTPTFTGEKTARPNNGSIRAFEVVDEIKSKVEKECPGVVSCADILAIAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W+VKLG
Sbjct: 137 RDSVKI-----LGGPKWDVKLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD++TAS SAAN+G IP PTS L LI+RF A GLSTKD+VALSG

Sbjct: 154 RRDSKTASFSAANSVIPPTSTLGNLINRFKAKGLSTKDMVALSG 199

Score = 84.3 bits (207), Expect = 7e-14
Identities = 39/64 (60%), Positives = 51/64 (79%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHD 771
L + LA+ V+ G+++A+LSTNFI SCP +FS+V+S V SA+SK+ R GASLLRL FHD
Sbjct: 15 LIVSLAVLVIFTGNSSAKLSTNFYSKCPKVFSTVQSVVHSAVSKQPRQGASLLRLHFHD 74

Query: 772 CFVN 783
CFVN
Sbjct: 75 CFVN 78

>gb|AAR31106.1| peroxidase precursor [Quercus suber]
Length = 330

Score = 187 bits (474), Expect = 8e-45
Identities = 87/125 (69%), Positives = 108/125 (86%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSTG-SGDNNLAPLDLQTPTSFNYYFKNL 1983
QARCT FR RIY + NI+++FA+TRQ +CP+T+G GDN +APLDLQTPT+FDNYY+KNL
Sbjct: 205 QARCTVFRDRIYKDKNIDSSFAKTRQNTCPKTTGLPGDNKIAPLDLQTPTAFDNYYKKNL 264

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSGEIRKN 2163
+++KGLL SDQQLFNGGSTDS+V+ YS + +F SDF AMIKMGDI PLTGS+GEIRKN
Sbjct: 265 IKQKGLLRSDQQLFNGGSTDSLVKKYSQDTKSFYSDFVNAMIKMGDIQPLTGSSGEIRKN 324

Query: 2164 CRRIN 2178
CR++N
Sbjct: 325 CRKVN 329

Score = 162 bits (410), Expect = 2e-37
Identities = 92/170 (54%), Positives = 105/170 (61%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDT +FTGEK A PN+ S RGFE +D IKS VEK CPGVVSCADILAIAA
Sbjct: 77 VNGCDGSVLLDDTPTFTGEKTAGPNKGSIRGFEFVDEIKSKVEKECPGVVSCADILAIAA 136

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W+VKLG
Sbjct: 137 RDSVKI-----LGGPKWDVKLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS AAN+G IP PTS L+ LI+RF A GLSTKD+VALSG I
Sbjct: 154 RRDSKTASLKAANSVIPPTSTLSNLINRFKAKGLSTKDMVALSGAHTI 203

Score = 87.8 bits (216), Expect = 6e-15
Identities = 41/64 (64%), Positives = 52/64 (81%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L + LA+ V+ G+++A+LSTNFYY SCP +FS+V+S V SAISK+ R GASLLRL FHD
Sbjct: 15 LIVSLAVLVIFSGNSSAKLSTNFYYKSCP KVFSTVQSVVHSAISKQPRQGASLLRLHFHD 74

Query: 772 CFVN 783
CFVN
Sbjct: 75 CFVN 78

>ref|NP_001131000.1| hypothetical protein LOC100192105 [Zea mays]
gb|ACF79421.1| unknown [Zea mays]
gb|ACL53914.1| unknown [Zea mays]
Length = 320

Score = 186 bits (473), Expect = 1e-44
Identities = 89/126 (70%), Positives = 107/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRA IYN+T+I+ AFARTRQ CP TSG+G DNNLAPLDLQTPT F+N Y++NL
Sbjct: 195 QARCTNFRAHIYNDTDIDAAFARTRQSGCPSTSGAGGDNNLAPLDLQTPTVFENNYRNL 254

Query: 1984 VQKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS-NGEIRK 2160
+ KKGLLHSDQ+LFNGG+TD++V+ Y + F +DF A MIKMGDI+PLTGS NG+IRK
Sbjct: 255 LAKKGLLHSDQELFNNGGATDALVQSYVGSQSAFFADFVAGMIKMGDITPLTGSNNGQIRK 314

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 315 NCRRVN 320

Score = 160 bits (406), Expect = 6e-37
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEK+CPGVVSCADILAIAA

Sbjct: 68 VQGCDAALLDDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKLCPGVVSCADILAI 127

Query: 1331 RDSVQIVSGGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G

Sbjct: 128 RDSVVIL-----GGPTWDVKVG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 145 RRDSTTASFGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 193

Score = 81.6 bits (200), Expect = 5e-13
Identities = 37/65 (56%), Positives = 51/65 (78%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
+R L L + + G+++AQLST FY +SCP ++ +VKS +QSAI++E RMGAS+LRLFF

Sbjct: 4 TRAAATLLLLLALAGTSSAQLSTGFYSYSCPGVYGAVKSVMQSAIAREKRMGASILRLFF 63

Query: 766 HDCFV 780
HDCFV

Sbjct: 64 HDCFV 68

>gb|AAD43561.1|AF155124_1 bacterial-induced peroxidase precursor [Gossypium hirsutum]
Length = 316

Score = 185 bits (470), Expect = 2e-44
Identities = 86/123 (69%), Positives = 104/123 (84%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT FR RIYN+TNI+ FA TR+ +CP + GDNNLAPLD+QTPT FDN YF+NLV

Sbjct: 196 ARCTTFRGRIYNDTNIDANFAATRRANCP--ASGGDNNLAPLDIQTPTFRFDNDYFRNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YS NP TFS+DFAAAM+KMG+ISPLTG+ GEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSNNPATFSADFAAAMVKMGNISPLTGTQGEIRRNCR 313

Query: 2170 RIN 2178
+N

Sbjct: 314 VVN 316

Score = 159 bits (403), Expect = 1e-36
Identities = 90/165 (54%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCDGSILLDDT++FTGEKNA PNRNSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 68 VNGCDGSILLDDTATFTGEKNAVPNRNSARGFEVIDTIKTNVEAACSATVSCADILALAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW V LG
Sbjct: 128 RDGVALL-----GGPTWQVPLG 144

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANN IP+P +NL L S F+A GLST+DL ALSG
Sbjct: 145 RRDARTASQSAANNQIPSPFANLATLTSSFAAKGLSTRDLTALSG 189

Score = 76.6 bits (187), Expect = 1e-11
Identities = 35/62 (56%), Positives = 48/62 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCF 777
+ L + +L +ANAQLS NFY SCPNL + V++ + A+++ETR+GAS+LRLFFHDCF
Sbjct: 8 VTLIVMLSCHAANAQLSPNFYASSCPNLQTIVRNAMSRVNRRETRIGASILRLFFHDCF 67

Query: 778 VN 783
VN
Sbjct: 68 VN 69

>gb|ACN33662.1| unknown [Zea mays]
Length = 320

Score = 184 bits (468), Expect = 4e-44
Identities = 88/126 (69%), Positives = 107/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRA IYN+T+I+ AFARTRQ CP TSG+G D+NLAPLDLQTPT F+N Y++NL
Sbjct: 195 QARCTNFRAHIYNDTDIDAAFARTRQSGCPSTSGAGGDSNLAPLDLQTPTVFENNYRNL 254

Query: 1984 VQKKGLLHSDQQLFNCGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS-NGEIRK 2160
+ KKGLLHSDQ+LFNCGG+TD++V+ Y + F +DF A MIKMGDI+PLTGS NG+IRK
Sbjct: 255 LAKKGLLHSDQELFNCGGATDALVQSYVGSQSAFFADFVAGMIKMGDITPLTGSNNGQIRK 314

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 315 NCRRVN 320

Score = 160 bits (406), Expect = 6e-37
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDT SF GEK ANPN S RGFVID +KSAVEK+CPGVVSCADILAI
Sbjct: 68 VQGCASLLDDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKLCPGVVSCADILAI 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G
Sbjct: 128 RDSVVIL-----GGPTWDVKVG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 145 RRDSTTASFSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 193

Score = 81.6 bits (200), Expect = 5e-13
Identities = 37/65 (56%), Positives = 51/65 (78%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPFLSSVKSTVQSAISKETRMGASLLRLFF 765
+R L L + + G+++AQLST FY +SCP ++ +VKS +QSAI++E RMGAS+LRLFF
Sbjct: 4 TRAAATLLLLALAGTSSAQLSTGFYSYSCPGVYGAVKSVMQSAIAREKRMGASILRLFF 63

Query: 766 HDCFV 780
HDCFV
Sbjct: 64 HDCFV 68

>emb|CBI25393.1| unnamed protein product [Vitis vinifera]
Length = 179

Score = 184 bits (466), Expect = 7e-44
Identities = 100/169 (59%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDTSSF GEKNA PN NS RGF+V+D+IKS VE CPGVVSCAD+LAI
Sbjct: 15 VNGCDGSVLLDDTSSFIGEKNAAPNANSVRGFDVDDIKSVETACPGVVSCADVLAIA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGP+WNVNLG
Sbjct: 75 RDSVVIL-----GGPSWNVNLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNLISRF ALGLST+DLVAL+G+ I
Sbjct: 92 RRDARTASQAAANNSIPPPTSNNLNLISRFQALGLSTRDLVALAGSHTI 140

Score = 57.8 bits (138), Expect = 7e-06
Identities = 24/31 (77%), Positives = 29/31 (93%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR 1899
QARCT+FRARIYNETNI+ +FA+TRQ +CPR
Sbjct: 142 QARCTSFARIYNETNIDNSFAKTRQSNCP 172

Score = 38.1 bits (87), Expect = 5.8
Identities = 16/16 (100%), Positives = 16/16 (100%)
Frame = +1

Query: 736 MGASLLRLFFHDCFVN 783
MGASLLRLFFHDCFVN
Sbjct: 1 MGASLLRLFFHDCFVN 16

>gb|ACU23223.1| unknown [Glycine max]
Length = 328

Score = 182 bits (462), Expect = 2e-43
Identities = 86/124 (69%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR RIYN+TNI+ FA RQ+ CPRT+G+GDNNLA LD +TP FDN YFKNL+
Sbjct: 205 KARCTSFDRINQTNIDRTFALARQRRCPRTNGTGDNNLANLDFRTPNHFDNYYFKNLL 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLL+SDQ LFNNGGSTDS+VR YS N F +DF AMI+MGDI PLTGS GEIRKNC
Sbjct: 265 IKRGLLNSDQVLFNNGGSTDSLVRTYSQNNKAFDTDFVKAMIRMGDIKPLTGSQGEIRKNC 324

Query: 2167 RRIN 2178
RR+N
Sbjct: 325 RRVN 328

Score = 152 bits (383), Expect = 3e-34
Identities = 88/166 (53%), Positives = 100/166 (60%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILIAA 1330
+QGCDGSILLDDT +F GEK A N NS RGFEVID IKS VEK+CPGVVSCADIL IA+

Sbjct: 77 VQCGDGSILLDDTPTFQGEKTAAANNNSVRGFEVIDAIKSEVEKICPGVVSCADILDIAS 136

Query: 1331 RDSVQIVSGGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W V+LG

Sbjct: 137 RDSVVL-----LGGPFWKVRLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+RTA+ +AAN G IP PTSNL LI+RF GLS +D+VALSG

Sbjct: 154 RRDSRTANFTAANTGVIPPPTSNTLNLTRFRDQGLSARDMVALSG 199

Score = 87.0 bits (214), Expect = 1e-14
Identities = 39/77 (50%), Positives = 59/77 (76%)
Frame = +1

Query: 550 VCLSKLTMAFSCRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKE 729
+ LS + +SF S + LA+ +L+ G+++A LS NFY +CPN+F++VKS V+SA+ +E

Sbjct: 1 MALSPIRSSSFSSSAIVALAVLLLLTGTSSANLSKNFYSKTCPNVFNTVKS VVKS AVVRE 60

Query: 730 TRMGASLLRLFFHDCFV 780
R+GAS++RLFFHDCFV

Sbjct: 61 PRIGASIVRLFFHDCFV 77

>emb|CAA71491.1| peroxidase [Spinacia oleracea]
Length = 323

Score = 182 bits (462), Expect = 2e-43
Identities = 84/123 (68%), Positives = 102/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFR IYN++NI+ FA TR+ SCPR +G+GD NLAP+D+QTP +FDN Y+KNLV

Sbjct: 201 ARCTNFRDHIYNDNSNIDPNFAATRKASCPRPRTGTGDFNLAPMDIQTPTNTFDNDYYKNLVA 260

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+L+NGGS DS+V+ YSTN F DFAAAMI+MGD+ PLTG+NGEIR NCR

Sbjct: 261 KRGLLHSDQELYNGGSQDSL VKMYSTNQALFFQDFAAAMIRMGDLKPLTGTNGEIRNNCR 320

Query: 2170 RIN 2178
IN

Sbjct: 321 VIN 323

Score = 123 bits (308), Expect = 1e-25
Identities = 74/166 (44%), Positives = 89/166 (53%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+ GCDGS+LLDDT + GEK A PNRN S RGFEVID IKS VE C G VSCADILA+A
Sbjct: 72 VNGCDGSVLLDDTPTSQGEKMAFPNRNNSIRGFEVIDAIKSNVEAACSGTVSCADILALA 131

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD VQ++ G PTWNVKL
Sbjct: 132 ARDGVQLLGG-----PTWNVKL 148

Query: 1508 GRRDARTASQSAANGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
GRRDARTA+ + AN +P + L L F+ L+ +++ ALSG
Sbjct: 149 GRRDARTANMTLANLNLPPGNAPLANLTELFAQQNLNIREMTALSG 194

Score = 66.6 bits (161), Expect = 2e-08
Identities = 32/60 (53%), Positives = 46/60 (76%), Gaps = 1/60 (1%)
Frame = +1

Query: 607 ALFVLIWGSANAQL-STNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
++ +L+ G+++A L +FY SCPN+ V +T++ A+SKE RMGAS+LRLFFHDCFVN
Sbjct: 14 SIILLLAGTSDAWLRKPHFYASSCPNVEQIVFNTMKQAVSKEPRMGASILRLFFHDCFVN 73

>gb|ABK21858.1| unknown [Picea sitchensis]
Length = 326

Score = 180 bits (457), Expect = 7e-43
Identities = 86/124 (69%), Positives = 104/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR RI++E+NI+ +FAR RQ +CP T G D+NLAPLDL TPT+FDN Y+KNL
Sbjct: 205 QARCTNFRNRIHSESNIIDLSFARARQANCPSTGG--DDNLAPLDLLTPTTFDNYYKNLE 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+++GLLHSDQQLFNGGSTD++V Y+T P FS DFA AM+KMG I PLTG+NGEIRKNC
Sbjct: 263 RRRGLLHSDQQLFNGGSTDNLVSFYTTYPIAFSIDFAVAMVKMGIEPLTGNGEIRKNC 322

Query: 2167 RRIN 2178
R+IN
Sbjct: 323 RKIN 326

Score = 153 bits (386), Expect = 1e-34
Identities = 88/169 (52%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTS+F GEK A PN+NS RGFEVID IK+ VE CPGVVSCADI+AIAA
Sbjct: 78 VNGCDGSILLDDTSTFQGEKTAVPNKNSVRGFEVIDAIKTQVEAACPGVVSCADIVAIAA 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LGGPTW V LG
Sbjct: 138 RDAV-----VQLGGPTWLVLLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ +P P SNL+ LIS F + GLS +DLVALSG+ I
Sbjct: 155 RRDSTTASLSAANSNLPPASNLSALISSFQSHGLSIRDLVALSGSHTI 203

Score = 67.8 bits (164), Expect = 7e-09
Identities = 35/65 (53%), Positives = 42/65 (64%)
Frame = +1

Query: 589 RLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFH 768
R +CL+ V + + QL FY SCP+ FS V S V A++KE RMGASLLRL FH
Sbjct: 16 RSLCLLLILVRL-SAVYGQLCPRFYDISCPSAFSIVNSVVTQAVAKEKRMGASLLRLHFH 74

Query: 769 DCFVN 783
DCFVN
Sbjct: 75 DCFVN 79

>emb|CAD67477.1| peroxidase [Asparagus officinalis]
Length = 315

Score = 179 bits (455), Expect = 1e-42
Identities = 82/124 (66%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FR+ IYN+++I+ +FA R+ +CP+ SGSGD NLAPLDLQTPT+FDN Y++NLV
Sbjct: 192 QARCTSFRRSHIYNDSDIDPSFATLRKSNCPKQSGSGDMNLAPLDLQTPTTFDNNYYRNLV 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGL+HSDQ+LFNGGSTDS+V+ YS G F S F MIKMGD+SPL GSNGEIRK C
Sbjct: 252 VKKGLMHSDQELFNGGSTDSLVSYS DGTGKFYS AFVEGMIKMGDV SPLVGSNGEIRKIC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 162 bits (409), Expect = 3e-37

Identities = 92/169 (54%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILL DT F GE++ANPN SARGF+VID IK+AVEK CPGVVSCADILAIAA

Sbjct: 65 VNGCDGSILLADTPHFVGEQHANPNRNSARGFKVIDRIKTAVEKACPGVVSCADILAIAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG

Sbjct: 125 RDSVVI-----LGGPNWDVKLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+RTA+++AANN IP PTS+L L S F+A GLSTKD+VALSG I

Sbjct: 142 RRDSRTANKTAANNEIPPPTSSLANLTSLFAAKGLSTKDMVALSGAHTI 190

Score = 82.8 bits (203), Expect = 2e-13
Identities = 40/64 (62%), Positives = 51/64 (79%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771

L I L+L ++ S+NAQLST FY +SCPN+F+++K +Q AI KE RMGAS+LRLFHD

Sbjct: 6 LAIILSLCIV---SSNAQLSTTFYSNSCPNVFTTIKPVLQHAIEKEKRMGASILRRLFHD 62

Query: 772 CFVN 783

CFVN

Sbjct: 63 CFVN 66

>emb|CAA62597.1| korean-radish isoperoxidase [Raphanus sativus]
Length = 315

Score = 179 bits (455), Expect = 1e-42
Identities = 89/124 (71%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

Q+RCTNFR RIYNETNI AFA RQ+SCPR + PLD+ +PTSFDN YFKNL+

Sbjct: 193 QSRCTNFRTRIYNETNINAAFATLRQKSCPRAAFRR-RKPQPLDINSPTSFDNSYFKNLM 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNP GTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

++GLLHSDQ LFNGGSTDSIVRGYS +P +F+SDFAAAMIKMGDISPLTGS+GEIRK C

Sbjct: 252 AQRGLLHSDQVLFNGGSTDSIVRGYSNSPSSFN SDFAAAMIKMGDISPLTGSSGEIRKVC 311

Query: 2167 RRIN 2178

R N

Sbjct: 312 GRTN 315

Score = 176 bits (445), Expect = 2e-41
Identities = 99/169 (58%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTS FTGE+NA PNRNSARGF VIDNIKSAVEK CPGVVSCADILAI AA
Sbjct: 67 VNGCDGSILLDDTS-FTGEQNAGPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAI AA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 126 RDSV-----VQLGGPNWNVKVG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSA LGLSTKDLVALSGTKHI 1657
RRDA+TASQ+AA N+ IPAP+ +L+QLIS F A+GLST+D+VALSG I
Sbjct: 143 RRDARTASQSAANNSIPAPSM SLSQLISSFRAVGLSTRDMVALSGAHTI 191

Score = 82.8 bits (203), Expect = 2e-13
Identities = 39/66 (59%), Positives = 49/66 (74%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S + I + + L+ AQL+TNFY SCPNL S+VKS V+SA+S + RMGAS+LRLFF
Sbjct: 3 SNIAILVIVITLLLQGGEAQLTTFYSTSCP NLLSTVKSGVKS AVSSQPRMGASILRLFF 62

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 63 HDCFVN 68

>gb|AC090366.1| peroxidase precursor [Triticum aestivum]
Length = 180

Score = 179 bits (454), Expect = 2e-42
Identities = 83/123 (67%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFR IYN+TNI+ FAR+RQ CP +GS DNNLAPLDLQT T F+N+Y+KNLVQ
Sbjct: 58 ARCTNFRDHIYNDTNIDAGFARSRQSGCPHATGSRDNNLAPLDLQTLTVFENHYK NLVQ 117

Query: 1990 KKGLLHSDQQLFN GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+LFNGG+ D++VR Y + F DF MI MGDI+PLTGSNG+IR NCR
Sbjct: 118 KRGLLHSDQELFN GGAADALVREYVGSQS AFFQDFVEGMIMMGDITPLTGSNGQIRMNCR 177

Query: 2170 RIN 2178

RIN
Sbjct: 178 RIN 180

Score = 64.7 bits (156), Expect = 6e-08
Identities = 33/55 (60%), Positives = 38/55 (69%)
Frame = +2

Query: 1493 WNVKLGRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
W VK+GRRD+ TAS + A N IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 1 WEVKMGRRDSTTASFNGAENNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 55

>gb|ACN34270.1| unknown [Zea mays]
Length = 332

Score = 179 bits (453), Expect = 2e-42
Identities = 85/127 (66%), Positives = 103/127 (81%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG---DNNLAPLDLQTPTSFDNYYFK 1977
QARCTNFRA +YN+TNI+ AFAR R+ CP + SG DNNLAPLDLQTPT F+N Y++
Sbjct: 206 QARCTNFRAHVYNDTNIDGAFARARRSVCPAASSGSGGDNNLAPLDLQTPTVFENDYYR 265

Query: 1978 NLVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIR 2157
NLV +KGLLHSDQ+LFNG +TD+ V+ Y ++ F +DF A M+KMGDISPLTGSGEIR
Sbjct: 266 NLVCRKGLLHSDQELFNGAATDAQVQAYVSSQSAFFADVFAGMVKMGDISPLTGSSGEIR 325

Query: 2158 KNCRRIN 2178
KNCRRIN
Sbjct: 326 KNCRRIN 332

Score = 159 bits (401), Expect = 2e-36
Identities = 92/169 (54%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK A PN S RGFEVID IKS AV+K CPGVVSCADILAIAA
Sbjct: 79 VQGCDASLLDDTPSFQGEKMAKPNGSVRGFEVIDAIKSAVDKACPGVVSCADILAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 139 RDSV-----VTLGGPNWDVKLG 155

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 156 RRDSRTASFGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 204

Score = 76.6 bits (187), Expect = 1e-11
Identities = 35/61 (57%), Positives = 47/61 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRRLFHDCF 777
+ LAL +++AQLST FY HSCP + +V+S +Q+AI++E RMGAS+LRLFHDCF
Sbjct: 19 LLLALLAAGTSTSSAQLSTGFYSHSCPGVHDAVRSVLQAAIAREQRMGASILRRLFHDCF 78

Query: 778 V 780
V
Sbjct: 79 V 79

>gb|ACU24215.1| unknown [Glycine max]
Length = 329

Score = 178 bits (451), Expect = 4e-42
Identities = 85/124 (68%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR RIYN+TNI+ FA RQ+ CPRT+G+GDNNLA LD +TP FDN YFKNL
Sbjct: 206 KARCTSFDRDIYNQTNIDRTFALARQRRCPRTNGTGDNNLANLDFRTPNHFDNYYFKNLF 265

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLL+ DQ LFNGGSTDS+VR YS N F DF AMI+MGDI PLTGS GEIRKNC
Sbjct: 266 IKRGLLNFDQVLFNGGSTDSLVRTYSQNNKAFDFDFVKAMIRMGDIKPLTGSQGEIRKNC 325

Query: 2167 RRIN 2178
RR+N
Sbjct: 326 RRVN 329

Score = 152 bits (383), Expect = 3e-34
Identities = 86/166 (51%), Positives = 102/166 (61%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCDGSILLDDT +F GEK A N NS RG+E+ID+IKS VEK+CPGVVSCADIL IA+
Sbjct: 78 VQGCDGSILLDDTPTFQGEKTAANNNSVRGYELIDDIKSKVEKICPGVVSCADILDIAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNV+LG
Sbjct: 138 RDSVVL-----LGGPFWNVRLG 154

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+R+A+ +AAN G IP PTSNL LI+RF GLS +D+VALSG
Sbjct: 155 RRDSRSANFTAANTGVIPPTSNLTNLITRFQDQGLSARDMVALSG 200

Score = 80.1 bits (196), Expect = 1e-12
Identities = 39/78 (50%), Positives = 59/78 (75%), Gaps = 1/78 (1%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTIC-LALFVLIWGSANAQLSTNFYVHSCPNIFFSSVKSTVQSAISK 726
+ LS + ++F S I LA+ +L+ +++A LS NFY +CPN+F++VKS V+SA++K
Sbjct: 1 MALSPIRSSTFSSSSAIVTLAVLLLLTRTSSATLSKNFYSKTCPNVFNTVKS VVKS AVAK 60

Query: 727 ETRMGASLLRLFFHDCFV 780
E R+GAS++RLFFHDCFV
Sbjct: 61 EPRIGASIVRLFFHDCFV 78

>gb|AAB48184.1| peroxidase precursor [Linum usitatissimum]
Length = 323

Score = 178 bits (451), Expect = 4e-42
Identities = 83/123 (67%), Positives = 100/123 (81%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC +FR RIYNETNI+ +FA +++CP SGD+NLAPLDL+TPTSFDN Y+ NL++
Sbjct: 201 ARCVSFRDRIYNETNIDPSFASQSEENCPLAPNSGDDNLAPLDLKTPTSFDNNYYNNLIE 260

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+KGLLHSDQ LFNGGSTDS+VR YS +P F++DFAAAM+KMGDI PLTGS GEIR C
Sbjct: 261 QKGLLHSDQVLFNGGSTDSLRSYSQSPKRFAADFAAAMVKMGDIKPLTGSQGEIRNVCS 320

Query: 2170 RIN 2178
R N
Sbjct: 321 RPN 323

Score = 143 bits (361), Expect = 1e-31
Identities = 82/170 (48%), Positives = 101/170 (59%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILL+DT SFTGE+ A PN S RG+ VI++IKS VE+VCPGVVSCADI+AIAA
Sbjct: 72 VNGCDGSILLEDTDSFTGEQTAAPNNGSVRGYYVIEDIKSKVEQVCPGVVSCADIVAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I GQ +W VK+G
Sbjct: 132 RDSTVIAGGQ-----SWEVKVG 148

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS +AAN+G+ PAPTS+LN+LI F GLS D+V LSG+ I
Sbjct: 149 RRDSKTASFNAANSGLVPAPTSSLNELIKSFGDQGLSANDMVVLSGSHTI 198

Score = 73.9 bits (180), Expect = 1e-10
Identities = 37/66 (56%), Positives = 45/66 (68%), Gaps = 2/66 (3%)
Frame = +1

Query: 592 LTICLALFVLIWGSANA--QLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
L CL L V + G+ QLST+FY SCP L +V+ V+SA+ KETR+ ASLLRL F
Sbjct: 8 LRSCLVLLVAVCGAGKCWGLSTDFYSESCPMLMDTVRCEVESAVDKETRIAASLLRLHF 67

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 68 HDCFVN 73

>emb|CBI27506.1| unnamed protein product [Vitis vinifera]
Length = 266

Score = 177 bits (450), Expect = 5e-42
Identities = 89/125 (71%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RI+ N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 142 QARCVTFRDRIHDNGTNIDAGFASTRRRRC PVDNGNGDDNLAPLDLVT P NSFDNYYFKNL 201

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS + TFSSDFAAAM+KM GDI PLTGSNGEIRK
Sbjct: 202 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSRSTFSSDFAAAMVKMGDIDPLTGSNGEIRKL 261

Query: 2164 CRRIN 2178
C IN
Sbjct: 262 CNAIN 266

Score = 138 bits (347), Expect = 4e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+QGCD SILLDD+++ EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
 Sbjct: 15 VQGCDASILLDDSATIQSEKNAPNNNSVRGFEVIDNVKSQVESICPGVVSCADILAVAA 74

 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDS S+ +GGPTW VKLG
 Sbjct: 75 RDS-----SVAVGGPTWTVKLG 91

 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ T+ S A +P+ L++L+S FS+ GL+T+++VALSG+ I
 Sbjct: 92 RRDSTTSGLSQAAANLPSFRDGLDKLVSLFSSKGLNTREMAVALSGSHTI 140

>ref|XP_002274550.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length = 320

Score = 177 bits (450), Expect = 5e-42
 Identities = 89/125 (71%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
 Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
 QARC FR RI+ N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
 Sbjct: 196 QARCVTFRDRIHDNGTNIDAGFASTRRRRCVPDNGNGDDNLAPLDLVTNSFDNYYFKNL 255

 Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
 +Q+KGLL SDQ LFNGGSTDSIV YS + TFSSDFAAAM+KMGGI PLTGSNGEIRK
 Sbjct: 256 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSRSTFSSDFAAAMVKGMDIDPLTGSNGEIRKL 315

 Query: 2164 CRRIN 2178
 C IN
 Sbjct: 316 CNAIN 320

Score = 138 bits (347), Expect = 4e-30
 Identities = 77/169 (45%), Positives = 99/169 (58%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
 +QGCD SILLDD+++ EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
 Sbjct: 69 VQGCDASILLDDSATIQSEKNAPNNNSVRGFEVIDNVKSQVESICPGVVSCADILAVAA 128

 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDS S+ +GGPTW VKLG
 Sbjct: 129 RDS-----SVAVGGPTWTVKLG 145

 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ T+ S A +P+ L++L+S FS+ GL+T+++VALSG+ I
 Sbjct: 146 RRDSTTSGLSQAAANLPSFRDGLDKLVSLFSSKGLNTREMAVALSGSHTI 194

Score = 62.0 bits (149), Expect = 4e-07
Identities = 25/47 (53%), Positives = 38/47 (80%)
Frame = +1

Query: 640 AQLSTNFYHHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
AQLS+ FY ++CP S++++ +++A+S+E RM ASL+RL FHDCFV
Sbjct: 23 AQLSSKFYDNTCPKALSTIRTAIRTAVSRRERMAASLIRLHFHDCFV 69

>gb|ACN42168.1| peroxidase 1 [Sesuvium portulacastrum]
Length = 318

Score = 177 bits (449), Expect = 6e-42
Identities = 83/124 (66%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYN+++I +FA++ + +CP +G+GDNNLAPLD QTP FD+ YF+ LV
Sbjct: 195 QARCTNFRAHIYNDSDINASFASLKANCPPKNGTGDNNLAPLDPQTPNKFHDHIYFQGLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNP GTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KK LHSDQ+L NG ST S ++ YSTNP FSSDF +MIKMGDI PLTGSNGEIRKNC
Sbjct: 255 NKKAPLHSDQELTNGASTSSWIQKYSTNP SLFSSDFGTSMIKMGDIKPLTGSNGEIRKNC 314

Query: 2167 RRIN 2178
RRIN
Sbjct: 315 RRIN 318

Score = 157 bits (398), Expect = 5e-36
Identities = 89/165 (53%), Positives = 105/165 (63%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS LLDDTSSF GEK+A+PN SARGFEVID IK+AVE+VCPGVVSCADILA+ A
Sbjct: 68 VNGCDGSNLLDDTSSFKGEKSASP NFQSARGFEVIDQIKAAVERVCPGVVSCADILAVTA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW+VKLG
Sbjct: 128 RDSV-----VGLGGPTWDVKLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RRDARTA+Q+AA N+ IP +S+L++LIS F GL+ KDLVAL G
Sbjct: 145 RRDARTANQAAANSSIPPASSSLRLISSFQNNQGLTIKDLVALYG 189

Score = 86.3 bits (212), Expect = 2e-14
Identities = 46/68 (67%), Positives = 55/68 (80%), Gaps = 2/68 (2%)
Frame = +1

Query: 586 SRLTICLAL-FVLIW-GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRL 759
+RLT LAL FV+++ GS++AQL+TNFY SCP+LF V+ VQSAI KE RMGASLLRL
Sbjct: 2 ARLTCFLALAFVIVFVGSSSAQLTTNFYEKSCPHLFPVVRDVVQSAIRKEARMGASLLRL 61

Query: 760 FFHDCFVN 783
FHDCFVN
Sbjct: 62 HFHDCFVN 69

>ref|XP_002269058.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 319

Score = 177 bits (448), Expect = 8e-42
Identities = 88/125 (70%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP TSG GD+N+A LDL TP SFDN YFKNL
Sbjct: 195 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPATSGDGDNNIAALDLVTPNSFDNYYFKNL 254

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV GYS +P TFSSDFA+AM+KMG+I PLTGS GEIRK
Sbjct: 255 IQKKGLLQSDQVLFSGGSTDSIVTGYSKSPSTFSSDFASAMVKMGNIEPLTGSAGEIRKL 314

Query: 2164 CRRIN 2178
C IN
Sbjct: 315 CSAIN 319

Score = 127 bits (318), Expect = 9e-27
Identities = 73/169 (43%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILL+D+SS EKNA N NS RG++VID++KS VE +CPG+VSCADILA+AA
Sbjct: 68 VQGCDASILLNDSSSIQSEKNAPNNLSVRGYDVIDDVKEVESICPGIVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VSG PTW V LG
Sbjct: 128 RDASVAVSG-----PTWTVNLG 144

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P + L++LIS F + GLS +D+VALSG+ I

Sbjct: 145 RRDSTTSGLSQAATNLPNFSGLDRLISLFGSKGLSERDMVALSGSHTI 193

Score = 63.9 bits (154), Expect = 1e-07
Identities = 28/57 (49%), Positives = 42/57 (73%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
LF+ AQLS++FY ++CP S++++ V++A+S+E RM ASL+RL FHDCFV
Sbjct: 12 LFIFSNMPCEAQLSSSFYDNTCPKALSTIRTAVRTAVSRERRMAASLIRLHFHDCFV 68

>emb|CBI27505.1| unnamed protein product [Vitis vinifera]
Length = 302

Score = 177 bits (448), Expect = 8e-42
Identities = 88/125 (70%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP TSG GD+N+A LDL TP SFDN YFKNL
Sbjct: 178 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPATSGDGDNNIAALDLVTPNSFDNYYFKNL 237

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV GYS +P TFSSDFA+AM+KMG+I PLTGS GEIRK
Sbjct: 238 IQKKGLLQSDQVLFSGGSTDSIVTGYSKSPSTFSSDFASAMVKGNIPLTGSAGEIRKL 297

Query: 2164 CRRIN 2178
C IN
Sbjct: 298 CSAIN 302

Score = 127 bits (318), Expect = 9e-27
Identities = 73/169 (43%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+QGCD SILL+D+SS EKNA N NS RG++VID++KS VE +CPG+VSCADILA+AA
Sbjct: 51 VQGCDA SILLNDSSSIQSEKNAPNNLSVRGYDVIDDVKSEVESICPGIVSCADILAVAA 110

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VSG PTW V LG
Sbjct: 111 RDASVAVSG-----PTWTVNLG 127

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P + L++LIS F + GLS +D+VALSG+ I
Sbjct: 128 RRDSTTSGLSQAATNLPNFSGLDRLISLFGSKGLSERDMVALSGSHTI 176

Score = 62.8 bits (151), Expect = 2e-07
Identities = 26/47 (55%), Positives = 39/47 (82%)
Frame = +1

Query: 640 AQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
AQLS++FY ++CP S++++ V++A+S+E RM ASL+RL FHDCFV
Sbjct: 5 AQLSSSFYDNTCPKALSTIRTAVRTAVSRERRMAASLIRLHFHDCFV 51

>emb|CAL25300.1| properoxidase [Picea abies]
Length = 310

Score = 176 bits (447), Expect = 1e-41
Identities = 81/124 (65%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFRA IYNETNI++ ++ + Q CP T+GSGD+NL+PLD TPT+FD Y+ NL
Sbjct: 187 QARCVNFRAHIYNETNIDSTYSTSLQSKCPSTAGSGDSNLSPLDYVTPATAFDKNYYSNLK 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS V Y++N +F SDFAAAM+KMG+I PLTG++G+IRKNC
Sbjct: 247 SKKGLLHSDQELFNGGSTDSQVTTYASNQNSFFSDFAAAMVKMGNIKPLTGTSGQIRKNC 306

Query: 2167 RRIN 2178
R+ N
Sbjct: 307 RKPN 310

Score = 159 bits (401), Expect = 2e-36
Identities = 88/165 (53%), Positives = 103/165 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDD+S+ TGEK ANPN NSARGF+VID IKS VEK C GVVSCADILAI+A
Sbjct: 60 VNGCDGSVLLDDSSITGEKTANPNANSARGFDVIDTIKSNEKACSGVVSCADILAISA 119

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 120 RDSV-----VELGGPSWTVM LG 136

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RRD+ TAS++ ANN IP PTS+L+ LIS F A GLSTK++VALSG
Sbjct: 137 RRDSTTASKNGANNIPPTSSLSNLISLFFQAQGLSTKEMVALSG 181

Score = 69.7 bits (169), Expect = 2e-09
Identities = 32/51 (62%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+AN QLS+ FY SCP S VK+ V+ A++ E RMGASLLRL FHDCFVN
Sbjct: 11 TANGQLSSTFYAQSCPTALSVVKA AVRQAVANEKRMGASLLRLHFHDCFVN 61

>ref|XP_002269145.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 175 bits (444), Expect = 2e-41
Identities = 87/125 (69%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGGTNIDAGFASTRRRRC PADNGNGDDNLAPLDLVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS GEIRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGEIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDA SILLDDSP TIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQT TNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 1e-07
Identities = 32/72 (44%), Positives = 49/72 (68%), Gaps = 1/72 (1%)
Frame = +1

Query: 568 TMAFCSRLTICLA-LFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGA 744
T S S I +A L +L AQLS++FY ++CP+ S++++ +++A+S+E RM A
Sbjct: 9 TWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNTCPSALSTIRTAIRTAIVSRERRMAA 68

Query: 745 SLLRLFFHDCFV 780
SL+RL FHDCFV
Sbjct: 69 SLIRLHFHDCFV 80

>gb|ACJ85500.1| unknown [Medicago truncatula]
Length = 229

Score = 174 bits (441), Expect = 5e-41
Identities = 99/169 (58%), Positives = 106/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEKNA PN+NS RGF+VIDNIK+AVE VCPGVVSCADILAIAA
Sbjct: 72 VNGCDGSILLDDTSNFTGEKNALPNKNSVRGFDVIDNIKTAVENVCPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
DSV I+ G PTWNVKLG
Sbjct: 132 TDSVAILGG-----PTWNVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA TASQS AN IP PTSNLN L S F +GLSTKDLVALSG I
Sbjct: 149 RRDATTASQSDANTAIPRPTSNLNILTSMFKNVGLSTKDLVALSGAHTI 197

Score = 95.1 bits (235), Expect = 4e-17
Identities = 49/68 (72%), Positives = 55/68 (80%), Gaps = 1/68 (1%)
Frame = +1

Query: 583 CSRLTI-CLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRL 759
CSR+T+ L LFVLI GS NAQLSTNFY +CP L S V+ VQSAISKE R+GAS+LRL
Sbjct: 6 CSRITMFSLVLFVLIIGSVNAQLSTNFYSKTCPKLSSIVQRQVQSAISKEARIGASILRL 65

Query: 760 FFHDCFVN 783
FFHDCFVN
Sbjct: 66 FFHDCFVN 73

Score = 43.1 bits (100), Expect = 0.18
Identities = 18/24 (75%), Positives = 21/24 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFART 1878
QA+CT FR RIYNETNI+T+FA T
Sbjct: 199 QAKCTTFRVRIYNETNIDTSFAST 222

>emb|CAN80097.1| hypothetical protein [Vitis vinifera]
Length = 331

Score = 173 bits (438), Expect = 1e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGGTNIDAGFASTRRRRCPADNGNGDDNLAPLDLVTNPSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGXIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDASILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.9 bits (154), Expect = 1e-07

Identities = 32/78 (41%), Positives = 52/78 (66%), Gaps = 8/78 (10%)
Frame = +1

Query: 571 MASFCSRLTICLA-LFVLIWG-----SANAQLSTNFYYHSCPRLFSSVKSTVQSAISK 726
+A+ SR C++ F+L+ G AQLS++FY + CP+ S++++ +++A+S+
Sbjct: 3 LAAGSSRWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNXCPSALSTIRTAIRTAIVSR 62

Query: 727 ETRMGASLLRLFFHDCFV 780
E RM ASL+RL FHDCFV
Sbjct: 63 ERRMAASLIRLHFHDCFV 80

>emb|CBI27503.1| unnamed protein product [Vitis vinifera]
Length = 357

Score = 172 bits (437), Expect = 2e-40
Identities = 85/121 (70%), Positives = 97/121 (80%), Gaps = 1/121 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSFGSDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYGNGTNI DAGFASTRRRRC PADNGNGDDNLAPLDLVT P NSF DN NY FKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KM GDI PL GS GEIRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGEIRKF 326

Query: 2164 C 2166
C
Sbjct: 327 C 327

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDASILLDDSP TI QSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 1e-07
Identities = 32/72 (44%), Positives = 49/72 (68%), Gaps = 1/72 (1%)
Frame = +1

Query: 568 TMAFCSRLTICLA-LFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGA 744
T S S I +A L +L AQLS++FY ++CP+ S++++ +++A+S+E RM A
Sbjct: 9 TWPSCVSHAFILVAGLLILSNMPCEAQLSSSFYDNTCPSALSTIRTAIRTAIVSRERRMAA 68

Query: 745 SLLRLFFHDCFV 780
SL+RL FHDCFV
Sbjct: 69 SLIRLHFHDCFV 80

>emb|CBI27502.1| unnamed protein product [Vitis vinifera]
Length = 266

Score = 172 bits (437), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 142 QARCVTFRDRIYGNGTNIDAGFASTRRRRCPADNGNGDDNLAPLDLVTNPSFDNYYFKNL 201

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 202 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGVIRKF 261

Query: 2164 CRRIN 2178
C IN
Sbjct: 262 CNVIN 266

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 15 VQGCDASILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 75 RDA-----SVAVGGPTWTLKLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 92 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 140

>ref|XP_002269169.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 172 bits (437), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGGTNIDAGFASTRRRRCPADNGGDDNLAPLDLVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGGDI PL GS G IRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGVIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 1e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDA SILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 64.7 bits (156), Expect = 6e-08
Identities = 32/78 (41%), Positives = 53/78 (67%), Gaps = 8/78 (10%)
Frame = +1

Query: 571 MASFCSRLTICLA-LFVLIWG-----SANAQLSTNFYHSCPNLFSSVKSTVQSAISK 726
+A+ SR C++ F+L+ G AQLS++FY ++CP+ S++++ +++A+S+

Sbjct: 3 LAAGSSRWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNACPSALSTIRTAIRTAISR 62

Query: 727 ETRMGASLLRLFFHDCFV 780
E RM ASL+RL FHDCFV

Sbjct: 63 ERRMAASLIRLHFHDCFV 80

>gb|AA013838.1|AF405326_1 peroxidase 2 [Lupinus albus]
Length = 260

Score = 172 bits (437), Expect = 2e-40
Identities = 81/126 (64%), Positives = 102/126 (80%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSQSG--DNNLAPLDLQTPTSFDNYYFKN 1980
+ARC+++R RIY++TNI+ FA++RQ++CPR S DNN+A LD +TPT FDN Y+KN
Sbjct: 135 KARCSSYRDRIYDDTNIDKLFAKSRQRNCPRKSSGTVKDNNVAVLDFKTPTHFDNLYYKN 194

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ KKGLLHSDQ+LFNGGSTDS+V YS N F+SDF AMIKMG+I PLTGSNG+IRK
Sbjct: 195 LINKKGLLHSDQELFNGGSTDSLVTYTSNNEKAFNSDFVTAMIKMGNIKPLTGSNGQIRK 254

Query: 2161 NCRRIN 2178
+CRR N
Sbjct: 255 HCRRAN 260

Score = 155 bits (392), Expect = 2e-35
Identities = 92/170 (54%), Positives = 102/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILLDDTSSF GEK A PN NS RGFEVID IKS VE+ CPGVVSCADI+AIAA
Sbjct: 7 VNGCDGSILLDDTSSFRGEKTAPPNNNSVRGFEVIDAIKSKVEEACPGVVSCADIVAIAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP WNVK+G
Sbjct: 67 RDSTAI-----LGGPYWNVKVG 83

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD++TAS S A++G IP P S L+ LISRF A GLS KD+VALSG I
Sbjct: 84 RRDSKTASFS DASSGVIPPPFSTLSNLISRFQAQGLSIKDMVALSGAHTI 133

>gb|ABA96220.1| Cationic peroxidase 1 precursor, putative, expressed [Oryza sativa
(japonica cultivar-group)]
gb|EAY79691.1| hypothetical protein OsI_34838 [Oryza sativa Indica Group]
gb|EAY19422.1| hypothetical protein OsJ_34979 [Oryza sativa Japonica Group]

Length = 291

Score = 172 bits (437), Expect = 2e-40
Identities = 78/124 (62%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 170 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYAFDNFYKLL 227

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AAM+KMG+I+P+TGS+G+IRKNC
Sbjct: 228 NKKGVLSHSDQQLFNGGSADSQTTTYSNMATFFTFSAAMVKMGNNINPITGSSGQIRKNC 287

Query: 2167 RRIN 2178
R++N
Sbjct: 288 RKNV 291

Score = 146 bits (369), Expect = 1e-32
Identities = 82/170 (48%), Positives = 98/170 (57%)
Frame = +2

Query: 1148 QMQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1327
++ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ +E +CP VVSCADILA+A
Sbjct: 42 RIAGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAHIEGICPQVVSCADILAVA 101

Query: 1328 ARDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
AR+SV + LGGPTW V+L
Sbjct: 102 ARESV-----VALGGPTWVVQL 118

Query: 1508 GRRDARTASQSAANNGIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 119 GRRDSTTASLDTANNDIPAPTFDLGDLTKSFSNKGLSATDMIALSGAHTI 168

>tpe|CAH69378.1| TPA: class III peroxidase 136 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 317

Score = 172 bits (437), Expect = 2e-40
Identities = 78/124 (62%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 196 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYAFDNFYKLL 253

QARC R RIY N TNI+T FA TR++ CP +G+GD+NLAPLD+ TP SFDN YFKNL
Sbjct: 75 QARCVTVRDRIYDNGTNIDTGFSTRRRRCVPDNGNGDDNLAPLDVVTTPNSFDNNYFKNL 134

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSS+FA+AM+KMGGDI PL GS GEIRK

Sbjct: 135 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSEFASAMVKMGDIEPLLGSAGEIRKI 194

Query: 2164 CRRIN 2178

C IN

Sbjct: 195 CNVIN 199

Score = 38.9 bits (89), Expect = 3.4
Identities = 22/42 (52%), Positives = 31/42 (73%)
Frame = +2

Query: 1532 SQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

SQ+AAAN +P+ L++LI FS+ GLST+D+VALSG+ I

Sbjct: 34 SQAAAN--LPSFRDGLDRLIPLFSSKGLSTRDMVALSGSHTI 73

>emb|CAH10839.1| peroxidase [Picea abies]
Length = 317

Score = 172 bits (436), Expect = 2e-40
Identities = 83/124 (66%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FRARIYNE+NI+T+FA + + SCP S GDN L+PLDL TPT+FDN Y+ +L

Sbjct: 196 QARCTTFRARIYNESNIDTSFATSVKSSCP--SAGGDNTLSPLDLATPTTFDNKYITDLG 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

+KGLLHSDQQLF+GGST+S V YS N TF +DFAAAM+KMG+ISPLTG++G+IRKNC

Sbjct: 254 NRKGLLHSDQQLFSGGSTNSQVTTYSANQNTFFTFDFAAAMVKMGNISPLTGTSGQIRKNC 313

Query: 2167 RRIN 2178

R+ N

Sbjct: 314 RKAN 317

Score = 158 bits (400), Expect = 3e-36
Identities = 91/165 (55%), Positives = 100/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AA 1330

+ GCDGSILLDD S+FTGEK A PN NS RGF+VID IK+ VE C GVVSCADILAI A

Sbjct: 69 VNGCDGSILLDDNSTFTGEKTALPNANSVRGFDVIDTIKTQVEAACSGVWSCADILAIVA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 129 RDSV-----VQLGGPTWTVLLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSAALGLSTKDLVALSG 1645
RRD+ TAS SAANN IP+P SNL+ LIS F+A GLSTKDLVALSG

Sbjct: 146 RRDSTTASLSAANNIPSPASNLSALISSFTAHLSTKDLVALSG 190

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/64 (48%), Positives = 41/64 (64%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
+ +C+ I +A+ QL++ FY CP S VK+ V A++ E RMGASLLRL FHD

Sbjct: 7 IVLCVLCISSINNAHGLTSTFYNKLCPALSIVKAAVNKAVNNEKRMGASLLRLHFHD 66

Query: 772 CFVN 783
CFVN

Sbjct: 67 CFVN 70

>ref|XP_002266365.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 328

Score = 172 bits (435), Expect = 3e-40
Identities = 81/124 (65%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYNE NI+ +F + Q +CP S GDN L+PLD QTPT+FDN Y+ NLV

Sbjct: 207 QARCTTFRTRIYNEANIDASFKTSLQANCP--SSGGDNTLSPLDTQTPTTFDNAYYTNLV 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNGGSTD++V YST TF +DFA AM+KMG++SPLTG++G+IR NC

Sbjct: 265 NKKGLLHSDQQLFNGGSTDAVVNTYSTRSTTFFTDANAMVKMGNSPLTGTSGQIRTNC 324

Query: 2167 RRIN 2178
R+ N

Sbjct: 325 RKTN 328

Score = 147 bits (372), Expect = 5e-33
Identities = 83/169 (49%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RG+EV+D IKS +E CPGVVSCADILA+AA
Sbjct: 80 VNGCDASILLDDTSNFTGEKTAGPNANSVRGYEVVDTIKSQLEASCPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GP+W V+LG
Sbjct: 140 RDSV-----VALRGPSWMVRLG 156

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LIS F+ G + +++VALSG+ I
Sbjct: 157 RRDSTTASLSAANSNIPAPTLNLSGLISAFTNKGFNAREMVALSGSHTI 205

Score = 76.3 bits (186), Expect = 2e-11
Identities = 35/52 (67%), Positives = 40/52 (76%)
Frame = +1

Query: 628 GSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
G A+AQL+TNFY +CPN S +KS V SA+ E RMGASLLRL FHDCFVN
Sbjct: 30 GMSAQLTTFYAKTCPNALSIIKSAVNSAVKSEARMGASLLRLHFHDCFVN 81

>ref|NP_001106040.1| plasma membrane-bound peroxidase 2b precursor [Zea mays]
sp|A5H452.1|PER70_MAIZE RecName: Full=Peroxidase 70; AltName: Full=Plasma membrane-bound
peroxidase 2b; Short=pmPOX2b; Flags: Precursor
gb|ABN48843.1| plasma membrane-bound peroxidase 2b [Zea mays]
Length = 321

Score = 172 bits (435), Expect = 3e-40
Identities = 77/123 (62%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C NFRA IYN+TN+ AFA R+ +CP +G+GD NLAPLD TPT+FDN Y+ NL+
Sbjct: 199 AQCKNFRAHIYNDTNVNAAFATLRRANCPAAAGNGDGNLAPLDTATPTAFDNAYYTNLLA 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQQLFNGG+TD +VR Y++ P FS DFAAAMI+MG+ISPLTG+ G+IR+ C
Sbjct: 259 QRGLLHSDQQLFNGGATDGLVRTYASTPRRFSRDFAAAMIRMGNISPLTGTGQGIIRRACS 318

Query: 2170 RIN 2178
R+N
Sbjct: 319 RVN 321

Score = 140 bits (353), Expect = 8e-31

Identities = 80/169 (47%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGS+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE VCPGVVSCADILA+AA

Sbjct: 71 VQGCDGSVLLNDTATFTGEQTANPNVGSIRFGVVDNIKAQVEAVCPGVVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 131 RDSV-----VALGGPSWRVLLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS + AN+ +PAP+ +L L + F+ LS DLVALSG I

Sbjct: 148 RRDSTTASLALANSDLPAPSLDLANLTAAFAKKRLSRTDLVALSGAHTI 196

Score = 68.2 bits (165), Expect = 5e-09
Identities = 34/72 (47%), Positives = 49/72 (68%)
Frame = +1

Query: 565 LTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGA 744
+ +SF S L++ + L + A+AQLS FY SCP +++K+ V +A+++E RMGA

Sbjct: 1 MASSSFTS-LSVMVLLCLAAA AVASAQLSPTFYSRSCPRLATIKAAVTA AAVAQEARMGA 59

Query: 745 SLLRLEFFHDCFV 780

SLLRL FHDCFV

Sbjct: 60 SLLRLHFHDCFV 71

>gb|EAY82023.1| hypothetical protein OsI_37207 [Oryza sativa Indica Group]
gb|EAZ17184.1| hypothetical protein OsJ_32691 [Oryza sativa Japonica Group]
Length = 291

Score = 171 bits (434), Expect = 3e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+

Sbjct: 170 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYTFDNFYKNNL 227

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC

Sbjct: 228 NKKGVLEHSDQQLFNGGSADSQTTTYSNMATFFTFDSAAIVKMGNIPLTGSSGQIRKNC 287

Query: 2167 RRIN 2178

R++N

Sbjct: 288 RKNV 291

Score = 146 bits (368), Expect = 2e-32
Identities = 83/167 (49%), Positives = 95/167 (56%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AARD
Sbjct: 45 GCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAARD 104

Query: 1337 SVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR R 1516
SV + GGPTW V+LGRR
Sbjct: 105 SVFAL-----GGPTWVVLGR R 121

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 122 DSTTASLDTANNDIPAPTLDLGLTKSFSNKGLSATDMIALSGAHTI 168

>gb|ABA91154.1| Cationic peroxidase 1 precursor, putative, expressed [Oryza sativa
(japonica cultivar-group)]
Length = 254

Score = 171 bits (434), Expect = 3e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 133 QARCVNFRNRIYSETNIDTSLATSLKSNC PNTTG--DNNISPLDASTPYTFDNFYK NLL 190

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC
Sbjct: 191 NKKGV LHS DQQLFNGGSADSQT TTYSSNMATFFTFDSAAIVKMGNIDPLTGSSGQIRKNC 250

Query: 2167 RRIN 2178
R++N
Sbjct: 251 R KVN 254

Score = 148 bits (374), Expect = 3e-33
Identities = 84/169 (49%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
M+GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AA
Sbjct: 6 MKGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAA 65

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + GGPTW V+LG
Sbjct: 66 RDSVFAL-----GGPTWVVLG 82

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSLGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 83 RRDSTTASLDTANNDIPAPTLDLGLTKSFSNKGLSATDMIALSGAHTI 131

>ref|NP_001065566.1| Os11g0112200 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69373.1| TPA: class III peroxidase 131 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF27411.1| Os11g0112200 [Oryza sativa Japonica Group]
Length = 317

Score = 171 bits (434), Expect = 3e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 196 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYTFDNFYKNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC
Sbjct: 254 NKKGVHLHSDQQLFNGGSADSQTTTYSSNMATFFTDFAAIVKMGNIDPLTGSSGQIRKNC 313

Query: 2167 RRIN 2178
R++N
Sbjct: 314 RKNV 317

Score = 146 bits (369), Expect = 1e-32
Identities = 83/169 (49%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + GGPTW V+LG
Sbjct: 129 RDSVFAL-----GGPTWVVLG 145

Query: 1511 RRDARTASQAANNIPAPTSNLNQLISRFSLGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 146 RRDSTTASLDTANNDIPAPTLDLGLTKSFSNKGLSATDMIALSGAHTI 194

Score = 74.7 bits (182), Expect = 6e-11
Identities = 36/67 (53%), Positives = 48/67 (71%)
Frame = +1

Query: 583 CSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLF 762
CS + + A ++ +AQLS NFY SCPN S++++ V+SA++KE RMGASLLRL
Sbjct: 9 CSVIALLFAAHLV-----SAQLSANFYDKSCPNALSTIRTAVRSAVAKENRMGASLLRLH 63

Query: 763 FHDCFVN 783
FHDCFVN
Sbjct: 64 FHDCFVN 70

>gb|EEE67815.1| hypothetical protein OsJ_25569 [Oryza sativa Japonica Group]
Length = 324

Score = 171 bits (433), Expect = 4e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
Sbjct: 200 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 260 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGQIRLSC 319

Query: 2167 RRIN 2178
++N
Sbjct: 320 SKVN 323

Score = 116 bits (290), Expect = 2e-23
Identities = 71/167 (42%), Positives = 86/167 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD
Sbjct: 80 GCDASVLLSQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 198

Score = 71.6 bits (174), Expect = 5e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNI FSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SSSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792
HDCFV +
Sbjct: 67 HDCFVQASF 75

>ref|NP_001060628.1| Os07g0677200 [Oryza sativa (japonica cultivar-group)]
dbj|BAC83103.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAF22542.1| Os07g0677200 [Oryza sativa Japonica Group]
dbj|BAG93342.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96895.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 317

Score = 171 bits (433), Expect = 4e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGQIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 3e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
 Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAA 125

 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV + LGGP+W V LG
 Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
 Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 6e-10
 Identities = 34/65 (52%), Positives = 45/65 (69%)
 Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
 S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
 Sbjct: 7 SSSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITAAVNSEARMGASLLRLHF 66

 Query: 766 HDCFV 780
 HDCFV
 Sbjct: 67 HDCFV 71

>tpe|CAH69353.1| TPA: class III peroxidase 111 precursor [Oryza sativa (japonica
 cultivar-group)]
 Length = 323

Score = 171 bits (433), Expect = 4e-40
 Identities = 78/124 (62%), Positives = 98/124 (79%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
 Sbjct: 199 QAQCQNFDRDIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 258

 Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
 Sbjct: 259 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTGQGIIRLSC 318

 Query: 2167 RRIN 2178
 ++N
 Sbjct: 319 SKVN 322

Score = 113 bits (283), Expect = 1e-22

Identities = 69/162 (42%), Positives = 84/162 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD

Sbjct: 80 GCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTNNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALS 1642
D+ TAS++ AN +PAP+S+L +LI FS GL D+VALS

Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALS 193

Score = 71.6 bits (174), Expect = 5e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SSLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792
HDCFV +

Sbjct: 67 HDCFVQASF 75

>emb|CBI27501.1| unnamed protein product [Vitis vinifera]
Length = 265

Score = 170 bits (431), Expect = 7e-40
Identities = 82/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+

Sbjct: 142 QARCVTFRDRVYNGTDIDAGFASTRRRRC PADNGGDANLAPLELVTPNSFDNYYFKNLI 201

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTD+IV YS +P TF SDFA+AM+KMGGDI PLTGS G IRK C

Sbjct: 202 QRKGLLQSDQVLFGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEPLTGSAGVIRKFC 261

Query: 2167 RRIN 2178
IN

Sbjct: 262 NVIN 265

Score = 134 bits (337), Expect = 6e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 15 VQGCDASILLDDSSSIQSEKNAPNNLSVRGYEVIDNIKSKVESICPGVVSCADIVAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VS GPTW VKLG
Sbjct: 75 RDASVAVS-----GPTWTVKLG 91

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I
Sbjct: 92 RRDSTTGLSLAATNLPSFRDSLDKLVSLFGSKGLSARDMVALSGSHTI 140

>ref|XP_002269266.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 326

Score = 170 bits (431), Expect = 7e-40
Identities = 82/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+
Sbjct: 203 QARCVTFRDRVYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTD+IV YS +P TF SDFA+AM+KMGGDI PLTGS G IRK C
Sbjct: 263 QRKGLLQSDQVLFGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEPLTGSAGVIRKFC 322

Query: 2167 RRIN 2178
IN
Sbjct: 323 NVIN 326

Score = 134 bits (337), Expect = 6e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 76 VQGCDASILLDDSSSIQSEKNAPNNLSVRGYEVIDNIKSKVESICPGVVSCADIVAVAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD+ VS GPTW VKLG
Sbjct: 136 RDASVAVS-----GPTWTVKLG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I

Sbjct: 153 RRDSTTSGLSLAATNLPsFRDSDLKLVSLFGSKGLSARDMVALSGSHTI 201

Score = 62.4 bits (150), Expect = 3e-07
Identities = 31/69 (44%), Positives = 46/69 (66%), Gaps = 1/69 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGS-ANAQLSTNFYYHSCPnLFSSVKSTVQSAISKETRMGASLL 753
S S I LA+F+++ AQLS FY +CP +++++ V++A+S+E RM ASL+
Sbjct: 8 SCISPACIFLAVFLILSNMPCEAQLSPTFYDDTCPTALTIRTAVRTAVSRERRMAASLI 67

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 68 RLHFHDCFV 76

>ref|XP_002509730.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF51117.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 323

Score = 170 bits (431), Expect = 7e-40
Identities = 82/125 (65%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIYN ++I+ FA TR++ CP +G+GD NLA LDL TP SFDN YF+NL
Sbjct: 199 QARCLTFRGRIYNNASDIDAGFASTRRRRQCPANNGNGDGNLAALDLVTPNSFDNYYFRNL 258

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTD+IV YS +P TFSSDFA+AM+KMGGDI PLTGS GEIR+
Sbjct: 259 IQKKGLLQSDQVLFSGGSTDNIVNEYSRSPSTFSSDFASAMVKMGDIEPLTGSQGEIRRL 318

Query: 2164 CRRIN 2178
C +N
Sbjct: 319 CNVVN 323

Score = 141 bits (355), Expect = 5e-31
Identities = 79/169 (46%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+QGCDGSILLDDTSS TGEK A N NS RGF+VIDN K+ VE +CPG+VSCADI+A+AA
Sbjct: 72 VQGCDGSILLDDTSSMTGEKFARNNNNSVRGFQVIDNAKAQVESICPGIVSCADIVAVAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W VKLG
Sbjct: 132 RDA-----SVAVGGPSWTVKLG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ +ASQ A+ +P T +L LIS F GLS +D+VALSG I
Sbjct: 149 RRDSTSASQRLADANLPGFTDSLESLSLIFERKGLSARDMVALSGAHTI 197

Score = 74.7 bits (182), Expect = 6e-11
Identities = 33/67 (49%), Positives = 51/67 (76%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
F +R+ + + L VL ++AQLS+NFY ++CPN S++++ ++SA+S+E RM ASL+RL
Sbjct: 6 FFNRMLTIFLIVLSSMQSHAQLSSNFYDNTCPNALSTIRTAIRSAVSRERRMSASLRL 65

Query: 760 FFHDCFV 780
FHDCFV
Sbjct: 66 HFHDCFV 72

>emb|CBI18066.1| unnamed protein product [Vitis vinifera]
Length = 263

Score = 170 bits (430), Expect = 1e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETNI+ +F + Q +CP S GDNNL+PLD ++PT+FDN YF NLV
Sbjct: 142 QARCTNFRDRLYNETNIDASQSSLQANCP--SSGGDNNLSPLDTKSPTTFDNAYFTNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLFNGGSTDS V YST TF +DFA A++KMG++SPLTG++G+IR NC
Sbjct: 200 NNKGLLHSDQQLFNGGSTDSQVTTYSTKSTTFFTFANAIKMGNSPLTGTSGQIRTNC 259

Query: 2167 RRIN 2178
R+ N
Sbjct: 260 RKTN 263

Score = 150 bits (379), Expect = 8e-34
Identities = 86/169 (50%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RGF+VID IKS VE CPGVVSCADILA+ A
Sbjct: 15 VNGCDASILLDDTSNFTGEKTAVPNANSVRGFDVIDTIKSQVESSCPGVVSCADILAVVA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 75 RDSV-----VALGGPSWTVRLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ IPAPT NL+ LIS FS G S ++VALSG+ I
Sbjct: 92 RRDSTTASLSTANS DIPAPTLNLSGLISSFSNKGFSANEMVALSGSHTI 140

>ref|XP_002268259.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 298

Score = 170 bits (430), Expect = 1e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETNI+ +F + Q +CP S GDDNL+PLD ++PT+FDN YF NLV
Sbjct: 177 QARCTNFRDRLYNETNIDASFQSSLQANCP--SSGGDNNLSPLDTKSPTTFDNAYFTNLV 234

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQQLFNGGSTDS V YST TF +DFA A++KMG++SPLTG++G+IR NC
Sbjct: 235 NNKGLLHSDQQLFNGGSTDSQVTTYSTKSTTFFTFANAIKMGNSPLTGTSGQIRTNC 294

Query: 2167 RRIN 2178
R+ N
Sbjct: 295 RKTN 298

Score = 150 bits (380), Expect = 6e-34
Identities = 86/169 (50%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCD SILLDDTS+FTGEK A PN NS RGF+VID IKS VE CPGVVSCADILA+ A
Sbjct: 50 VKGCDASILLDDTSNFTGEKTAVPNANSVRGFDVIDTIKSQVESSCPGVVSCADILAVVA 109

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 110 RDSV-----VALGGPSWTVRLG 126

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ IPAPT NL+ LIS FS G S ++VALSG+ I
Sbjct: 127 RRDSTTASLSTANS DIPAPTLNLSGLISSFSNKGFSANEMVALSGSHTI 175

Score = 71.2 bits (173), Expect = 6e-10
Identities = 32/49 (65%), Positives = 39/49 (79%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
A+ AQL+TN+Y SCPN S +KS V +A++ E RMGASLLR L FHDCFV
Sbjct: 2 ASAQLTTNYSSCPNALSI IKS AVNTAVNNEARMGASLLR LFFHDCFV 50

>ref|XP_002299006.1| predicted protein [Populus trichocarpa]
gb|EEE83811.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 170 bits (430), Expect = 1e-39
Identities = 82/125 (65%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N ++I+ FA TR+++CP SG+G+NNLAPLDL TP SFDN YF+NL
Sbjct: 198 QARCVTFRGRIYDNSSDIDAGFASTRRRNCPSASGNGNNN LAPLDLVTPNSFDNYYFRNL 257

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTGSNGEIRKN 2163
+Q++GLL SDQ LF+G STDSIV YS NP FSSDFAAAM++MGDI PLTGS GEIR+
Sbjct: 258 IQRRGLLQSDQVLFSGQSTDSIVTEYSRNP SLFSSDFAAAML RMGDIEPLTGSQGEIRRV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSVVN 322

Score = 126 bits (317), Expect = 1e-26
Identities = 72/169 (42%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNI KSAVEKVC PGVVSCADILAIAA 1330
+QGCD SI+LD++ S EK + N NS RGFEVID+ K+ VE +CPGVVSCADI A+AA
Sbjct: 71 VQGCDASIMLDNSPSIDSEKFSFSNNNSIRGFEVIDDAKAQVESIC PGVVSCADIAAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 131 RDA-----SVAVGGPSWTVRLG 147

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ IP T++L LI F+ GLS +D+VALSG+ I
Sbjct: 148 RRDSTTASRLADSDIPRATTSLVNLIGMFNGKGLSERDMVALSGSHTI 196

Score = 66.2 bits (160), Expect = 2e-08
Identities = 32/69 (46%), Positives = 47/69 (68%), Gaps = 4/69 (5%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSA----NAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
SRL++ +F L S+ AQLS+NFY +CPN +++++ ++ A+S E RM ASL+
Sbjct: 3 SRLSLACVVFSFLFISSCLPCQAQLSSNFYDSTCPNALTIRTAIRRAVSSERRMAASLI 62

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 63 RLHFHDCFV 71

>ref|XP_002333334.1| predicted protein [Populus trichocarpa]
gb|EEE74658.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 170 bits (430), Expect = 1e-39
Identities = 82/125 (65%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSKSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N ++I+ FA TR+++CP SG+G+NNLAPLDL TP SFDN YF+NL
Sbjct: 198 QARCVTFRGRIDNSSDIDAGFASTRRRNCPSASGNGNNLAPLDLVTNPSFDNNYFRNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q++GLL SDQ LF+G STDSIV YS NP FSSDFAAAM++MGDI PLTGS GEIR+
Sbjct: 258 IQRRGLLQSDQVLFSGQSTDSIVTEYSRNP SLFSSDFAAAMLRMGDIEPLTGSQGEIRRV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSVVN 322

Score = 126 bits (316), Expect = 2e-26
Identities = 71/169 (42%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SI+LD++ S EK + N NS RGFEV+D+ K+ VE +CPGVVSCADI A+AA
Sbjct: 71 VQGCDASIMLDNPSIDSEKFSFSNNNSIRGFEVVDDAKAQVESICPGVVSCADIAAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 131 RDA-----SVAVGGPSWTVRLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ IP T++L LI F+ GLS +D+VALSG+ I
Sbjct: 148 RRDSTTASRLADSDIPRATTSVLNLIGMFNGKGLSERDMVALSGSHTI 196

Score = 66.2 bits (160), Expect = 2e-08
Identities = 32/69 (46%), Positives = 47/69 (68%), Gaps = 4/69 (5%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSA----NAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
SRL++ +F L S+ AQLS+NFY +CPN +++++ ++ A+S E RM ASL+
Sbjct: 3 SRLSLACVVFSLFLISSCLPCQAQLSSNFYDSTCPNALTTIRTAIRRAVSSERRMAASLI 62

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 63 RLHFHDCFV 71

>ref|XP_002285723.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 170 bits (430), Expect = 1e-39
Identities = 84/124 (67%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR+RIYNETNI+ AFA ++Q+ CP T G DNNL+ LD +T T FDN YF+NL
Sbjct: 195 KARCTSFRRSRIYNETNIDAAFATSKQKICPSTGG--DNNLSDLD-ETTTVFDNVYFRNLK 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQL+NGGSTDSIV YSTN TF +D A AMIKMG++SPLTG+NGEIR +C
Sbjct: 252 AKKGLLHSDQQLYNGGSTDSIVETYSTNSATFFTDVANAMIKMGNLSPLTGTNGEIRTDC 311

Query: 2167 RRIN 2178
++IN
Sbjct: 312 KKIN 315

Score = 155 bits (391), Expect = 3e-35
Identities = 85/167 (50%), Positives = 103/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLDDT+SFTGEK A PN++S RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTASFTGEKTAGPNKDSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW ++LGRR
Sbjct: 130 SV-----VALGGPTWTLQLGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +P P S+L+ LISRFS G +TK++VALSGT I
Sbjct: 147 DSTTASLSTANS DLPGPASDLSTLISRFSNKGFTTKEMVALSGTHTI 193

Score = 75.1 bits (183), Expect = 4e-11
Identities = 38/70 (54%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSLFCVFSFLL--GMAHAQLSSNFYASSCPKALSTIRAAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAA46916.1| peroxidase [Oryza sativa (japonica cultivar-group)]
prf||1909367A peroxidase
Length = 317

Score = 170 bits (430), Expect = 1e-39
Identities = 77/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAP+D TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTSGGDSNLAPVDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGQIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 3e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 6e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SSLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITAAVNSEARMGASLLRLHF 66

Query: 766 HDCFV 780
HDCFV
Sbjct: 67 HDCFV 71

>ref|XP_002319967.1| predicted protein [Populus trichocarpa]
gb|EEE95890.1| predicted protein [Populus trichocarpa]
Length = 312

Score = 169 bits (429), Expect = 1e-39
Identities = 82/120 (68%), Positives = 94/120 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q +C FRARIYNETNI+ +FA RQ+ CP T+G D+NLAPLD QTP FDN Y+KNL+
Sbjct: 191 QTKCKTFRARIYNETNIDKSFATMRQKMCPLTTG--DDNLAPLDFQTPNVFDNNYYKNLI 248

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ LF+G STDS+VR YS NP F SDFAAAM+KMGGDI P TG+ GEIRK C
Sbjct: 249 HKKGLLHSDQVLFSGESTDSLVRTYSNPNPDIFFSDFAAAMVKMGDIDPRTGTRGEIRKNC 308

Score = 140 bits (352), Expect = 1e-30
Identities = 75/169 (44%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCD SILL+DT++F GE+ A PN NS RG+ V+ IKS +EKVCPG+VSCADI+ IAA
Sbjct: 64 VKGCDASILLEDATATFKGEQGAGPNNSVRGYNVVAIKSKLEKVCPGIVSCADIVVIAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP W VKLG
Sbjct: 124 RDS-----TVLLGGPYWKVKLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TA+ +AA+ +P+ TS ++QLI RF + GLS D+VALSG+ I
Sbjct: 141 RRDSKTANMNAASKSLPSDTSTVSQLIKRFKSKGLSATDMVALSGSHTI 189

Score = 84.3 bits (207), Expect = 7e-14
Identities = 40/63 (63%), Positives = 51/63 (80%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
+++ LAL ++ S++A LST+FY SCP LF +VKS VQSAI+KE RMGASL+RLFFHD
Sbjct: 2 VSVTLALLLIYTSSSSAHLSTDFYDKSCPQLFGTVKSVVQSAIAKERRMGASLVRLFFHD 61

Query: 772 CFV 780
CFV
Sbjct: 62 CFV 64

>gb|ABK24123.1| unknown [Picea sitchensis]
Length = 208

Score = 169 bits (427), Expect = 2e-39
Identities = 81/124 (65%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN++NI+TA+A++ Q CPR+ G DN L+PLD QTPT F+N Y+KNLV
Sbjct: 87 KARCTSF RDHIYNSNIDTAYAKSLQAKCPRSGG--DNRLSPLDYQTPTKFENNYKLV 144

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNG STDS+V YS N F +DFAAAMIKMGI PLTGS G+IRKNC
Sbjct: 145 ARKGLLHSDQELFNGVSTDSLVTKYSKNLKLFENDFAAAMIKMGNIMPLTGSQGIIRKNC 204

Query: 2167 RRIN 2178
R+ N
Sbjct: 205 RKRN 208

Score = 91.7 bits (226), Expect = 4e-16
Identities = 54/124 (43%), Positives = 66/124 (53%)
Frame = +2

Query: 1274 VEKVC PGV VSCADILAI AARDSVQIVSGQTTNKNTLN*IIKLYISK LITNLVPHMQLKRT 1453
+EK C GVVSCADILA+AARDSV
Sbjct: 1 MEKACSGV VSCADILAVAARDSV----- 23

Query: 1454 FC*F*SI*LGGPTWNVKLGRRDARTASQSAANN GIPAPTSNLNLISRFSALGLSTKDLV 1633
+ LGGPTW V LGRRD+ TA+++AAN IPAPT+NL L S+F A GLS +++V
Sbjct: 24 -----VTLGGPTWTVMLGRRD SGTANRTAANTNIPAPTANLANLTSKFGAQGLSKREMV 77

Query: 1634 ALSG 1645
LSG
Sbjct: 78 VLSG 81

>gb|AAA20473.1| peroxidase [Cenchrus ciliaris]
Length = 313

Score = 169 bits (427), Expect = 2e-39
Identities = 78/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR IYN+TNI T FA + + +CPR +GSGD NLA LD TP +FDN YFKNL+
Sbjct: 190 QAQCLNFRDHIYNDTNINTGFASSLKANCPRPTGSGDGNLASLDTSTPYTFDNAYFKNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++NP FSS FAAAM+KM +SPLTGS G+IR C
Sbjct: 250 SQKGLLHSDQQLFNGGSTDNTVRNFASNP SAFSSAFAAAMVKMASLSPLTGSQQGQIRLTC 309

Query: 2167 RRIN 2178
+ N
Sbjct: 310 SKAN 313

Score = 103 bits (258), Expect = 9e-20
Identities = 67/170 (39%), Positives = 85/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI A 1330
+QGCD S+LLD GE+ A PN S RGF+VI NIK+ VE +C VSCADILA+ A
Sbjct: 66 VQGCDASVLLDSG----GEQGAIPNAGSLRGFDVIANIKAQVEAICKQTVSCADILAVGA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R SV + LGGP+W V LG
Sbjct: 122 RHSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNNGIPAPTS-NLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ + S + AN+ +PA S NL+QLI F G + ++VALSG I
Sbjct: 139 RRDSTSGSAALANSDLPASRSFNLSQLIGSFDNKGFTATEMVALSGAHTI 188

Score = 73.2 bits (178), Expect = 2e-10
Identities = 39/70 (55%), Positives = 47/70 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L + + A+AQLS FY SCPN S++KS V +A+ KE RMGASL
Sbjct: 1 MASSVSGLLLMLCMAAV----ASAQLSATFYDTSCPNALSTIKSAVTAAVKKENRMGASL 56

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 57 LRLHFHDCFV 66

>gb|ABK23423.1| unknown [Picea sitchensis]
Length = 318

Score = 168 bits (426), Expect = 3e-39
Identities = 81/124 (65%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNE+NI+T+ A + CPRT G DN L+PLDL TP +FD +Y+ NL
Sbjct: 197 QARCTSFARIYNESNIDTSLATAVKPKCPRTGG--DNTLSPLDLATPITFDKHYECNLR 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNGGSTDS V YSTN F +DFAAAM+ MG+I PLTG++G+IR+NC
Sbjct: 255 SKKGLLHSDQQLFNGGSTDSQVTTYSTNQNNFFTDFAAAMVMGNIKPLTGTSGQIRRNC 314

Query: 2167 RRIN 2178
R+ N
Sbjct: 315 RKS N 318

Score = 149 bits (377), Expect = 1e-33
Identities = 86/169 (50%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+ GCDGSILLDD S+FTGEK A PN NS RG++VID IK+ VE C GVVSCADI+AIAA
 Sbjct: 70 VNGCDGSILLDDNSTFTGEKTATPNNSVRGYDVIDTIKTQVEAACSGVVSCADIVAIAA 129

 Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV + LGGPTW V LG
 Sbjct: 130 RDSV-----VALGGPTWTVLLG 146

 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TAS +AAN+ IP+P SNL+ LIS F + LS KDLVALSG I
 Sbjct: 147 RRDSTTASFNAANSSIPASNLSTLISSFRSHNLSPKDLVALSGAHTI 195

Score = 66.6 bits (161), Expect = 2e-08
 Identities = 33/64 (51%), Positives = 44/64 (68%), Gaps = 2/64 (3%)
 Frame = +1

Query: 598 ICLALFVL--IWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
 I + LF++ I + QL++ FY SCP S V++ V+ A++KE RMGASLLRL FHD
 Sbjct: 8 IPIVLFIICSIPNIVHGLTSTFYSESCPRALSIVQAAVEQAVAKERRMGASLLRLHFHD 67

 Query: 772 CFVN 783
 CFVN
 Sbjct: 68 CFVN 71

>ref|NP_001060629.1| Os07g0677300 [Oryza sativa (japonica cultivar-group)]
 sp|Q0D3N0.1|PER2_ORYSJ RecName: Full=Peroxidase 2; Flags: Precursor
 dbj|BAA03911.1| peroxidase [Oryza sativa Japonica Group]
 dbj|BAC79528.1| peroxidase [Oryza sativa Japonica Group]
 dbj|BAC83104.1| peroxidase [Oryza sativa Japonica Group]
 tpe|CAH69354.1| TPA: class III peroxidase 112 precursor [Oryza sativa (japonica
 cultivar-group)]
 dbj|BAF22543.1| Os07g0677300 [Oryza sativa Japonica Group]
 dbj|BAG93552.1| unnamed protein product [Oryza sativa Japonica Group]
 gb|EEE67816.1| hypothetical protein OsJ_25570 [Oryza sativa Japonica Group]
 Length = 314

Score = 168 bits (426), Expect = 3e-39
 Identities = 76/124 (61%), Positives = 99/124 (79%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QA+C NFR R+YNETNI+++FA + +CPR +GSGD+NLAPLD TP +FD+ Y+ NL+
 Sbjct: 191 QAQCQNFRDRLYNETNIDSSFATALKANCPRTGSGDSNLAPLDTTTPNAFDSAYYTNLL 250

 Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 KLLHSDQ LFNGGSTD+ VR +S+N F+S F AAM+KMG+ISPLTG+ G+IR NC
 Sbjct: 251 SNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTAAMVKGNIPLTGTGQIRLNC 310

Query: 2167 RRIN 2178

++N

Sbjct: 311 SKVN 314

Score = 121 bits (303), Expect = 5e-25

Identities = 72/169 (42%), Positives = 89/169 (52%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+QGCD S+LL E+NA PN S RGF V+DNIK+ VE +C VSCADILA+AA

Sbjct: 69 VQGCDAVLLSGQ-----EQNAGPNAGSLRGFNVVDNIKTQVEAICSQTVSCADILAVAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGP+W V LG

Sbjct: 124 RDSV-----VALGGPSWTVLLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TA++S AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 141 RRDSTTANESQANTDLPAPSSSLAELIGNFSRKGLDVTDMVALSGAHTI 189

Score = 70.5 bits (171), Expect = 1e-09

Identities = 36/70 (51%), Positives = 49/70 (70%)

Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750

MAS S +++ L + + +A+AQLS FY SCPN S++KS V +A++ E RMGASL

Sbjct: 1 MAS-ASSVSLMLLVAAAMASAASAQLSATFYDTSCPNALSTIKSAVTA AVNSEPRMGASL 59

Query: 751 LRLFFHDCFV 780

+RL FHDCFV

Sbjct: 60 VRLHFHDCFV 69

>gb|ACJ11762.1| class III peroxidase [Gossypium hirsutum]

Length = 323

Score = 168 bits (425), Expect = 4e-39

Identities = 80/124 (64%), Positives = 101/124 (81%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FR RIYNETNI++ FA + + +CP S GDN+L+PLD + TSFDN YFKNL

Sbjct: 202 QARCTTFRTRIYNETNIDSTFATSLRANCP--SNGGDNSLSPLDTTSSTSF DNAYFKNLQ 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLF+GGSTDS V YS+N G+F++DFA AM+KMG++SPLTG++G+IR NC
Sbjct: 260 GQKGLLHSDQQLFSGGSTDSQVNAYSSNLGSFTTDFANAMVKMGNLSPLTGTSGQIRTNC 319

Query: 2167 RRIN 2178
R+ N
Sbjct: 320 RKAN 323

Score = 152 bits (384), Expect = 2e-34
Identities = 87/169 (51%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILATAA 1330
+ GCDGSILLDDT++ TGEK A PN NSARGFEVID IKS VE +CPGVVSCADI+A+AA
Sbjct: 75 VNGCDGSILLDDTANMTGEKTAVPNSNSARGFEVIDTIKSQVESLCPGVVSCADIVAVAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 135 RDSV-----VALGGPSWIVLLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LI+ FS G + K++VALSG+ I
Sbjct: 152 RRDSTTASLSAANSNIPAPTLNLSGLITAFSNKGFTAKEMVALSGSHTI 200

Score = 72.0 bits (175), Expect = 4e-10
Identities = 39/75 (52%), Positives = 48/75 (64%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRM 738
SK S R + + LF+L+ A AQLS+ FY +CP S++KS V SA+S E RM
Sbjct: 3 SKTCSPSNKLRFLLGMVFLLM-NMATAQLSSTFYSTTCPRALSTIKSAVNSAVSNEARM 61

Query: 739 GASLLRLFFHDCFVN 783
GASL RL FHDCFVN
Sbjct: 62 GASLPRLHFHDCFVN 76

>gb|ABK25962.1| unknown [Picea sitchensis]
Length = 323

Score = 168 bits (425), Expect = 4e-39
Identities = 79/124 (63%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARC NFRA IYN+TNI + ++ + + CP T+GSGDNNL+PLD +PT+FD Y+ NL
 Sbjct: 200 QARCFNFRAHIYNDTNILSTYSTSLRSKCPPTNGSGDNNLSPLDYVSPTAFDKNYYCNLK 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 KKGLLHSDQ+LFNGGSTDS V Y++N F SDFAAAM+KMG+I PLTG++G+IRKNC
 Sbjct: 260 IKKGLLHSDQELFNGGSTDSQVTTYASNQNIFFSDFAAAMVKGNIKPLTGTSGQIRKNC 319

Query: 2167 RRIN 2178
 R+ N
 Sbjct: 320 RKPN 323

Score = 153 bits (387), Expect = 9e-35
 Identities = 87/169 (51%), Positives = 102/169 (60%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
 + GCDGS+LLDD+S TGEK A PN NSARGF+VID IKS VEK C GVVSCADILAIAA
 Sbjct: 73 VNGCDGSVLLDDSSKITGEKTAVPNANSARGFDVIDTIKSQVEKSCSGVVSCADILAIAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV + LGGP+W V LG
 Sbjct: 133 RDSV-----VELGGPSWTVLLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TAS+S ANN IP PTS+L+++IS F A GLS K++VAL+G I
 Sbjct: 150 RRDSTTASKSGANNIPPTSSLSKIISLFQAQGLSAKEMVALAGAHTI 198

Score = 69.3 bits (168), Expect = 2e-09
 Identities = 36/65 (55%), Positives = 45/65 (69%), Gaps = 4/65 (6%)
 Frame = +1

Query: 601 CLALFVLIWGS----ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFH 768
 C+A+ V I S ++ QLS+ FY SCP S VK+ V+ A++KE RMGASLLRL FH
 Sbjct: 10 CIAVMVFIICSIANLSHGQLSSTFYDKSCPAALS VVKA AVKQAVAKEQRMGASLLRLHFH 69

Query: 769 DCFVN 783
 DCFVN
 Sbjct: 70 DCFVN 74

>gb|EAO5133.1| hypothetical protein OsI_27326 [Oryza sativa Indica Group]
 Length = 324

Score = 168 bits (425), Expect = 4e-39
 Identities = 77/124 (62%), Positives = 97/124 (78%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLA LD TP +FDN Y+ NL+

Sbjct: 200 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTGSGDSNLAALDTTPNAFDNAYYSNLL 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR ++N FSS F AM+KMG+ISPLTG+ G+IR +C

Sbjct: 260 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTGGQIRLSC 319

Query: 2167 RRIN 2178

++N

Sbjct: 320 SKVN 323

Score = 116 bits (290), Expect = 2e-23

Identities = 71/167 (42%), Positives = 86/167 (51%)

Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD

Sbjct: 80 GCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 198

Score = 71.6 bits (174), Expect = 5e-10

Identities = 34/69 (49%), Positives = 46/69 (66%)

Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SSLSLMLLVAAAMASVASAQLSATFYDTSCP NALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792

HDCFV +

Sbjct: 67 HDCFVQASF 75

>ref|NP_001046400.1| Os02g0240100 [Oryza sativa (japonica cultivar-group)]

Length = 335

Score = 168 bits (425), Expect = 4e-39
Identities = 74/123 (60%), Positives = 101/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFR R+YN+TNI+ AFA R++ CP GSGD++LAPLD QT FDN Y++NL+
Sbjct: 211 SQCANFRDRVYNDTNIDPAFAALRRRGCPAAPGSGDSSLAPLDAQTNVFDNAYYRNLLA 270

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I PLTG+ G+IR++CR
Sbjct: 271 QRGLLHSDQELFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNIKPLTGAAGQIRRSR 330

Query: 2170 RIN 2178
+N
Sbjct: 331 AVN 333

Score = 134 bits (337), Expect = 6e-29
Identities = 80/171 (46%), Positives = 97/171 (56%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 81 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRNVELLCPGVVSCADIVAL 140

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 141 AARDSTAL-----LGGPSWAVP 157

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS SAAN+ +PAP+S+L LI+ F GLS +D+ ALSG I
Sbjct: 158 LGRRDSTTASLSAANS DLPAPSSDLATLIAGFGNKGLSPRDMTALSGAHTI 208

Score = 70.1 bits (170), Expect = 1e-09
Identities = 42/82 (51%), Positives = 52/82 (63%), Gaps = 4/82 (4%)
Frame = +1

Query: 547 LVCLSKLTMASFCSRLTICLALFVLIWGSANA----QLSTNFYHSCPNLFSSVKSTVQS 714
L+ + ++TMAS S CL F L+ +A A QLST FY SCP L V++TV
Sbjct: 1 LIKICEITMASRSS-WHCCLLAFFLLSSAAGAAYGQQLSTTFYAASCP TLQVVVRATVLG 59

Query: 715 AISKETRMGASLLRLFFHDCFV 780
A+ E RMGASL+RLFFHDCFV
Sbjct: 60 ALLAERRMGASLVRLLFFHDCFV 81

>gb|AAC49818.1| peroxidase [Oryza sativa Indica Group]
Length = 317

Score = 168 bits (425), Expect = 4e-39
Identities = 77/124 (62%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLA LD TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFDRRIYNETNIDSAFATQRQANCPRPTGSGDSNLAALDTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNGGSADNTRNFASNAAFSSAFTTAMVKMGNISPLTGTGQIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 3e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 6e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SSLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFV 780

HDCFV
Sbjct: 67 HDCFV 71

>dbj|BAD28869.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69272.1| TPA: class III peroxidase 30 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAG98261.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAF08314.2| Os02g0240100 [Oryza sativa Japonica Group]
Length = 327

Score = 168 bits (425), Expect = 4e-39
Identities = 74/123 (60%), Positives = 101/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFR R+YN+TNI+ AFA R++ CP GSGD++LAPLD QT FDN Y++NL+
Sbjct: 203 SQCANFRDRVYNDTNIDPAFAALRRRGCPAAPGSGDSSLAPLDAQTNVFDNAYYRNLLA 262

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I PLTG+ G+IR++CR
Sbjct: 263 QRGLLHSDQELFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNIKPLTGAAGQIRRSCR 322

Query: 2170 RIN 2178
+N
Sbjct: 323 AVN 325

Score = 134 bits (337), Expect = 6e-29
Identities = 80/171 (46%), Positives = 97/171 (56%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 73 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRNVELLCPGVVSCADIVAL 132

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 133 AARDSTAL-----LGGPSWAVP 149

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS SAAN+ +PAP+S+L LI+ F GLS +D+ ALSG I
Sbjct: 150 LGRRDSTTASLSAANS DLPAPSSDLATLIAGFGNKGLSPRDMTALSGAHTI 200

Score = 66.6 bits (161), Expect = 2e-08

Identities = 36/64 (56%), Positives = 42/64 (65%), Gaps = 4/64 (6%)
Frame = +1

Query: 601 CLALFVLIWGSANA----QLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFH 768
CL F L+ +A A QLST FY SCP L V++TV A+ E RMGASL+RLFFH
Sbjct: 10 CLLAFFLLSSAAGAAYGQQLSTTFYAASCPTLQVVVRATVLGALLAERRMGASLVRLFFH 69

Query: 769 DCFV 780
DCFV
Sbjct: 70 DCFV 73

>ref|XP_002274693.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 324

Score = 167 bits (424), Expect = 5e-39
Identities = 85/125 (68%), Positives = 96/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP +G GD+NLA LDL TP SFDN YFKNL
Sbjct: 200 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPADNGDGDNNLAALDLVTPNSFDNYYFKNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV YS N TFSSDFA AM+KMGGDI PLTG+ GEIR+
Sbjct: 260 IQKKGLLQSDQVLFSGGSTDSIVSEYSKNRKTFFSSDFALAMVKMGDIEPLTGAAGEIREF 319

Query: 2164 CRRIN 2178
C IN
Sbjct: 320 CNAIN 324

Score = 136 bits (343), Expect = 1e-29
Identities = 76/169 (44%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+SS EKNA N NSARG+EVI ++KS VE +CPG+VSCADILA+AA
Sbjct: 73 VQGCDASILLDDSSSIQSEKNAPNNLNSARGYEVHDKVKSQVESICPGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW VKLG
Sbjct: 133 RDA-----SVAVGPTWTVKLG 149

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S ++ +P+ +L++LIS F + GLST+D+VALSG+ I
Sbjct: 150 RRDSTTSGLSQVSSNLPSFRDSLRLISLFGSKGLSTRDMVALSGSHTI 198

Score = 63.2 bits (152), Expect = 2e-07
Identities = 31/73 (42%), Positives = 46/73 (63%), Gaps = 3/73 (4%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS---ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMG 741
M S C+ + VL+ S AQLS++FY ++CP S++++ + A+S+E RM
Sbjct: 1 MGSIAGNYGACIFVAVLLILSIMPCEAQLSSSFYDNTCPKALSTIRTATRKAVSRERRMA 60

Query: 742 ASLLRLFFHDCFV 780
ASL+RL FHDCFV
Sbjct: 61 ASLIRLHFHDCFV 73

>gb|EEC82680.1| hypothetical protein OsI_27324 [Oryza sativa Indica Group]
Length = 318

Score = 167 bits (424), Expect = 5e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 195 QAQCQNFRDRLYNETNIDAAFAAALKASCPRTGSGDGNLAPLDTTPTAFDNAYYTLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 255 SNKGLLHSDQVLFNGGAVDGGVRSYASGPSRFRDFAAAMVKMGNIAPLTGTGQGIIRLVC 314

Query: 2167 RRIN 2178
++N
Sbjct: 315 SKVN 318

Score = 130 bits (327), Expect = 9e-28
Identities = 73/165 (44%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 68 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 128 RDSV-----VALGGPSWRVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645

RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 145 RRDSTTASLALANSDLPPPSFDVANLTAAFAAKGLSQADMVALSG 189

Score = 64.3 bits (155), Expect = 8e-08
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFS SVKSTVQSAISKETRMGASLLRLFFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYSRSCPRLAIIRAGVRAAVAQEPRMGASLLRLHFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>ref|NP_001060626.1| Os07g0676900 [Oryza sativa (japonica cultivar-group)]
dbj|BAF22540.1| Os07g0676900 [Oryza sativa Japonica Group]
Length = 333

Score = 167 bits (424), Expect = 5e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 210 QAQCQNFRDRLYNETNIDAAFAAALKASCPRTSGSGDGNLAPLDTTPTAFDNAYYT NLL 269

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 270 SNKGLLHSDQVLFNGGAVDGGVRSYASGPSRFR R DFAAAMVKMGNIAPLTGTGQGI R LVC 329

Query: 2167 RRIN 2178
++N
Sbjct: 330 SKVN 333

Score = 130 bits (327), Expect = 9e-28
Identities = 73/165 (44%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DN IK+ VE C VSCADILA+AA
Sbjct: 83 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGP+W V LG
Sbjct: 143 RDSV-----VALGGPSWRVLLG 159

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 160 RRDSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 204

Score = 68.6 bits (166), Expect = 4e-09
Identities = 38/74 (51%), Positives = 50/74 (67%), Gaps = 1/74 (1%)
Frame = +1

Query: 562 KLTMAFCS-RLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRM 738
+LTMAS S L +CLAL + G QLS FY SCP + +++ V++A+++E RM
Sbjct: 13 RLTMASCLSVLLLLCLALAGSVSGQ---QLSATFYRSCPRALAIIRAGVRAAVAQEPRM 69

Query: 739 GASLLRLFFHDCFV 780
GASLLRL FHDCFV
Sbjct: 70 GASLLRLHFHDCFV 83

>emb|CAH10840.1| peroxidase [Picea abies]
Length = 320

Score = 167 bits (424), Expect = 5e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ TPT+FDN Y+ NL
Sbjct: 199 QSRCAFFRTRIYNESNINAAAFATSVKPNCP--SAGGDNTLSPLDVVTPTTFDNKYYSNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIRKNC 2166
+KGLLHSDQQLFNGGSTDS V YSTN +F +DFAAAM+KMG+ISPLTG++G+IRKNC
Sbjct: 257 VQKGLLHSDQQLFNGGSTDSQVTTYSTNQNSFFTFDFAAAMVKMGNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 151 bits (381), Expect = 5e-34
Identities = 87/169 (51%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AA 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA

Sbjct: 72 VNGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS+ + L GPTW V LG

Sbjct: 132 RDSI-----VELQGPTWTVM LG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS SAANN IP+P S+L+ LI+ F GLSTKDLVALSG I

Sbjct: 149 RRDSPTASLSAANNIPSPASSLSTLITSFQNHGLSTKDLVALSGAHTI 197

Score = 69.3 bits (168), Expect = 2e-09
Identities = 34/70 (48%), Positives = 46/70 (65%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGS-----ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + ++ S N QLS+ FY SCP + S VK+ V+ A++KE RMGASL+

Sbjct: 4 RTLVCIGVMVALLCSININAVNGQLSSTFYAKSCP RVQSIVKTVVKQAVAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783
RL FHDCFVN

Sbjct: 64 RLHFHDCFVN 73

>dbj|BAC83101.1| putative peroxidase precursor [Oryza sativa Japonica Group]
gb|EEE67813.1| hypothetical protein OsJ_25567 [Oryza sativa Japonica Group]
Length = 318

Score = 167 bits (424), Expect = 5e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+

Sbjct: 195 QAQCQNFRDRLYNETNIDAAFAAALKASCP RPTSGSGDGNLAPLDTTPTAFDNAYYTNLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C

Sbjct: 255 SNKGLLHSDQVLFNGGAVDGGVRSYASGPSRFR R DFAAAMVKMGNIAPLTGTGGQIRLVC 314

Query: 2167 RRIN 2178
++N

Sbjct: 315 SKVN 318

Score = 130 bits (327), Expect = 9e-28
Identities = 73/165 (44%), Positives = 94/165 (56%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 68 VQGCDAVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 128 RDSV-----VALGGPSWRVLLG 144

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 145 RRDSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 189

Score = 64.3 bits (155), Expect = 8e-08
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYSRSCPRLAIIRAGVRAAVAQEPRMGASLLRLHFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>tpe|CAH69351.1| TPA: class III peroxidase 109 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 322

Score = 167 bits (424), Expect = 5e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 199 QAQCQNFRDRLYNETNIDAAFAAALKASCPRPTGSGDGNLAPLDTTPTAFDNAYYTNLL 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 259 SNKGLLHSDQVLFNGGAVDGGVRSYASGPSRFRRDFAAAMVKMGNIAPLTGTGQGIQLVC 318

Query: 2167 RRIN 2178
++N
Sbjct: 319 SKVN 322

Score = 128 bits (321), Expect = 4e-27
Identities = 72/163 (44%), Positives = 92/163 (56%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AARD
Sbjct: 74 GCDASVLLNDTANFTGEQG ANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAARD 133

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 134 SV-----VALGGPSWRVLLGRR 150

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
D+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 151 DSTTASLALANS DLPPPSFDVANLTASFAAKGLSQADMVALSG 193

Score = 64.3 bits (155), Expect = 8e-08
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYSRSCPRA LAIIRAGVRAAVAQEPRMGASLLRLHFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>ref|XP_002451848.1| hypothetical protein SORBIDRAFT_04g008620 [Sorghum bicolor]
gb|EES04824.1| hypothetical protein SORBIDRAFT_04g008620 [Sorghum bicolor]
Length = 278

Score = 167 bits (423), Expect = 6e-39
Identities = 79/124 (63%), Positives = 100/124 (80%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNLV 1986
++C NFR IYN+T+I+ AFA RQ+SCP G+G D NLA LD+QT FDN Y++NL+
Sbjct: 153 SQCQNRFRGHIYNDTDIDAAFAALRQRSCPAAPGTGGDTNLAALDVQTQLVFDNAYYRNLL 212

Query: 1987 QKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGISPLTGSNGEIRKNC 2166
K+GLLHSDQ+LFNGGS D++VR YS+NP F+SDFAAAMIKMGI+ISPLTG+ G+IR NC
Sbjct: 213 AKRGLLHSDQELFNNGSQDALVRQYSSNPALFASDFAAAMIKMGNISPLTGTAGQIRANC 272

Query: 2167 RRIN 2178
R +N
Sbjct: 273 RVVN 276

Score = 134 bits (338), Expect = 5e-29
Identities = 78/169 (46%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGSILLDD SF GEK A PN NS RGF+VID IK+ VE +CPGVVSCADI+A+AA
Sbjct: 25 VQGCDGSILLDDVGSFVGEKGAGPNVNSVRGFDVIDQIKTNVELICPGVVSCADIVALAA 84

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R F + LGGP+W V LG
Sbjct: 85 R-----FGTFLLGGPSWAVPLG 101

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P+P S L L++ F GLS DL ALSG I
Sbjct: 102 RRDSTTASLTANSDLSPASGLATLVTAFGNKGLSPGDLTALSGAHTI 150

Score = 39.3 bits (90), Expect = 2.6
Identities = 17/22 (77%), Positives = 19/22 (86%)
Frame = +1

Query: 715 AISKETRMGASLLRLFFHDCFV 780
A+ E RMGASL+RLFFHDCFV
Sbjct: 4 ALLAERRMGASLVRLFFHDCFV 25

>gb|ACN33811.1| unknown [Zea mays]
Length = 320

Score = 167 bits (423), Expect = 6e-39
Identities = 77/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR IYN+TNI FA + + +CPR +GSGD NLAPLD TP SFDN Y+ NL+
Sbjct: 197 QAQCKNFRDHIYNDTNINQGFASSLKANCPRPTGSGDGNLAPLDTTTPYSFDNAYYSNLL 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++N FSS FAAAM+KMG++SPLTGS G+IR C
Sbjct: 257 SQKGLLHSDQELFNGGSTDNTVRNFASNSAAFSSAFAAAMVKMGNLSPLTGSQGGQIRLTC 316

Query: 2167 RRIN 2178

+N
Sbjct: 317 STVN 320

Score = 118 bits (296), Expect = 3e-24
Identities = 72/171 (42%), Positives = 89/171 (52%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD S+LL D ++ FTGE+ A PN S RGF+VI NIK+ VE VC VSCADILA+
Sbjct: 68 VQGCDAVLLADNAATGFTGEQGAAPNAGSLRGFDVIANIKAQVEAVCKQTVSCADILAV 127

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDSV + LGGP+W V
Sbjct: 128 AARDSV-----VALGGPSWTVP 144

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS S AN+ +P P NL QLI+ F G + ++ LSG I
Sbjct: 145 LGRRDSTTASLSLANSIDLPPPFNLGQLITAFGNKGFTATEMATLSGAHTI 195

Score = 75.1 bits (183), Expect = 4e-11
Identities = 36/65 (55%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
S ++ CL L + + A+AQLS FY SCPN S++K V +A+ KE RMGASLLRL F
Sbjct: 4 SSVSSCLLLLCLAAVASAQLSPTFYDSSCPNALSTIKIAVNAAVQKENRMGASLLRLHF 63

Query: 766 HDCFV 780
HDCFV
Sbjct: 64 HDCFV 68

>gb|ABR18139.1| unknown [Picea sitchensis]
Length = 327

Score = 167 bits (423), Expect = 6e-39
Identities = 83/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR RIYNE+NI FA R+ +CP T G DNNLAPLDL TPT+FDN Y+ NL
Sbjct: 206 QARCTNFRNRIYNESNIALLFAGLRKANCPVTGG--DNNLAPLDLFTPTAFDINSYNNLQ 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ GLLHSDQQLF GGSTD+ V Y+ +P F +DFAAAM+KMG+I PLT +NGEIRKNC

Sbjct: 264 FQNGLLHSDQQLFKGGSTDNRVSFYAVHPDAFFNDFAAAMVKMGNIKPLTVNNGEIRKNC 323

Query: 2167 RRIN 2178
R+IN

Sbjct: 324 RKIN 327

Score = 162 bits (410), Expect = 2e-37
Identities = 91/169 (53%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEK ANPN NS RGF+VID IK+ VE C GVVSCADI+AIAA
Sbjct: 79 VNGCDGSILLDDTSTFTGEKTANPNNSVRGFDVIDTIKTQVEATCSGVVSCADIVAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 139 RDSV-----VQLGGPTWTVM LG 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ +AS+SAANN IP PTSNL+ LIS F A GL+T+D+VALSG+ I
Sbjct: 156 RRDSTSASKSAANNNIPPTSNSALISFFQAQGLTTEDMVALSGSHTI 204

Score = 76.3 bits (186), Expect = 2e-11
Identities = 39/78 (50%), Positives = 52/78 (66%), Gaps = 4/78 (5%)
Frame = +1

Query: 562 KLTMAFCS---RLTICLALFVLIWG-SANAQLSTNFYYHSCP NFLSSVKSTVQSAISKE 729
++ MA F + R+ +C++L V++ S QL +FY SCPN+ S V S V A++KE
Sbjct: 3 RIVMAFFSTMGIRIACISLLVIVCSTSVYGGQLCPDFYDKSCP NVLSIVNSVVMQAVAKE 62

Query: 730 TRMGASLLRLFFHDCFVN 783
RMGASLLRL FHDCFVN
Sbjct: 63 KRMGASLLRLHFHDCFVN 80

>sp|A2YPX3.2|PER2_ORYSI RecName: Full=Peroxidase 2; Flags: Precursor
gb|AAC49821.1| peroxidase [Oryza sativa Indica Group]
gb|EEC82682.1| hypothetical protein OsI_27327 [Oryza sativa Indica Group]
Length = 314

Score = 167 bits (422), Expect = 8e-39
Identities = 75/124 (60%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QA+C NFR R+YNETNI+++FA + +CPR +GSGD+NLAPLD TP +FD+ Y+ NL+
Sbjct: 191 QAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAFDSAYYTNLL 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGSTD+ VR +S+N F+S F AM+KMG+ISPLTG+ G+IR NC

Sbjct: 251 SNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTVAMVKGNISPLTGTQGQIRLNC 310

Query: 2167 RRIN 2178

++N

Sbjct: 311 SKVN 314

Score = 121 bits (303), Expect = 5e-25
Identities = 72/169 (42%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF V+DNIK+ VE +C VSCADILA+AA

Sbjct: 69 VQGCDAVLLSGQ-----EQNAGPNAGSLRGFNVDNIKTQVEAICSQTVSCADILAVAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 124 RDSV-----VALGGPSWTVLLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TA++S AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 141 RRDSTTANESQANTDLPAPSSSLAELIGNFSRKGLDVTDMVALSGAHTI 189

Score = 70.5 bits (171), Expect = 1e-09
Identities = 36/70 (51%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S +++ L + + +A+AQLS FY SCPN S++KS V +A++ E RMGASL

Sbjct: 1 MAS-ASSVSLMLLVAAAMASAASAQLSATFYDTSCPNALSTIKSAVTA AVNSEPRMGASL 59

Query: 751 LRLFFHDCFV 780

+RL FHDCFV

Sbjct: 60 VRLHFHDCFV 69

>ref|XP_002461208.1| hypothetical protein SORBIDRAFT_02g042850 [Sorghum bicolor]
gb|EER97729.1| hypothetical protein SORBIDRAFT_02g042850 [Sorghum bicolor]
Length = 319

Score = 166 bits (421), Expect = 1e-38

Identities = 76/124 (61%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR IYN+TNI +AFA + + +CPR++GSGD NLAPLD TP FDN Y+ NL+

Sbjct: 196 QAQCQFFRDHIYNDTNINSAFATSLKANCPRSTGSGDGNLAPLDTTPYKFDNAYYSNLL 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGBISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++N FSS FAAAM+KMG++SPLTGS G+IR C

Sbjct: 256 NQKGLLHSDQELFNGGSTDNTVRNFASNSAAFSSAFAAAMVKMGNLSPLTGSQGQIRLTC 315

Query: 2167 RRIN 2178

++N

Sbjct: 316 SKVN 319

Score = 118 bits (296), Expect = 3e-24
Identities = 71/171 (41%), Positives = 89/171 (52%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD S+LL D ++ FTGE+ A PN S RGF+VI NIK+ VE +C VSCADILA+

Sbjct: 67 VQGCDA SVLLADNAATGFTGEQGALPNAGSLRGFDVIANIKTQVEAICKQTVSCADILAV 126

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDSV + LGGP+W V

Sbjct: 127 AARDSV-----VALGGPSWTVP 143

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

LGRRD+ TAS S AN+ +P P+ NL QLI F G + ++ LSG I

Sbjct: 144 LGRRDSTTASLSANSDLPSPFNLEQLIKAFGNKGFTATEMATLSGAHTI 194

Score = 74.7 bits (182), Expect = 6e-11
Identities = 36/59 (61%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

L LF+ + A+AQLS FY SCPN S++KS V +A+ KE RMGASLLRL FHDCFV

Sbjct: 9 LLLFLCLAAVASAQLSPTFYDTSCPNALSTIKSAVNAAVQKENRMGASLLRLHFHDCFV 67

>ref|XP_002320417.1| predicted protein [Populus trichocarpa]
gb|EEE98732.1| predicted protein [Populus trichocarpa]
Length = 316

Score = 166 bits (421), Expect = 1e-38

Identities = 82/123 (66%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT FR RIYN+TNI+ +FA TR+ SCP + GD LAPLD T T FDN Y+ NLV

Sbjct: 197 ARCTTFRNRIYNDTNIDASFATRRASCP--ASGGDATLAPLD-GTQTRFDNYYTNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YSTN TF+ DFAAAM+KMG+ISPLTG NGEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSTNGATFARDFAAAMVKMGNISPLTGRNGEIRRNCR 313

Query: 2170 RIN 2178
+N

Sbjct: 314 VVN 316

Score = 157 bits (396), Expect = 9e-36
Identities = 89/165 (53%), Positives = 100/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDT++FTGEKNANPNRNSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDGSILLDDTATFTGEKNANPNRNSARGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + GGP+W V LG

Sbjct: 129 RDGVVL-----RGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAAN+ IP+P S+L LIS FSA GLS D+ ALSG

Sbjct: 146 RRDARTASQSAANSQIPSPASSLATLISMFSAKGLSAGDMTALSG 190

Score = 62.8 bits (151), Expect = 2e-07
Identities = 32/78 (41%), Positives = 45/78 (57%)
Frame = +1

Query: 550 VCLSKLTMASFC SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKE 729
+C+ L +SFCS AQLS FY +CPNL + V++ + A++ +

Sbjct: 10 LCVVPLLASSFCS-----AQLSATFYASTCPNLQTIVRNAMTGAVNGQ 52

Query: 730 TRMGASLLRLFFHDCFVN 783
R+ AS+LRLFFHDCFVN

Sbjct: 53 PRLAASILRLFFHDCFVN 70

>ref|NP_001130666.1| hypothetical protein LOC100191769 [Zea mays]

gb|ACF78975.1| unknown [Zea mays]
Length = 324

Score = 166 bits (421), Expect = 1e-38
Identities = 77/123 (62%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFRA IYN+T+I+ AFA RQ++CP G+GD++LAPLD+QT FDN Y++NL+
Sbjct: 200 SQCQNFRAHIYNDTDIDPAFASLRQRTCPAAPGTGDSSLAPLDVQTQLVFDNAYYRNLLA 259

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLL SDQ LFNGGS D++VR YS NP F+SDFA AMIKMG+ISPLTG+ G+IR NCR
Sbjct: 260 KRGLLRSDQALFNGGSQDALVRQYSANPALFASDFANAMIKMGNISPLTGTAGQIRANCR 319

Query: 2170 RIN 2178
+N
Sbjct: 320 VVN 322

Score = 134 bits (338), Expect = 5e-29
Identities = 77/169 (45%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLDD SF GEK A PN NS RGF+VID IK+ VE +CPGVVSCADI+A+AA
Sbjct: 72 VQGCDGSILLDDVGSFVGEKGAGPNVNSLRGFDVIDQIKANVELICPGVVSCADIVALAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + LGGP+W V LG
Sbjct: 132 RDGTFL-----LGGPSWAVPLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P+P S L L++ F GL DL ALSG I
Sbjct: 149 RRDSTTASLALANS DLPSPVSGLAALLA AFGNKGLGPGDLTALSGAHTI 197

Score = 63.9 bits (154), Expect = 1e-07
Identities = 36/72 (50%), Positives = 48/72 (66%), Gaps = 2/72 (2%)
Frame = +1

Query: 571 MASFCSRLTICLA--LFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
MASF + LA LF+L + QLS++FY +CP L V++T+ +A+ E RMGA
Sbjct: 1 MASFRTSWHCLLAACLFLLASAAHQQLSSSFYAATCPTLELIVRTTMTLALLAERRMGA 60

Query: 745 SLLRLFFHDCFV 780
SL+RLFFHDCFV

Sbjct: 61 SLVRLFFHDCFV 72

>ref|NP_200648.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9LV1.1|PER68_ARATH RecName: Full=Peroxidase 68; Short=Atperox P68; Flags: Precursor
dbj|BAA96931.1| peroxidase [Arabidopsis thaliana]
dbj|BAC42892.1| putative peroxidase [Arabidopsis thaliana]
gb|AAP40354.1| putative peroxidase [Arabidopsis thaliana]
Length = 325

Score = 166 bits (421), Expect = 1e-38
Identities = 82/124 (66%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARC FR+RIYN TNI+ +FA +R++SCP +GSGDNN A LDL+TP FD YF LV
Sbjct: 202 QARCVTFRSRIYNSTNIDLSFALSRRRSCPAATGSGDNNAILDLRTPEKFDGSYFMQLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
+GLL SDQ LFNGGSTDSIV YS + F DF AAMIKMGDISPLTGSNG+IR++C
Sbjct: 262 NHRGLTSDQVLFGNGGSTDSIVVSYSRSVQAFYRDFVAAMIKMGDISPLTGSNGQIRRSC 321

Query: 2167 RRIN 2178
RR N
Sbjct: 322 RRPN 325

Score = 144 bits (362), Expect = 7e-32
Identities = 85/170 (50%), Positives = 99/170 (58%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILATAA 1330
+ GCD SILLDDT SF GEK A PN NS RG+EVID IKS VE++CPGVVSCADILAI A
Sbjct: 74 VNGCDASILLDDTRSFLGEKTAGPNNSVRYEVIDAIKSRVERLCPGVVSCADILAITA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + +GG W+VKLG
Sbjct: 134 RDSVLL-----MGGRGWSVKLG 150

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+G+ P PTS L+ LI+ F A GLS +D+VALSG I
Sbjct: 151 RRDSITASFSTANSGLVPPPTSTLDNLINLFRANGLSPRDMVALSGAHTI 200

Score = 73.2 bits (178), Expect = 2e-10
Identities = 36/66 (54%), Positives = 47/66 (71%), Gaps = 1/66 (1%)
Frame = +1

Query: 589 RLTICLALFVLIWGS-ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFF 765
R + LF+++ GS A AQL T+FY SCP+L +V+ VQ ++KE R+ ASLLRLFF
Sbjct: 10 RAAFVLLFIVMLGSQAQAQLRTDFYSDSCPSLLPTVRRVVQREVAKERRIAASLLRLFF 69

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 70 HDCFVN 75

>ref|XP_002338628.1| predicted protein [Populus trichocarpa]
gb|EEF10179.1| predicted protein [Populus trichocarpa]
Length = 183

Score = 166 bits (420), Expect = 1e-38
Identities = 83/124 (66%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR G NLAPLDL TP SFDN YFKNL+
Sbjct: 62 QAQCFTFRDRIYNASNIDAGFASTRKRRCPRAGGQA--NLAPLDLVTPNSFDNYYFKNLM 119

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLL SDQ LFNGGSTDSIV YS NP FSSDFA+AMIKMGDI PLTGS G+IR+ C
Sbjct: 120 RNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPKFSSDFASAMIKMGDIRPLTGSAGQIRRIC 179

Query: 2167 RRIN 2178
+N
Sbjct: 180 SAVN 183

Score = 65.5 bits (158), Expect = 3e-08
Identities = 31/57 (54%), Positives = 43/57 (75%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
+GGP+W VK GRRD+ TAS++ AN +PA L++LISRF GL+ +D+VALSG+
Sbjct: 1 VGGPSWAVKFGRRDSTASRTLANAELPAFFDRLDRLISRFAQKGLTARDMVALSGS 57

>ref|XP_002336344.1| predicted protein [Populus trichocarpa]
gb|EEE73229.1| predicted protein [Populus trichocarpa]
Length = 316

Score = 166 bits (420), Expect = 1e-38
Identities = 83/124 (66%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR G NLAPLDL TP SFDN YFKNL+
Sbjct: 195 QAQCFTFRDRIYNASNIDAGFASTRKRRCPRAGGQA--NLAPLDLVTPNSFDNYYFKNLM 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLL SDQ LFNGGSTDSIV YS NP FSSDFA+AMIKMGDI PLTGS G+IR+ C
Sbjct: 253 RNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPKFSDFASAMIKMGDIRPLTGSAGQIRRIC 312

Query: 2167 RRIN 2178
+N
Sbjct: 313 SAVN 316

Score = 135 bits (339), Expect = 3e-29
Identities = 76/166 (45%), Positives = 97/166 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLD+TSS EK A N+NSARG+EVID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 68 VQGCDASILLDETSSIKSEKTAGANKNSARGYEVIDKAKAEVEKICPGVVSCADIIAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP+W VKLG
Sbjct: 128 RDA-----SAYVGGPSWAVKLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS + A +PA + +L +LISRF GL+ +D+VALSG+
Sbjct: 145 RRDSTTASPTLAITELPAFSDDLGRLISRFQQKGLTARDMVALSGS 190

Score = 63.5 bits (153), Expect = 1e-07
Identities = 26/50 (52%), Positives = 40/50 (80%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+ A+LS+ FY+ SCPN S++++ ++AI++E RM ASL+RL FHDCFV
Sbjct: 19 ACQAKLSSTFYHKSCPNAESAIRTAIRTAIRERRMAASLIRLHFHDCFV 68

>emb|CAA71493.1| peroxidase [Spinacia oleracea]
Length = 309

Score = 166 bits (420), Expect = 1e-38
Identities = 76/123 (61%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARC +FR IYN+T+I+ F TR+ +CP ++ +G+ NLAPLDLQ+PT FDN Y+KNL+
Sbjct: 187 ARCVSFRHHIYNDTDIDANFEATRKNVNCPLSNNTGNTNLAPLDLQSPTKFDNSYYKNLIA 246

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+L+NGGS D++V YS + F+ DF AA+IKMG+ISPLTGS+GEIRKNCR

Sbjct: 247 KRGLLHSDQELYNGGSQDALVTRYSKSNAFAKDFVAAIIKMGNISPLTGSSGEIRKNCR 306

Query: 2170 RIN 2178

IN

Sbjct: 307 FIN 309

Score = 131 bits (329), Expect = 5e-28

Identities = 79/170 (46%), Positives = 95/170 (55%), Gaps = 1/170 (0%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S+LLDDTS+FTGEK A NRN S RGFEVID+IK+ VE C VSCADILA+A

Sbjct: 58 VNGCDASLLDDTSTFTGEKTAISNRNNSVRGFEVIDSIKTNVEASCKATVSCADILALA 117

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V + LGGP+W V L

Sbjct: 118 ARDGVFL-----LGGPSWKVPL 134

Query: 1508 GRRDARTASQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

GRRDARTAS +AA N +P +S+L+ L + F+ GLS KD+ ALSG I

Sbjct: 135 GRRDARTASLTAAATNNLPPASSSLSNLTTLFNNKGLSPKDMTALSGAHTI 184

Score = 70.9 bits (172), Expect = 8e-10

Identities = 32/50 (64%), Positives = 39/50 (78%)

Frame = +1

Query: 634 ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFVN 783

+NAQLS+ Y SCPNL V+ T++ A+ KE RMGAS+LRLFFHDCFVN

Sbjct: 10 SNAQLSSKHYASSCPNLEKIVRKT MKQAVQKEQRMGASILR LFFHDCFVN 59

>gb|AA53172.1| peroxidase [Populus alba x Populus tremula var. glandulosa]

Length = 316

Score = 166 bits (420), Expect = 1e-38

Identities = 81/123 (65%), Positives = 99/123 (80%)

Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT FR RIYN+TNI+ +FA TR+ SCP + GD LAPLD T T FDN Y+ NLV

Sbjct: 197 ARCTTFRNRIYNDTNIDASFATRRASCP--ASGGDATLAPLD-GTQTRFDNNYYTNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YSTN TF+ DFAAAM++MG+ISPLTG+NGEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSTNGATFARDFAAAMVRMGNISPLTGTNGEIRRNCR 313

Query: 2170 RIN 2178

+N

Sbjct: 314 VVN 316

Score = 159 bits (402), Expect = 2e-36
Identities = 90/165 (54%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDT++FTGEKNANPNRNSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDGSILLDDTATFTGEKNANPNRNSARGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG

Sbjct: 129 RDGVVL-----LGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645

RRDARTASQSAAN+ IP+P S+L LIS FSA GLS D+ ALSG

Sbjct: 146 RRDARTASQSAANSQIPSPASSLATLISMFSAGLSAGDMTALSG 190

Score = 63.2 bits (152), Expect = 2e-07
Identities = 32/78 (41%), Positives = 45/78 (57%)
Frame = +1

Query: 550 VCLSKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKE 729
+C+ L +SFCS AQLS FY +CPNL + V++ + A++ +

Sbjct: 10 LCIVPLLASSFCS-----AQLSATFYASTCPNLQTIVRNAMTGAVNGQ 52

Query: 730 TRMGASLLRLFFHDCFVN 783

R+ AS+LRLFFHDCFVN

Sbjct: 53 PRLAASILRLFFHDCFVN 70

>ref|XP_002509738.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]

gb|EEF51125.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]

Length = 320

Score = 166 bits (419), Expect = 2e-38
Identities = 80/125 (64%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ CP SGSGD+NLAPLDL TP FDN YF+NL
Sbjct: 196 QAQCVTFRGRIYNNASDIDAGFAATTRSQCPAASGSGDSNLAPLDLVTNIFDNNYFRNL 255

Query: 1984 VQKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GG+TDSIV YS + FSSDFA+AM+KMG+ISPLTGS G+IR+
Sbjct: 256 IQKKGLLQSDQVLFSGGATDSIVNQYSRDSSVFSSDFASAMVKMGNISPLTGSQQGIRRV 315

Query: 2164 CRRIN 2178
C +N
Sbjct: 316 CNVVN 320

Score = 137 bits (346), Expect = 5e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AA 1330
+QGCDGSILLDDT + TGEK A N NS RGF+VIDNIKS +E CPG+VSCADI+A+AA
Sbjct: 69 VQGCDGSILLDDTPTMTGEKTARNNANSVRGFDVIDNIKSQLESRCPGIVSCADIVAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GP+W+V LG
Sbjct: 129 RDA-----SVAASGPSWSVNLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ +PA T +L++L S F + GLS +D+VALSG I
Sbjct: 146 RRDSTTASRLADSNLPAFTDSLRLTSLFGSKGLSQRDMVALSGAHTI 194

Score = 70.1 bits (170), Expect = 1e-09
Identities = 32/67 (47%), Positives = 49/67 (73%), Gaps = 2/67 (2%)
Frame = +1

Query: 586 SRLTICLALFVLIWGS--ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
SRL++ + ++I+ S AQLS+NFY ++CP+ S++K + +A+S+E RM ASL+RL
Sbjct: 3 SRLSLLCMVLMIFSSLPCKAQLSSNFYDNTCPSALSTIKGAISTAVSREQRMAASLIRL 62

Query: 760 FFHDCFV 780
FHDCFV
Sbjct: 63 HFHDCFV 69

>ref|XP_002453592.1| hypothetical protein SORBIDRAFT_04g008630 [Sorghum bicolor]
gb|EES06568.1| hypothetical protein SORBIDRAFT_04g008630 [Sorghum bicolor]
Length = 321

Score = 165 bits (418), Expect = 2e-38
Identities = 76/123 (61%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A C +FR IYN+TN++ AFA RQ++CP SGSGD NLAPLD+QT FDN Y++NL+
Sbjct: 197 AECEDFRGHIYNDTNVDPFAALRQRNCPAESGSGDTNLAPLDVQTRYVFDNAYYRNLMV 256

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YST+PG F+S F AAMIKMG+I LTGS G+IR +CR
Sbjct: 257 RQGLLHSDQELFNGGSQDALVQQYSTDPGLFASHFVAAMIKMGNIGTLTGSQGGIRADCR 316

Query: 2170 RIN 2178
+N
Sbjct: 317 VVN 319

Score = 135 bits (339), Expect = 3e-29
Identities = 81/169 (47%), Positives = 92/169 (54%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGSILLDD SF GEK A PN S RG+EVID IK+ VE VCPGVVSCADI+A+AARD
Sbjct: 72 GCDGSILLDDAGSFVGEKTALPNA-SIRGYEVIDQIKANVEAVCPGVVSCADIVALAARD 130

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
++ GGPTW V LGRR
Sbjct: 131 GTVLL-----GGPTWAVPLGRR 147

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHISH 1663
D+ TAS S AN+ IPAPT NL+ LI F GLS D+ ALSG I +
Sbjct: 148 DSTTASLSQANS DIPAPTLNLDLILAFGKKGLSPADMTALSGAHTIGY 196

Score = 60.8 bits (146), Expect = 8e-07
Identities = 34/70 (48%), Positives = 40/70 (57%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MA L CL L + QL+ FY SCP L V++T+ AI + RMGASL
Sbjct: 1 MACSFRALLHCLLALSLCSTAYGGQLTPTFYALSCP ALEPIVRTTMTKAI INDRRMGASL 60

Query: 751 LRLFFHDCFV 780

LRLFFHDCFV
Sbjct: 61 LRLFFHDCFV 70

>gb|ACN60163.1| class III peroxidase [Tamarix hispida]
Length = 320

Score = 164 bits (415), Expect = 5e-38
Identities = 77/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI ++FA++ Q +CP T G DNNL+PLD +PT+FD Y+ +L+
Sbjct: 199 QARCTSFARIYNETNINSSFAKSLQANCPSTGG--DNNLSPLDTSSPTTFDVGYYTDLI 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQL+NGGSTDS V YS++ TF +DF +MI MG+ISPLTGS G++R NC
Sbjct: 257 GQKGLLHSDQQLYNGGSTDSQVTSYSSSSSTFLTDFGTSMINMGNISPLTGSRGQVRTNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKTN 320

Score = 125 bits (313), Expect = 4e-26
Identities = 78/170 (45%), Positives = 89/170 (52%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGS-ILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S + K A PN S RGF+V+D IKS VE VCPGVV CADILA+A
Sbjct: 71 VNGCDASGSIRRHCQLHRKRKTAQPNNGSLRGFDVVDTIKSKVESVCPGVPCADILAVA 130

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGG +W V L
Sbjct: 131 ARDSV-----VALGGKSWGVL 147

Query: 1508 GRRDARTASQAANN GIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS SAAN GIPAPT NL+ LI+ FS +GLSTKDLV LSG I
Sbjct: 148 GRRDSTTASLSAANTGIPAPTLNLSGLITSFSNVGLSTKDLVVLGAHTI 197

>ref|XP_002450134.1| hypothetical protein SORBIDRAFT_05g001030 [Sorghum bicolor]
gb|EES09122.1| hypothetical protein SORBIDRAFT_05g001030 [Sorghum bicolor]
Length = 317

Score = 163 bits (413), Expect = 9e-38
Identities = 76/124 (61%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+E NI+T+ A + + +CP +G DNN++PLD TP FDN+Y+KNL+
Sbjct: 196 QARCVNFRDRIYSEANIDTSLATSLKNCNPKTG--DNNISPLDASTPYVFDNFYKNNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N F +DF+ AM+KM +ISPLTGS+G+IRKNC
Sbjct: 254 NKKGVLHSDQQLFNGGSADSQTTTYSSNMAKFFTFSTAMLKMSNISPLTGSSGQIRKNC 313

Query: 2167 RRIN 2178
RR+N
Sbjct: 314 RRVN 317

Score = 147 bits (370), Expect = 9e-33
Identities = 81/165 (49%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VID+IK+ +E++CP VVSCADI+A+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAVPNNNSLRGFDVIDSIKAQLERICPVVSCADIVAA 128

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 129 RDSV-----VALGGPTWAVNLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS AANN IPAPT +L L FS GLS D++ALSG
Sbjct: 146 RRDSL TASLDAANNDIPAPTLDLTLTKSFSNKGLSASDMIALSG 190

Score = 68.9 bits (167), Expect = 3e-09
Identities = 36/71 (50%), Positives = 47/71 (66%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS LALF ++QL+ NFY SCPN ++++ V+SA+++E RMGASL
Sbjct: 1 MASHKPLTCSVLALFFAA-SLVSSQLNANFYDKSCPNAlyTIQTAVRSAVARENRMGASL 59

Query: 751 LRLFFHDCFVN 783
LRL FHDCFVN
Sbjct: 60 LRLHFHDCFVN 70

>gb|AAC05277.1| peroxidase FLXPER4 [Linum usitatissimum]
Length = 305

Score = 163 bits (413), Expect = 9e-38
Identities = 81/124 (65%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYN+TNI+ AFA TR+ +CP+ +G+G N LAPLD TPT FDN Y+++LV
Sbjct: 185 QARCTTFRQRIYNDTNIDPAFATTRRGNC PQ-AGAGAN-LAPLD-GTPTQFDNRYQQDLV 241

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGNGEIRKNC 2166
++GLLHSDQ+LFN G+ D++VR YS N TF++DFAAAM++MG+ISPLTG+NGEIR NC
Sbjct: 242 ARRGLLHSDQELFNNGTQDALVRTYSNNAATFATDFAAAMVRMGNISPLTGNGEIRFNC 301

Query: 2167 RRIN 2178
RR N
Sbjct: 302 RRPN 305

Score = 144 bits (362), Expect = 7e-32
Identities = 80/169 (47%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AA 1330
+ GCDGS+LLDDT++FTGEKNA PN+NS RGF++ID IK+ VE C VSCADILA+AA
Sbjct: 58 VNGCDGSLLDDTATFTGEKNAGPNQNSVRGFDI IDTIKTRVEAACNATVSCADILALAA 117

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V +V GGPTW V LG
Sbjct: 118 RDGVVLV-----GGPTWTVP LG 134

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAAN IPAP S+L + + F+ GL+ +D+ LSG I
Sbjct: 135 RRDARTASQSAANAQIPAPGSSLGTITNLFTNKGLTARDVTILSGAHTI 183

Score = 65.1 bits (157), Expect = 4e-08
Identities = 29/55 (52%), Positives = 39/55 (70%)
Frame = +1

Query: 619 LIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
L+ S +AQL+ NFY SCP L + V++ + A++ E RM AS+LRL FHDCFVN
Sbjct: 5 LLASSGSAQLAANFYATSCPTLLTIVRNAMTQAVNSENMAASILRLHFHDCFVN 59

>ref|XP_002269343.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 163 bits (412), Expect = 1e-37

Identities = 81/125 (64%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP +G+GD+NLAPL+L TP SFDN YFKNL

Sbjct: 207 QARCVTFRDRIYDNGTDIDAGFASTRRRRC PANNGGDDNLAPLELVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQ LF+GGSTD+IV YS +P TF SDFA+AM+KMGDI LTGS G IRK

Sbjct: 267 IRRKGLLQSDQVLFSGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEALTGSAGVIRKF 326

Query: 2164 CRRIN 2178

C IN

Sbjct: 327 CNVIN 331

Score = 132 bits (332), Expect = 2e-28
Identities = 76/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA

Sbjct: 80 VQGC DASILLDDSSSIQSEKNAPNNLNSVRGYEVIDNIKSKVESLCPGVVSCADIVAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VS GPTW V+LG

Sbjct: 140 RDASVAVS-----GPTWTVRLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I

Sbjct: 157 RRDSTTSGLSQAATNLPSFRDSLDKLVSLFGSKGLSARDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 1e-07
Identities = 31/69 (44%), Positives = 46/69 (66%), Gaps = 1/69 (1%)
Frame = +1

Query: 577 SFC SRLTICLALFVLIWGS-ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753

S S I LA+F+++ A LS FY H+CP +++++ V++A+S+E RM ASL+

Sbjct: 12 SCISPACIFLAVFLILSNMPCEAHLSPTFYDHTCPRALTTIQTAVRTAVSRERRMAASLI 71

Query: 754 RLFFHDCFV 780

RL FHDCFV

Sbjct: 72 RLHFHDCFV 80

>gb|EAY85148.1| hypothetical protein OsI_06503 [Oryza sativa Indica Group]

Length = 323

Score = 163 bits (412), Expect = 1e-37
Identities = 74/123 (60%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFR RIYN+TNI+ AFA R+ CP GSGD +LAPLD T FDN Y++NL+
Sbjct: 199 SQCANFRDRIYNDTNIDPAFAALRRGGCPAAPGSGDTS LAPLDALTQNVFDNAYYRNLLA 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I+PLTG+ G+IR++CR
Sbjct: 259 QRGLLHSDQVLFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNINPLTGAAGQIRRSCR 318

Query: 2170 RIN 2178
+N
Sbjct: 319 AVN 321

Score = 139 bits (349), Expect = 2e-30
Identities = 80/171 (46%), Positives = 99/171 (57%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 69 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRRVELLCPGVVSCADIVAL 128

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 129 AARDSTAL-----LGGPSWEVP 145

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS SAAN+ +PAP+S+L L++RF + GLS +D+ ALSG I
Sbjct: 146 LGRRDSTTASLSAANSDLAPSSDLATLVARFGSKGLSPRDMTALSGAHTI 196

Score = 69.7 bits (169), Expect = 2e-09
Identities = 35/60 (58%), Positives = 41/60 (68%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
CL F L+ +A QLST FY SCP L V++TV S + E RMGASL+RLFFHDCFV
Sbjct: 10 CLLAFFLLSSAACGQLSTTFYAASCPTQLLVVRATVLSTLLAERRMGASLRLFFHDCFV 69

>ref|XP_002269301.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 213

Score = 162 bits (411), Expect = 2e-37
Identities = 81/124 (65%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q RC FR RIYN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+
Sbjct: 90 QGRCVTFRDRIYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 149

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTDSIV YS +P TF SDFA+AM+KMGI PLT S G IRK
Sbjct: 150 QRKGLLQSDQVLFSGGSTDSIVNEYSKSPKTFRSDFASAMLKMGDIEPLTRSAGVIRKIFY 209

Query: 2167 RRIN 2178
IN
Sbjct: 210 NVIN 213

Score = 62.0 bits (149), Expect = 4e-07
Identities = 30/60 (50%), Positives = 42/60 (70%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
+ GPTW VKLGRRD+ T+ S A +P+ +L++LIS F + GLS +D+VALSG+ I
Sbjct: 29 VSGPTWTVKLGRRDSTTSGLSLAATNLPSPFRDSLDKLISLFGSKGLSARDMVALSGSHTI 88

>gb|AAD37428.1|AF149278_1 peroxidase 3 precursor [Phaseolus vulgaris]
Length = 324

Score = 162 bits (411), Expect = 2e-37
Identities = 78/126 (61%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG--DNNLAPLDLQTPTSFDNYYFKN 1980
+ARC + +RIYNE NIE+ FA+ RQ++CPR S DNN+APL+ +TP FDN Y+KN
Sbjct: 199 KARCAVYGSRIYNEKNIESLFAKARQKNCPRNSNGTPKDNNVAPLEFKTPNHFDNYYKN 258

Query: 1981 LVQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ KKGLLHSDQ LF+GGSTDS+VR YS + F SDF AMIKMG+I PLTGSNG+IR+
Sbjct: 259 LINKKGLLHSDQVLFDDGGSTDSLVRAYSNDQRAFESDFVTAMIKMGNIKPLTGSNGQIRR 318

Query: 2161 NCRRIN 2178
C R N
Sbjct: 319 LCGRPN 324

Score = 126 bits (317), Expect = 1e-26
Identities = 79/170 (46%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLD SS EK A PN S RG+EVID IKS VE +CPG+VSCADI+AIAA
Sbjct: 74 VNGCDGSVLLDGPSS---EKTAPPNDKSLRGYEVIDAIKSKVEALCPGIVSCADIVAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W VKLG
Sbjct: 131 RDSVNI-----LGGPFWKVKLG 147

Query: 1511 RRDARTA-SQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T Q A++ +P+P S+L+ LIS F GLS KD+VALSG I
Sbjct: 148 RRDSTGFFQLASSGALPSPASSLDTLISSFKDQGLSAKDMVALSGAHTI 197

Score = 83.6 bits (205), Expect = 1e-13
Identities = 42/67 (62%), Positives = 50/67 (74%), Gaps = 1/67 (1%)
Frame = +1

Query: 586 SRLTICLALFVL-IWGSANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLF 762
S T +A F L + GS++AQLS NFY CP + +VKS VQSA++KE RMGASLLRLF
Sbjct: 9 STTTFAIAFFTLFLIGSSSAQLSENFYAKKCPKVLVAVKSVVQSAVAKEPRMGASLLRLF 68

Query: 763 FHDCFVN 783
FHDCFVN
Sbjct: 69 FHDCFVN 75

>ref|XP_002334243.1| predicted protein [Populus trichocarpa]
gb|EEF07510.1| predicted protein [Populus trichocarpa]
Length = 317

Score = 162 bits (410), Expect = 2e-37
Identities = 80/124 (64%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RI+++ NI+ FA TR++ CP D+ LAPLDL TP SFDN YFKNL+
Sbjct: 196 QAQCFTFRDRIHSDNNIDAGFASTRKRCPLVGS--DSTLAPLDLVTPNSFDNYYFKNLM 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKGLL SDQ+LF+GGSTDSIV YS NP FSSDFA+AMIKMGDISPLTG+ G+IR+ C
Sbjct: 254 QKKGLLQSDQELFSGGSTDSIVSEYSRNPAKFSSDFASAMIKMGDISPLTGTAGQIRRIC 313

Query: 2167 RRIN 2178
+N

Sbjct: 314 SAVN 317

Score = 133 bits (335), Expect = 1e-28
Identities = 76/166 (45%), Positives = 95/166 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+TSS EK A N NS RG+EVID KS VEK+CPGVVSCADI+A+AA
Sbjct: 69 VQGCDASILLDETSSIQSEKTAGGNNSVRGYEVIDKAKSKVEKICPGVVSCADIIAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP+W VKLG
Sbjct: 129 RDA-----SAYVGGPSWAVKLG 145

Query: 1511 RRDARTASQSAANN GIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS + A +PA + +L +LISRF GL+ +D+VALSG+
Sbjct: 146 RRDSTTASPTLAITELPAFSDDLGR LISR FQQKGLTARDMVALSGS 191

Score = 62.0 bits (149), Expect = 4e-07
Identities = 28/57 (49%), Positives = 42/57 (73%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
LF+L + A+LS+ FY SCP S++++ ++AI++E RM ASL+RL FHDCFV
Sbjct: 13 LFLSTTACQAKLSSAFYDKSCPKAESAIRTAIRTAIARERRMAASLIRLHFHDCFV 69

>ref|XP_002438530.1| hypothetical protein SORBIDRAFT_10g021630 [Sorghum bicolor]
gb|EER89897.1| hypothetical protein SORBIDRAFT_10g021630 [Sorghum bicolor]
Length = 329

Score = 162 bits (409), Expect = 3e-37
Identities = 73/126 (57%), Positives = 100/126 (79%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS--GSGDNNLAPLDLQTPTSFDNYYFKN 1980
QARCT FR+RIY +TNI FA RQQ+CP+ S G+GD LAP+D++TP +FDN Y++N
Sbjct: 204 QARCTTFRSRIYGD TNINATFASLRQQTCPQASDGGAGDAALAPIDVRTPEAFDNAYYQN 263

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ ++GL HSDQ+LFNGGS D++V+ YS N F++DFA AM++MG ISPLTG+ GE+R
Sbjct: 264 LMARQGLFHSDQQLFNGGSQDALVKKYSGNAAMFAADFAKAMVRMG AISPLTGTQGEVRL 323

Query: 2161 NCRRIN 2178
+CR++N

Sbjct: 324 DCRKVN 329

Score = 141 bits (356), Expect = 4e-31
Identities = 79/165 (47%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 77 VNGCDASILLDDTATFTGEKNAGPNANSVRGYEVIDAIKTQEASCNATVSCADILALAA 136

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW V LG
Sbjct: 137 RDAVNLL-----GGPTWTVYLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQS AN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 154 RRDARTASQSDANGNLPGPSLTLVTMFGNKGLSARDMTALSG 198

Score = 69.3 bits (168), Expect = 2e-09
Identities = 35/66 (53%), Positives = 48/66 (72%), Gaps = 2/66 (3%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQ--LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
LT+ L +L+ G+A A LST+FY CPN+ S V++ + SA++ E RMGAS+LR+FF
Sbjct: 13 LTVA AVL SLLMAGAAAAGGLSTSFYSKKCPNVQSIVRAGMASAVAAEKRMGASILRMFF 72

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 73 HDCFVN 78

>ref|XP_002281755.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 162 bits (409), Expect = 3e-37
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD+QT FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIQTMNKFDNYYQNLM 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR YS N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TQRGLLHSDQELFNGGSQDALVRTYSANNALFFGDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 RRIN 2178

R +N

Sbjct: 314 RVVN 317

Score = 152 bits (383), Expect = 3e-34

Identities = 85/169 (50%), Positives = 101/169 (59%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDASILDDTTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACKATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD V + LGGP+W V LG

Sbjct: 129 RDGVVL-----LGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ ALSG+ I

Sbjct: 146 RRDARTANQSAANNLPPFANLSALISGFAAKGLNADDMTALSGSHTI 194

Score = 70.9 bits (172), Expect = 8e-10

Identities = 37/71 (52%), Positives = 47/71 (66%)

Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750

MASF + + + VL S NAQLS NFY +CPN+ V+ + A+ +E RMGAS+

Sbjct: 1 MASFTNSFVFSIISVLAC-SINAQLSPNFYASTCPNVQKIVRVEMVQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783

LRLFFHDCFVN

Sbjct: 60 LRLFFHDCFVN 70

>ref|XP_002437128.1| hypothetical protein SORBIDRAFT_10g021610 [Sorghum bicolor]

gb|EER88495.1| hypothetical protein SORBIDRAFT_10g021610 [Sorghum bicolor]

Length = 314

Score = 161 bits (408), Expect = 3e-37

Identities = 76/125 (60%), Positives = 98/125 (78%), Gaps = 1/125 (0%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFART-RQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983

QARCT FR+RIY +TNI +FA RQQ+CP++ G G NLAP+D+QTPT FD Y+ NL

Sbjct: 191 QARCTTFRSRIYGDNTINASF AAALRQQTCPQSGGDG--NLAPMDVQTPTRFDTDYTNL 248

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GL HSDQ+LFNGGS D++VR YS NP F+SDF AAMIKMG++ LTG+ G+IR+N
Sbjct: 249 LSQRGLFHSDQELFNGGSQDALVRQYSANPSLFSDFMAAMIKMGNVGVLTGTAGQIRRN 308

Query: 2164 CRRIN 2178
CR +N
Sbjct: 309 CRVVN 313

Score = 134 bits (336), Expect = 8e-29
Identities = 80/169 (47%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCDGSILLD GEK A PN NSARGFEVID IK+ VE CPGVVSCADILA+AA
Sbjct: 68 VQGCDGSILLDAG----GEKTAGPNANSARGFEVIDTIKTNVEAACPGVVSCADILALAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD ++ G PTWNV LG
Sbjct: 124 RDGTNLLGG-----PTWNVPLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P T++L LIS FS GLS +D+ ALSG I
Sbjct: 141 RRDSTTASASLANSLPQSTASLGTLISLFSRQGLSARDMTALSGAHTI 189

Score = 71.6 bits (174), Expect = 5e-10
Identities = 36/60 (60%), Positives = 42/60 (70%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYYHSCP NLFS SVKSTVQSAISKETRMGASLLRLFFHDCFV 780
CL L+ A+ AQLST FY SCPNL S V+ + A+S + RMGASLLRLFFHDCFV
Sbjct: 9 CLVAISLLSCVAHAQLSTTFYASSCPNLQ SIVRRAMIQALSNDQRMGASLLRLFFHDCFV 68

>ref|XP_002517727.1| Cationic peroxidase 1 precursor, putative [Ricinus communis]
gb|EEF44659.1| Cationic peroxidase 1 precursor, putative [Ricinus communis]
Length = 264

Score = 160 bits (406), Expect = 6e-37
Identities = 79/124 (63%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YNETNI++A A + + CP T+GS D+NL+PLD +P FDN YFKNLV
Sbjct: 143 QARCLMFRGRLYNETNIDSALATSLKSDCP--TTGS--DDNLSPLDATSPVIFDNSYFKNLV 200

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLF+GGST+S V+ YST+P TF +DFA AMIKMG +SPLTG++G+IR +C
Sbjct: 201 NNKGLLHSDQQLFSGGSTNSQVKTYSTDPFTFYADFANAMIKMGKLSPLTGTGQIRTDC 260

Query: 2167 RRIN 2178
R++N
Sbjct: 261 RKNV 264

Score = 140 bits (354), Expect = 6e-31
Identities = 80/170 (47%), Positives = 98/170 (57%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTS-SFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+ GCD S+LLDD S SFTGEK A PN NS RGF+VID IKS VE +CPGVVSCADILA+A
Sbjct: 15 VNGCDASVLLDDISPSFTGEKTAGPNANSLRGFDVIDTIKSQVESICPGVVSCADILAVA 74

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 75 ARDSV-----VALGGPSWQVEL 91

Query: 1508 GRRDARTASQAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS AAN +P+P +L+ LIS S G + K++VAL+G+ I
Sbjct: 92 GRRDSTTASYDAANTDLPSPMLDSDLISALSRKGFTAKEMVALAGSHTI 141

>ref|NP_001057822.1| Os06g0547400 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54122.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69328.1| TPA: class III peroxidase 86 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF19736.1| Os06g0547400 [Oryza sativa Japonica Group]
gb|EEC80780.1| hypothetical protein OsI_23305 [Oryza sativa Indica Group]
gb|EEE65851.1| hypothetical protein OsJ_21628 [Oryza sativa Japonica Group]
Length = 324

Score = 160 bits (406), Expect = 6e-37
Identities = 74/124 (59%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSFGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR+RIY E NI +FA RQQ+CPR+ G D NLAP D+QTP +FDN Y++NLV
Sbjct: 203 RAQCQFFRSRIYTERNINASFASLRQQTCPRSSG--DANLAPFDVQTPDAFDNAYYQNLV 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D +VR YSTNP FSSDF +AM+KMG++ P +G+ E+R NC
Sbjct: 261 SQRGLLHSDQELFNGGSQDGLVRQYSTNPSQFSSDFVSAMVKGMLLPSSGTATEVRLNC 320

Query: 2167 RRIN 2178

R++N

Sbjct: 321 RKNV 324

Score = 149 bits (375), Expect = 2e-33

Identities = 84/169 (49%), Positives = 99/169 (58%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+ GCDGSILLDDTS+FTGEK+A PN NSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 76 VNGCDGSILLDDTSTFTGEKSAGPNANSARGFEVIDAIKTQVEASCKATVSCADILALAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD V ++ GGPTW+V LG

Sbjct: 136 RDGVNLL-----GGPTWSVALG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

R+D+RTASQSAAN+ +P P S+L LIS F GLS +D+ ALSG I

Sbjct: 153 RKDSRTASQSAANSNLPGPSSLATLISMFGNQGLSARDMTALSGAHTI 201

Score = 73.2 bits (178), Expect = 2e-10

Identities = 36/63 (57%), Positives = 47/63 (74%), Gaps = 1/63 (1%)

Frame = +1

Query: 598 ICLALFVLIWGSANAQ-LSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774

+ + + VL+ G+A AQ LS NFY +CPNL + V+S + SA+ E RMGAS+LRLFFHDC

Sbjct: 15 VAVVVAVLLGGAAEAQQLSPNFYSRTC PNLATIVRSGMASAVRTEPRMGASILRLFFHDC 74

Query: 775 FVN 783

FVN

Sbjct: 75 FVN 77

>ref|XP_002285724.1| PREDICTED: hypothetical protein [Vitis vinifera]

Length = 318

Score = 160 bits (405), Expect = 8e-37

Identities = 78/124 (62%), Positives = 99/124 (79%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L

Sbjct: 196 KARCTSFRNHIYNDTDIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLK 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+L+NGGSTDSIV YS N TF D A AM+KMG+ISPLTG+NG+IR NC
Sbjct: 253 EKKGLLHSDQELYNGGSTDSIVETYSINTATFFRDVANAMVKMGNISPLTGNGQIRTNC 312

Query: 2167 RRIN 2178
R++N
Sbjct: 313 RKNV 316

Score = 155 bits (391), Expect = 3e-35
Identities = 86/167 (51%), Positives = 100/167 (59%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 71 GCDASILLDDTATFTGEKTAGPNNNSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 130

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V+LGRR
Sbjct: 131 SV-----VALGGPTWTVRLGRR 147

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS SAA +P P NL+QLIS FS GL+TK++V LSGT I
Sbjct: 148 DSTTASFSAAARTDLPGNLNLSQLISAFSKKGLTTKEMVVLSTHTI 194

Score = 66.6 bits (161), Expect = 2e-08
Identities = 32/58 (55%), Positives = 41/58 (70%), Gaps = 1/58 (1%)
Frame = +1

Query: 610 LFVLIWGSANAQ-LSTNFYYHSCP NLFS SVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+F L+ G A+A LS NFY SCP ++++ V A++KE RMGASLLRL FHDCFV
Sbjct: 12 IFSLLGMAHAHYLSPNFYARSCPRLPTIRTAVNKAVAKEKRMGASLLRLHFHDCFV 69

>ref|XP_002521867.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF40503.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 326

Score = 160 bits (405), Expect = 8e-37
Identities = 83/125 (66%), Positives = 96/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQS CPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T I+ FA TR++SCP G D NLAPLDL TP SFDN YFKNL

Sbjct: 204 QAQCFTFRDRIYSNGTEIDAGFASTRKRSCPAVGG--DANLAPLDLVTPNSFDNNYFKNL 261

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ L +GGSTDIV GYS +P TFSSDFA+AMIKMG+I PLTG+ G+IR+

Sbjct: 262 MQRKGLLESDQILLSGGSTDSIVSGYSRSPSTFSSDFAAMIKMGIDPLTGTAGQIRRI 321

Query: 2164 CRRIN 2178

C IN

Sbjct: 322 CSAIN 326

Score = 137 bits (344), Expect = 9e-30
Identities = 75/165 (45%), Positives = 99/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LLD+TS+ EK A PN++SARG+EVID K+ VEK+CPGVVSCADIL++AA

Sbjct: 77 IQGCDASVLLDETSTIESEKTALPNKDSARGYEVIDKAKTEVEKICPGVVSCADILSVAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDS S +GGP+W V LG

Sbjct: 137 RDS-----SAYVGGPSWTVMLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645

RRD+ TAS++ AN+ +P+ L++LISRF + GLS +D+VALSG

Sbjct: 154 RRDSTTASRTLANSFELPSFKDGLDRLISRFQSKGLSARDMVALSG 198

Score = 60.8 bits (146), Expect = 8e-07
Identities = 27/56 (48%), Positives = 44/56 (78%), Gaps = 1/56 (1%)
Frame = +1

Query: 616 VLIWGA-NAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

+LI G+A +AQL++ FY CPN S+++++++I+ E RM ASL+RL FHDCF+

Sbjct: 22 LLILGTACHAQLTSTFYDSLCPNALSTIRTSIRNSIAAERRMAASLIRLHFHDCF 77

>emb|CAH10841.1| peroxidase [Picea abies]
Length = 320

Score = 160 bits (405), Expect = 8e-37
Identities = 78/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ TP F+N Y+ NL

Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKANCP--SAGGDNTLSPLDVVTPIKFNNKYGNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLFNGGSTDS V YSTN +F +DFAAAM+KM +ISPLTG++G+IRKNC
Sbjct: 257 IQKGLLHSDQQLFNGGSTDSQVTAYSTNQNSFFTDFAAAMVKMSNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 154 bits (388), Expect = 7e-35
Identities = 89/169 (52%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA
Sbjct: 72 VSGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GPTW V LG
Sbjct: 132 RDSV-----VELQGPTWTVM LG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAANN IP+P S+L+ LIS F GLSTKDLVALSG I
Sbjct: 149 RRDSTTASLSAANNIPSPASSLSALISSFKGHGLSTKDLVALSGAHTI 197

Score = 62.8 bits (151), Expect = 2e-07
Identities = 33/70 (47%), Positives = 43/70 (61%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGSAN-----AQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + + S N QLS+ FY SCP S VK V+ A++KE RMGASL+
Sbjct: 4 RNLLCIGIMAVFVCSININAVSGQLSSTFYDKSCPRAQSIVKRVVKQALAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783
RL FHDCFV+
Sbjct: 64 RLHFHDCFVS 73

>gb|EEE67814.1| hypothetical protein OsJ_25568 [Oryza sativa Japonica Group]
Length = 135

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 12 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTTPYSFDNAYYSNLL 71

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 72 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQGQIRLSC 131

Query: 2167 RRIN 2178
++N
Sbjct: 132 SKVN 135

>tpe|CAH69352.1| TPA: class III peroxidase 110 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 313

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 190 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTTPYSFDNAYYSNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 250 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQGQIRLSC 309

Query: 2167 RRIN 2178
++N
Sbjct: 310 SKVN 313

Score = 127 bits (319), Expect = 7e-27
Identities = 74/175 (42%), Positives = 94/175 (53%)
Frame = +2

Query: 1118 AS*ILMSKH*QMCGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV 1297
AS + + H GCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C
Sbjct: 53 ASLLRLHFHDC FVGCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQT 112

Query: 1298 VSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* 1477
VSCADILA+AARDSV +
Sbjct: 113 VSCADILAVAARDSV-----VA 129

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNLISRF SALGLSTKDLVALS 1642
LGGP+W V LGRRD+ TAS +ANN +P P +L LI F G S D+VALS

Sbjct: 130 LGGPSWTVGLGRRDSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALS 184

Score = 67.0 bits (162), Expect = 1e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTAAVNNEPRMGASLLRLHFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>ref|NP_001060627.1| Os07g0677100 [Oryza sativa (japonica cultivar-group)]
dbj|BAC83102.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAF22541.1| Os07g0677100 [Oryza sativa Japonica Group]
dbj|BAG95220.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 315

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 192 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTPYSFDNAYYSNLL 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR ++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 252 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQQGQIRLSC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 132 bits (331), Expect = 3e-28
Identities = 74/169 (43%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AA
Sbjct: 65 VQGCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVGLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 RRDSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 190

Score = 67.0 bits (162), Expect = 1e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTAANNNEPRMGASLLRLHFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>gb|ABD66594.1| peroxidase [Litchi chinensis]
Length = 234

Score = 159 bits (403), Expect = 1e-36
Identities = 88/169 (52%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTS+F GEK A PN NS RGF V+D IK+ +EK CPGVVSCAD+LAIAA
Sbjct: 4 VDGCDSLLDDTSTFVGEKTAVPNNNSVRGFNVVDQIKAKLEKACPGVVSCADLLAIAA 63

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 64 RDSV-----VHLGGPSWTVRLG 80

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS++ AN IP PTSNL+ LIS FSA GLS KDLVALSG I
Sbjct: 81 RRDSKTASRALANTSIPPPTSNSALISSFSAQGLSLKDLVALSGAHTI 129

Score = 113 bits (283), Expect = 1e-22
Identities = 54/98 (55%), Positives = 69/98 (70%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT+FR IYN+TNI+++FA + ++ CPR+ DN LA LD QTP FD Y+ NL++
Sbjct: 132 ARCTSFRGHIYNDTNIDSSFAMSLRRKCPRSGN--DNALANLDRQTPFCFDKLYDNLLK 189

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAA 2103
KKGLLHSDQ+LF GGS D V+ Y+ N F DFA A

Sbjct: 190 KKGLLHSDQELFKGGSADPFVKKYANNTSAFFKDFAGA 227

>emb|CBI19219.1| unnamed protein product [Vitis vinifera]
Length = 446

Score = 159 bits (403), Expect = 1e-36
Identities = 81/138 (58%), Positives = 105/138 (76%), Gaps = 1/138 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L

Sbjct: 194 KARCTSFNRHIYNDTDIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLK 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+L+NGGSTDSIV YS N TF D A AM+KMG+ISPLTG+NG+IR NC

Sbjct: 251 EKKGLLHSDQELYNGGSTDSIVETYSINTATFFRDVANAMVKMGNISPLTGTTNGQIRTNC 310

Query: 2167 RRIN*F-DSVLNIKGPTH 2217

R+I + + I+ PT+

Sbjct: 311 RKIQCIGPTPIEIRNPTN 328

Score = 155 bits (391), Expect = 3e-35
Identities = 86/167 (51%), Positives = 100/167 (59%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG+EVID IKS VE +CPGVVSCADI+A+AARD

Sbjct: 69 GCDASILLDDTATFTGEKTAGPNNSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 128

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V+LGRR

Sbjct: 129 SV-----VALGGPTWTVRLGR 145

Query: 1517 DARTASQSAANNGIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS SAA +P P NL+QLIS FS GL+TK++V LSGT I

Sbjct: 146 DSTTASFSAAARTDLPGNLNLSQLISAFSKGLTTKEMVVLSTGHTI 192

Score = 65.1 bits (157), Expect = 4e-08
Identities = 31/57 (54%), Positives = 40/57 (70%), Gaps = 1/57 (1%)

Frame = +1

Query: 610 LFVLIWGSANAQ-LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCF 777
+F L+ G A+A LS NFY SCP ++++ V A++KE RMGASLLRL FHDCF
Sbjct: 12 IFSLLLGMAHAHYLSPNFYARSCPRLPTIRTAVNKAVAKEKRMGASLLRLHFHDCF 68

>ref|XP_002334317.1| predicted protein [Populus trichocarpa]
gb|EEF08174.1| predicted protein [Populus trichocarpa]
Length = 224

Score = 159 bits (403), Expect = 1e-36
Identities = 80/124 (64%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR D LAPLDL TP SFDN YFKNL+
Sbjct: 103 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGS--DATLAPLDLVT PNSFDNYYFKNLM 160

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS+G+IR+ C
Sbjct: 161 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSSGQIRRIC 220

Query: 2167 RRIN 2178
+N
Sbjct: 221 SAVN 224

Score = 99.4 bits (246), Expect = 2e-18
Identities = 59/140 (42%), Positives = 77/140 (55%)
Frame = +2

Query: 1229 NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYIS 1408
NSARG+ VID K+ VEK+CPGVVSCADI+A+AARD+
Sbjct: 2 NSARGYNVIDKAKTEVEKICPGVVSCADIIA VAARDA----- 38

Query: 1409 KLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQL 1588
S +GGP++ VKLGRRD+ TAS++ AN +PA +L L
Sbjct: 39 -----SAYVGGPSYAVKLGRRDSTASRTLANAELPAFFESLESL 78

Query: 1589 ISRFSALGLSTKDLVALSGT 1648
ISRF GL+ +D+VALSG+
Sbjct: 79 ISRFQKKGLTARDMVALSGS 98

>emb|CAN73051.1| hypothetical protein [Vitis vinifera]
Length = 297

Score = 159 bits (403), Expect = 1e-36
Identities = 77/124 (62%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD+QT FDN Y++NL
Sbjct: 176 QAQCFTFRSRIYNDTNIDPNFAATTRSTCP-VSG-GNSNLAPLDIQTMNKFDNKYYENLE 233

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 234 AQRGLFHSDQELFNGGSQDALVRAYSANNALFFXDFAAAMVKMSNISPLTGNGEIRSNC 293

Query: 2167 RRIN 2178
R +N
Sbjct: 294 RVVN 297

Score = 151 bits (382), Expect = 4e-34
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 49 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 108

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 109 RDGVVL-----LGGPSWTVPLG 125

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ ALSG+ I
Sbjct: 126 RRDARTANQSAANNLPPFANLSALISGFAAKGLNADDMTALSGSHTI 174

Score = 62.4 bits (150), Expect = 3e-07
Identities = 28/49 (57%), Positives = 36/49 (73%)
Frame = +1

Query: 637 NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
N +LS NFY +CPN+ V+ + A+ +E RMGAS+LRLFFHDCFVN
Sbjct: 2 NYKLSPNFYASTCPNVQKIVRVEMVQAVIREPRMGASILRLFFHDCFVN 50

>gb|EEE67818.1| hypothetical protein OsJ_25573 [Oryza sativa Japonica Group]
Length = 323

Score = 159 bits (402), Expect = 2e-36

Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+

Sbjct: 200 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYYRNLLS 259

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C

Sbjct: 260 NKGLLHSDQELFSGSTDNVRSFASAAAFGAATAMVKMGNISPLTGTGQGIIRLICS 319

Query: 2170 RIN 2178

+N

Sbjct: 320 AVN 322

Score = 94.7 bits (234), Expect = 5e-17
Identities = 68/168 (40%), Positives = 85/168 (50%), Gaps = 1/168 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AARD

Sbjct: 79 GCDASILLAGN-----ERNAAPNF-SVRGYDVDSIKTQIEAVCKQTVSCADILTVAARD 132

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W+V LGRR

Sbjct: 133 SV-----VALGGPSWSVPLGRR 149

Query: 1517 DARTASQSAANNGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ A+ +A AP T +L QLIS +++ GLS DLVALSG I

Sbjct: 150 DSTGAATAAQVISSLAPSTDLSAQLISAYASKGLSATDLVALSGAHTI 197

Score = 67.8 bits (164), Expect = 7e-09
Identities = 39/70 (55%), Positives = 46/70 (65%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL

Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTSCPRAMSIKSTVTA AVNNEPRMGASL 58

Query: 751 LRLFFHDCFV 780

LRL FHDCFV

Sbjct: 59 LRLHFHDCFV 68

>gb|EEE56633.1| hypothetical protein OsJ_06032 [Oryza sativa Japonica Group]

Length = 303

Score = 159 bits (402), Expect = 2e-36
Identities = 74/123 (60%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 179 AQCQFFRGHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 238

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 239 RRGLLHSDQELFNGGSQDERVKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 298

Query: 2170 RIN 2178
+N
Sbjct: 299 VVN 301

Score = 95.9 bits (237), Expect = 2e-17
Identities = 48/70 (68%), Positives = 54/70 (77%), Gaps = 2/70 (2%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD S F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+
Sbjct: 80 VQGCDASILLDDVPSKGFVGEKTAGPNTNSIRGYEVIDKIKANVEAACPGVVSCADILAL 139

Query: 1325 AARDSVQIVS 1354
AAR+ V +VS
Sbjct: 140 AAREGVNLVS 149

Score = 60.5 bits (145), Expect = 1e-06
Identities = 34/76 (44%), Positives = 47/76 (61%), Gaps = 7/76 (9%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANA-----QLSTNFYYHSCPRLFSSVKSTVQSAISKET 732
+S +R + LAL + + SA A ++ ++Y SCP L + V+ T+ SAI E
Sbjct: 5 SSTTTRFCLLLALVLPMISSAAGDDALPLPMTPSYYRKSCPTLEAIVRGTMLSAIKAER 64

Query: 733 RMGASLLRLFFHDCFV 780
RMGAS+LRLFFHDCFV
Sbjct: 65 RMGASILRLFFHDCFV 80

>ref|XP_002281731.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 159 bits (402), Expect = 2e-36
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIRTMNRFDNIIYYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 151 bits (381), Expect = 5e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGV-----VQLGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I
Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 5e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSII SLLACSLNQLSPNFYASTCPNVQNI VRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>gb|EAZ05136.1| hypothetical protein OsI_27329 [Oryza sativa Indica Group]
Length = 338

Score = 159 bits (402), Expect = 2e-36
Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+
Sbjct: 215 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYYRNLLS 274

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C
Sbjct: 275 NKGLLHSDQELFSNGSTDNTVRSFASSAAAFGAATAMVKMGNISPLTGTQGQIRLICS 334

Query: 2170 RIN 2178
+N
Sbjct: 335 AVN 337

Score = 96.7 bits (239), Expect = 1e-17
Identities = 69/169 (40%), Positives = 86/169 (50%), Gaps = 1/169 (0%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAR 1333
QGCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AAR
Sbjct: 93 QGCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAAR 146

Query: 1334 DSVQIVSGQTNTKNLTN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W+V LGR
Sbjct: 147 DSV-----VALGGPSWSVPLGR 163

Query: 1514 RDARTASQSAANNGIPAP-TSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RD+ A+ +A AP T +L QLIS +++ GLS DLVALSG I
Sbjct: 164 RDSTGAATAAQVISSLAPSTDLSLAQLISAYASKGLSATDLVALSGAHTI 212

Score = 69.3 bits (168), Expect = 2e-09
Identities = 45/93 (48%), Positives = 55/93 (59%), Gaps = 1/93 (1%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSVVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL
Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTSCPRAMSIKSTVTAAVNNEPRMGASL 58

Query: 751 LRLFFHDCFVNV-IYLHLLPLTYKYAKLTYSSS 846

LRL FHDCFV +L P+ + Y L SS
Sbjct: 59 LRLHFHDCFVQARFHLTNHPVFFFYFDLMPKSS 91

>ref|NP_001046402.1| Os02g0240500 [Oryza sativa (japonica cultivar-group)]
dbj|BAD28874.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69270.1| TPA: class III peroxidase 28 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF08316.1| Os02g0240500 [Oryza sativa Japonica Group]
Length = 334

Score = 159 bits (402), Expect = 2e-36
Identities = 74/123 (60%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 210 AQCQFFRGHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 269

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 270 RRGLLHSDQELFNGGSQDERVKKYSTDPDFLAFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 329

Query: 2170 RIN 2178
+N
Sbjct: 330 VVN 332

Score = 134 bits (336), Expect = 8e-29
Identities = 76/173 (43%), Positives = 96/173 (55%), Gaps = 2/173 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD S F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+
Sbjct: 80 VQGCDASILLDDVPSKGFVGEKTAGPNTNSIRGYEVIDKIKANVEAACPGVVSCADILAL 139

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AAR+ V + LGGP+W V
Sbjct: 140 AAREGVNL-----LGGPSWEVP 156

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHISH 1663
LGRRD+ TAS+S A++ +P P+S+L L++ F GL+ +D+ ALSG I +
Sbjct: 157 LGRRDSTTASKSEADSDLPGPSSSLADLVAAFGKKGLAPRDMTALSGAHTIGY 209

Score = 60.5 bits (145), Expect = 1e-06

Identities = 34/76 (44%), Positives = 47/76 (61%), Gaps = 7/76 (9%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANA-----QLSTNFYHSCPNLFSSVKSTVQSAISKET 732
+S +R + LAL + + SA A ++ ++Y SCP L + V+ T+ SAI E
Sbjct: 5 SSTTTRFCLLLALVLPMISSAAAGDDALPLPMTPSYYRKSCPTLEAIVRGTMLSAIAER 64

Query: 733 RMGASLLRLFFHDCFV 780
RMGAS+LRLFFHDCFV
Sbjct: 65 RMGASILRLFFHDCFV 80

>ref|NP_001060630.1| Os07g0677400 [Oryza sativa (japonica cultivar-group)]
gb|AAC49820.1| peroxidase [Oryza sativa Indica Group]
dbj|BAC79530.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAD30310.1| peroxidase [Oryza sativa Japonica Group]
tpe|CAH69355.1| TPA: class III peroxidase 113 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF22544.1| Os07g0677400 [Oryza sativa Japonica Group]
Length = 314

Score = 159 bits (402), Expect = 2e-36
Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+
Sbjct: 191 ARCRGFRTRYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYYRNLLS 250

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C
Sbjct: 251 NKGLLHSDQELFNSGSTDNTVRSFASAAAFGAATAMVKMGNISPLTGTQGQIRLICS 310

Query: 2170 RIN 2178
+N
Sbjct: 311 AVN 313

Score = 97.1 bits (240), Expect = 1e-17
Identities = 69/170 (40%), Positives = 87/170 (51%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAI AA 1330
+QGCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AA
Sbjct: 68 VQGCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W+V LG

Sbjct: 122 RDSV-----VALGGPSWSVPLG 138

Query: 1511 RRDARTASQAANNIGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+ +A AP T +L QLIS +++ GLS DLVALSG I

Sbjct: 139 RRDSTGAATAAQVISSLAPSTDLSLAQLISAYASKGLSATDLVALSGAHTI 188

Score = 67.8 bits (164), Expect = 7e-09
Identities = 39/70 (55%), Positives = 46/70 (65%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL
Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPFYDTSCPRAMSIKSTVTAAVNNEPRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAA59487.1| peroxidase [Triticum aestivum]
gb|ACF08093.1| class III peroxidase [Triticum aestivum]
Length = 319

Score = 159 bits (401), Expect = 2e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+TAF A + + +CPR +GSGD++LAPLD TP +FDN Y++NL+
Sbjct: 196 QAQCQNFDRRLYNETNIDTAFATSLRANCPRPTGSGDSSLAPLDTTTPNAFDNAYYRNLM 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DF AAM+ MG+ISPLTG+ G++R +C
Sbjct: 256 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNDRDFRAAMVSMGNISPLTGTQGVRLSC 315

Query: 2167 RRIN 2178
R+N
Sbjct: 316 SRVN 319

Score = 131 bits (329), Expect = 5e-28
Identities = 76/169 (44%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA

Sbjct: 69 VQGCDAIILLSDTATFTGEQAGPNAGSIRGMNVIDNIKAQVEAVCTQTVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 129 RDSV-----VALGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P P+ ++ L + F+A GLS D+VALSG I

Sbjct: 146 RRDSTTASLSLANSDLPPPSFDVANLTANFAAKGLSVTDMVALSGAHTI 194

Score = 60.5 bits (145), Expect = 1e-06
Identities = 35/73 (47%), Positives = 44/73 (60%), Gaps = 1/73 (1%)
Frame = +1

Query: 565 LTMASFCS-RLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMG 741
+ MAS S L +CLA ++AQLS FY SCP + ++ V +A+ E RMG

Sbjct: 3 MAMASSLSVLLLLCLA-----APSSAQLSPRFYARSCPRAQAIIRRGVAAAVRSERRMG 56

Query: 742 ASLLRLFFHDCFV 780
ASLLRL FHDCFV

Sbjct: 57 ASLLRLHFHDCFV 69

>gb|AAB02554.1| cationic peroxidase [Stylosanthes humilis]
Length = 320

Score = 159 bits (401), Expect = 2e-36
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYNE+NI+ ++A++ Q +CP S GD+NL+P D+ TP FDN Y+ NL

Sbjct: 198 QARCTTFRTRIYNESNIDPSYAKSLQGNCP--SVGGDSNLSPFDVTPNKFNDAYYINLK 255

Query: 1987 QKKGLLHSDQQLFNGG-STDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
KKGLLH+DQQLFNGG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR N

Sbjct: 256 NKKGLLHADQQLFNGGGSTDSQVTAYSNNAAATFNTDFGNAMIKMGNLSPLTGTSGQIRTN 315

Query: 2164 CRRIN 2178
CR+ N

Sbjct: 316 CRKTN 320

Score = 152 bits (384), Expect = 2e-34
Identities = 85/169 (50%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+QGCD S+LLDDTS+FTGEK A PN NSARGF+VID IKS VE +CPGVVSCADILA+AA
Sbjct: 71 VQGCDASVLLDDTSTFTGEKTAFPNVNSARGFDVIDTIKSQVESLCPGVVSCADILALAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+WNV+LG
Sbjct: 131 RDSV-----VALGGPSWNVQLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ++AN+ +P P+ NL+ LIS FS G + K+LV LSG I
Sbjct: 148 RRDSTASLNSANSDLPGPSFNL SGLISAFSKKGFTAKELVTLSGAHTI 196

Score = 75.1 bits (183), Expect = 4e-11
Identities = 35/62 (56%), Positives = 45/62 (72%), Gaps = 1/62 (1%)
Frame = +1

Query: 598 ICLALFVLI-WGSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRLFFHDC 774
+C +F+ + G + QLS+NFY CPN S++KS V SA+SKE R+GASLLRL FHDC
Sbjct: 10 VCFIIFMCLNIGLGGSQLSSNFYATKCPNALSTIKSAVNSAVSKEARLGASLLRLHFHDC 69

Query: 775 FV 780
FV
Sbjct: 70 FV 71

>sp|P16147.2|PERX_LUPPO RecName: Full=Peroxidase
emb|CAA36066.1| peroxidase [Lupinus polyphyllus]
prf||1805332A peroxidase:ISOTYPE=basic isozyme
Length = 158

Score = 159 bits (401), Expect = 2e-36
Identities = 79/124 (63%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+ C F+ RIYN+TNI+T FA +RQ +CP ++G G+ NLAPLD TP FDN Y+K+LV
Sbjct: 36 QSECQFFKTRIYNDTNIDTNFATSRQANCPFSAG-GETNLAPLDSLTPNRFDNYYKDLV 94

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+GLLHSDQ LFNGGS D++VR YSTN F SDFAAA++KM ISPLTG GEIRKNC
Sbjct: 95 SNRGLLHSDQVLFNGGSQDTLVRTYSTNNVKKFSDFAAAIVKMSKISPLTG IAGEIRKNC 154

Query: 2167 RRIN 2178
R IN
Sbjct: 155 RVIN 158

>dbj|BAA77389.1| peroxidase 3 [Scutellaria baicalensis]
Length = 318

Score = 159 bits (401), Expect = 2e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYN+TNI AFA + +CPR+ G DNNLAPLD +P F+N Y++NL+
Sbjct: 197 QARCTTFRGRIYNDTNINGAFATGLRANCPRSGG--DNNLAPLDNVSPARFNNDYYRNLI 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+GLLHSDQ+LFN G+ D+ VR YSTN F +DFA AM+KM ++SPLTG+NG+IR+NC
Sbjct: 255 GLRGLLHSDQQLFNNGTADAQVRAYSTNSAAFFNDFANAMVKMSNLSPLTGNGQIRRNC 314

Query: 2167 RRIN 2178
RR N
Sbjct: 315 RRTN 318

Score = 135 bits (341), Expect = 2e-29
Identities = 76/169 (44%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD S+LLDD + FTGEK A PN NS RGF+VIDNIK+ VE CP +VSC+DIL++AA
Sbjct: 70 VNGCDASVLLDDRTGFTGEKTAGPNANSLRGFDVIDNIKTLVEGSCPNIVSCSDILSVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V V GGP+W V LG
Sbjct: 130 RDGVVAV-----GGPSWAVALG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +AAN IP P NLN LI+ FS G + +++VALSG+ I
Sbjct: 147 RRDSTTASLNAANTQIPGPGLNLNALITSFSNKGFTAREMVALSGSHTI 195

Score = 87.4 bits (215), Expect = 8e-15
Identities = 42/71 (59%), Positives = 53/71 (74%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MASF S + L L +L+ G +NAQLS NFY +CPNL + +++ V SA+S +TRMGASL
Sbjct: 1 MASFVSEFSTRMLVL LLLIGVSNAQLSANFYNTTCPNLLTIIRNAVNSAVSSDTRMGASL 60

Query: 751 LRLFFHDCFVN 783

LRL FHDCFVN
Sbjct: 61 LRLHFHDCFVN 71

>ref|XP_002461207.1| hypothetical protein SORBIDRAFT_02g042840 [Sorghum bicolor]
gb|EER97728.1| hypothetical protein SORBIDRAFT_02g042840 [Sorghum bicolor]
Length = 318

Score = 158 bits (400), Expect = 3e-36
Identities = 73/124 (58%), Positives = 93/124 (75%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++C NFRA IYN+TN+ AFA R+ SCP +G GD NL PLD T T+FDN Y+ NL+
Sbjct: 195 SQCKNFRAHIYNDTNVNAFATLRKVSPPAAAGDGDGNTPLDTATSTAFDNAYYTNLLS 254

Query: 1990 KKGLLHSDQQLFN-GGSTDSIVRGYSTNPGETSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ GLLHSDQQLFN GG+TD +VR Y++ P F+ DF AAMI+MG+ISPLTG G+IR+ C
Sbjct: 255 RSGLLHSDQQLFNNGGATDGLVRYASTPTRFNRDFTAAIRMGNISPLTGRQGIIRAC 314

Query: 2167 RRIN 2178
R+N
Sbjct: 315 SRVN 318

Score = 138 bits (347), Expect = 4e-30
Identities = 79/169 (46%), Positives = 98/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE VCPGVVSCADILA+AA
Sbjct: 67 VQGCDASVLLNDTATFTGEQTANPNVGSIRGFGVVDNIKAQVEAVCPGVVSCADILAVAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 127 RDSV-----VALGGPSWRVLLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +PAP+ +L L + F+ LS DLVALSG I
Sbjct: 144 RRDSTTASLALANSPLPAPSLDLANLTAFAKKRLSRTDLVALSGAHTI 192

Score = 67.0 bits (162), Expect = 1e-08
Identities = 30/49 (61%), Positives = 38/49 (77%)
Frame = +1

Query: 634 ANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

A+AQLS FY SCP +++KS V +A+++E RMGASLLRL FHDCFV
Sbjct: 19 ASAQLSATFYSRSCPRALATIKSAVTAAVAQEPRMGASLLRLHFHDCFV 67

>gb|EEC82684.1| hypothetical protein OsI_27330 [Oryza sativa Indica Group]
Length = 309

Score = 158 bits (400), Expect = 3e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 187 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 244

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 245 SNKGLLHSDQVLFNNGGSTDNTVRNFASNAAFSSAFATAMVMGNIAPKTGTNGQIRLSC 304

Query: 2167 RRIN 2178
++N
Sbjct: 305 SKVN 308

Score = 102 bits (254), Expect = 2e-19
Identities = 64/167 (38%), Positives = 85/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AARD
Sbjct: 67 GCDASVLLSGN-----EQDAPPNKDSL RGYGVDSIKAQIETVCNQTVSCADILTVAARD 121

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V LGRR
Sbjct: 122 SV-----VALGGPTWTVPLGRR 138

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 DSTGASAALAI SDLPFTASLQELVDAFAKGLSVTDMVALSGAHTI 185

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/61 (54%), Positives = 43/61 (70%), Gaps = 2/61 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC

Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTAAVNSEPRMGASLLRLHFHDC 65

Query: 775 F 777
F

Sbjct: 66 F 66

>gb|AAW52720.1| peroxidase 6 [Triticum monococcum]
Length = 322

Score = 158 bits (400), Expect = 3e-36
Identities = 73/123 (59%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++C NFR IYN TNI+ AFA R+++CP + +GD NLAP D+QT FDN Y++NLV
Sbjct: 199 SQCLNFRDHIYNGTNIDPAFATLRKRTCPAQAPNGDKNLAPFDVQTQLLFDNAYYRNVA 258

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLL+SDQ LFNGGS D++VR Y NP F+SDF AMIKMG+I+PLTG+ G+IR+NCR
Sbjct: 259 KRGLLNSDQVLFNNGSQDALVRQYVANPALFASDFVTAMIKMGNINPLTGTAGQIRRNCR 318

Query: 2170 RIN 2178
+N
Sbjct: 319 VVN 321

Score = 131 bits (329), Expect = 5e-28
Identities = 76/169 (44%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCDGSILLDD SF GEK A PN +S RG+EVID IK VE +CPG+VSCADI A+AA
Sbjct: 71 VQGCDGSILLDDVGSFVGEKTAFPNVDSVRGYEVIDEIKKNVELLCPGIVSCADIAALAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + LGGP+W+V LG
Sbjct: 131 RDGTFL-----LGGPSWSVPLG 147

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +PAP+ +L LI F LS +DL ALSG I
Sbjct: 148 RRDSTTASLTEANS DLPAPSLSLGLLIKAFDKKQLSPQDLTALSGAHTI 196

Score = 64.3 bits (155), Expect = 8e-08
Identities = 33/60 (55%), Positives = 39/60 (65%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNI FSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
CL L+ SA QLS +FY SCP L V++T+ A+ E RMGASLLRL FHD CFV
Sbjct: 12 CLLALFLLSSSAYGQLSPSFYAKSCPTLQLIVRATMIKALLAERRMGASLLRLHFHDCFV 71

>gb|AAQ55292.1| class III peroxidase GvPx2b [Vitis vinifera]
Length = 255

Score = 158 bits (400), Expect = 3e-36
Identities = 76/124 (61%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L
Sbjct: 135 KARCTSF RNHIYNDT DIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLE 191

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ L+NGGSTDS+V+ YS + TF +D A AM++MGDISPLTG+NG+IR NC
Sbjct: 192 EKKGLLHSDQVLYNGGSTDSL VKTYSIDTATFFTDVANAMVRMGDISPLTG TNGQIRTNC 251

Query: 2167 RRIN 2178
R++N
Sbjct: 252 RKNV 255

Score = 147 bits (372), Expect = 5e-33
Identities = 83/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLD T++FTGEK A PN NS RG+EVID IKS V +CPGVVSCADI+A+AARD
Sbjct: 10 GCDASILLDGTATFTGEKTAGPNNSVRGYEVIDTIKSQVGS LCPGVVSCADIVAVAARD 69

Query: 1337 SVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNV KLGRR 1516
SV I+ GGPTW V+LGRR
Sbjct: 70 SVVIL-----GGPTWTVRLGRR 86

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS SAA +P P +L+QLIS FS GL+TK++V LSGT I
Sbjct: 87 DSTTASFS AAGTDLPGPNLSLSQLISAFSKKGLTTKEMVVLSGTHTI 133

>gb|AAF65464.2|AF247700_1 peroxidase POC1 [Oryza sativa Indica Group]
Length = 311

Score = 158 bits (400), Expect = 3e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+

Sbjct: 189 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR ++N FSS FA AM+ MG+I+P TG+NG+IR +C

Sbjct: 247 SNKGLLHSDQVLFNNGSTDNTVRNFASNAAFSSAFATAMVNMGNIAPKTGTNGQIRLSC 306

Query: 2167 RRIN 2178

++N

Sbjct: 307 SKVN 310

Score = 104 bits (260), Expect = 5e-20

Identities = 65/169 (38%), Positives = 87/169 (51%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AA

Sbjct: 67 VQGCDASVLLSGN-----EQDAPPNKDSL RGYGVIDS IKAQIEAVCNQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISK LITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 122 RDSV-----VALGGPTWTVP LG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ AS + A + +P T++L +L+ F+ GLS D+VALSG I

Sbjct: 139 RRDSTGASAA LAISDLPPFTASLQELVDAFAKKGLSVTDMVALSGAHTI 187

Score = 68.2 bits (165), Expect = 5e-09

Identities = 34/62 (54%), Positives = 44/62 (70%), Gaps = 2/62 (3%)

Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774

C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC

Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSI IKS AVTAAVNSEPRMGASLLRLHFHDC 65

Query: 775 FV 780

FV

Sbjct: 66 FV 67

>ref|XP_002311022.1| predicted protein [Populus trichocarpa]

gb|EEE88389.1| predicted protein [Populus trichocarpa]

Length = 319

Score = 158 bits (399), Expect = 4e-36
Identities = 79/124 (63%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + + LAPLDL TP SFDN YFKNL+
Sbjct: 197 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSN--STLAPLDLVTPNSFDNYYFKNLM 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 255 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPFKSDFGSAMIKMGDIGLLTGSAGQIRRIC 314

Query: 2167 RRIN 2178
+N
Sbjct: 315 SAVN 318

Score = 126 bits (316), Expect = 2e-26
Identities = 74/166 (44%), Positives = 94/166 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLD+T S EK A N NSARG+ VID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 70 VQGCDA SILLDETLSIQSEKTALGNLNSARGYNVIDKAKTEVEKICPGVVSCADIIAVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP++ VKLG
Sbjct: 130 RDA-----SAYVGGPSYAVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGT 1648
RRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 147 RRDSTTASRTLANAELPAFFESLES LISR FQKKGLTARDMVALSGS 192

Score = 62.4 bits (150), Expect = 3e-07
Identities = 28/57 (49%), Positives = 40/57 (70%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
+ L+ + AQLS FY SCPN S++++ ++SAI+ + RM ASL+RL FHDCFV
Sbjct: 14 MLFLLNTACQAQLSPAFYDSSCPNAISAIRTAIRSAIASDRRMAASLIRLHFHDCFV 70

>gb|EEE67819.1| hypothetical protein OsJ_25574 [Oryza sativa Japonica Group]
Length = 309

Score = 158 bits (399), Expect = 4e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 187 QACSTFRGRIYNETNIDSAFATQRQANCPTSG--DMNLAPLDTTANAFDNAYYTNNL 244

Query: 1987 QKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 245 SNKGLLHSDQVLFNNGSTDNTVRNFASNAEFSSAFATAMVNMGNIAPKTGTNGQIRLSC 304

Query: 2167 RRIN 2178
++N
Sbjct: 305 SKVN 308

Score = 102 bits (254), Expect = 2e-19
Identities = 64/167 (38%), Positives = 85/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AARD
Sbjct: 67 GCDASVLLSGN-----EQDAPPNKDSLRYGVIDSIIKAQIEAVCNQTVSCADILTVAARD 121

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V LGRR
Sbjct: 122 SV-----VALGGPTWTVPLGRR 138

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 DSTGASAALAI SDLPFTASLQELVDAFAKGLSVTDMVALSGAHTI 185

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/61 (54%), Positives = 43/61 (70%), Gaps = 2/61 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC
Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTA AVNSEPRMGASLLRLHFHDC 65

Query: 775 F 777
F
Sbjct: 66 F 66

>ref|NP_001147216.1| LOC100280824 [Zea mays]
gb|ACG26145.1| peroxidase 52 precursor [Zea mays]
Length = 318

Score = 158 bits (399), Expect = 4e-36
Identities = 72/124 (58%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIY +T+I +FA RQQ+CPR+ G G NLAP+D+QTP FD YF NL+
Sbjct: 196 QARCTTFRGRIYGD TDINASFAALRQQTCPRSGGDG--NLAPIDVQTPVRFD TAYFTNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS + F++DF AAMI+MG++ LTG+ G+IR+NC
Sbjct: 254 SRRGLFHS DQELFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLTGTAGQIRRNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 134 bits (338), Expect = 5e-29
Identities = 83/169 (49%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGSILLD GEK A PN NS RGFEVID IK VE CPGVVSCADILA+AA
Sbjct: 73 VQGCDGSILLDAG----GEKTAGPNLSVRGFEVIDTIKRNV EACPGVVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD TNL LGGPTW+V LG
Sbjct: 129 RDG-----TNL-----LGGPTWSVPLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P PT++L LIS F GLS +D+ ALSG I
Sbjct: 146 RRDSTTASASLANSLPPPTASLGTLISLFGRQGLSPRDMTALSGAHTI 194

Score = 73.2 bits (178), Expect = 2e-10
Identities = 40/75 (53%), Positives = 49/75 (65%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETR 735
+ +L MAS L CL + L+ A+AQLS FY SCPNL S V++ + A+ E R
Sbjct: 1 MQLLAMAS--PTLMQCLVVVSLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVGSEQR 58

Query: 736 MGASLLRLFFHDCFV 780
MGASLLRLFFHDCFV
Sbjct: 59 MGASLLRLFFHDCFV 73

>ref|NP_001060631.1| Os07g0677500 [Oryza sativa (japonica cultivar-group)]
dbj|BAC79531.1| peroxidase POC1 [Oryza sativa Japonica Group]
dbj|BAD30311.1| peroxidase POC1 [Oryza sativa Japonica Group]
tpe|CAH69356.1| TPA: class III peroxidase 114 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF22545.1| Os07g0677500 [Oryza sativa Japonica Group]
Length = 311

Score = 158 bits (399), Expect = 4e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 189 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 247 SNKGLLHSDQVLFNNGGSTDNTVRNFASNAEFSSAFATAMVMGNIAPKTGTNGQIRLSC 306

Query: 2167 RRIN 2178
++N
Sbjct: 307 SKVN 310

Score = 104 bits (260), Expect = 5e-20
Identities = 65/169 (38%), Positives = 87/169 (51%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AA
Sbjct: 67 VQGCDASVLLSGN-----EQDAPPNKDSL RGYGVDSIKAQIEAVCNQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 122 RDSV-----VALGGPTWTVPPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 RRDSTGASAAALISDLPPFTASLQELVDAFAKKGLSVTDMVALSGAHTI 187

Score = 68.2 bits (165), Expect = 5e-09
Identities = 34/62 (54%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC
Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTA AVNSEPRMGASLLRLHFHDC 65

Query: 775 FV 780
FV
Sbjct: 66 FV 67

>pdb|1SCH|A Chain A, Peanut Peroxidase
pdb|1SCH|B Chain B, Peanut Peroxidase
Length = 294

Score = 158 bits (399), Expect = 4e-36
Identities = 76/124 (61%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CT FR RIYNE+NI+ +A++ Q +CP S GD NL+P D+ TP FDN Y+ NL
Sbjct: 173 QAQCTAFRTRIYNESNIDPTYAKSLQANCP--SVGGDTNLSPFDVTPNKF DNAYYINLR 230

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR NC
Sbjct: 231 NKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNC 290

Query: 2167 RRIN 2178
R+ N
Sbjct: 291 RKTN 294

Score = 152 bits (385), Expect = 2e-34
Identities = 87/169 (51%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDTS+FTGEK A PN NS RGFEVID IKS VE +CPGVVSCADILA+AA
Sbjct: 46 VQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAA 105

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGG +WNV LG
Sbjct: 106 RDSV-----VALGGASWNVLLG 122

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S+AN+ +PAP NL+ LIS FS G +TK+LV LSG I

Sbjct: 123 RRDSTTASLSSANSDLPAFFNLISAFSNKGFTTKELVTLGAHTI 171

Score = 68.9 bits (167), Expect = 3e-09
Identities = 31/45 (68%), Positives = 36/45 (80%)
Frame = +1

Query: 646 LSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
LS+NFY CPN S++KS V SA++KE RMGASLLRL FHDCFV
Sbjct: 2 LSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFV 46

>sp|P22195.2|PER1_ARAHY RecName: Full=Cationic peroxidase 1; AltName: Full=PNPC1; Flags:
Precursor
gb|AAB06183.1| cationic peroxidase [Arachis hypogaea]
Length = 316

Score = 158 bits (399), Expect = 4e-36
Identities = 76/124 (61%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CT FR RIYNE+NI+ +A++ Q +CP S GD NL+P D+ TP FDN Y+ NL
Sbjct: 195 QAQCTAFRTRIYNESNIDPTYAKSLQANCP--SVGGDTNLSPFDVTPNKFBNAYYINLR 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR NC
Sbjct: 253 NKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNC 312

Query: 2167 RRIN 2178
R+ N
Sbjct: 313 RKTN 316

Score = 152 bits (385), Expect = 2e-34
Identities = 87/169 (51%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSTFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDTS+FTGEK A PN NS RGFEVID IKS VE +CPGVVSCADILA+AA
Sbjct: 68 VQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGG +WNV LG
Sbjct: 128 RDSV-----VALGGASWNVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S+AN+ +PAP NL+ LIS FS G +TK+LV LSG I
Sbjct: 145 RRDSTTASLSSANSDDLPAFFNL SGLISAFSNKGFTTKELVTLSGAHTI 193

Score = 77.0 bits (188), Expect = 1e-11
Identities = 35/57 (61%), Positives = 44/57 (77%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+F+ + G +AQLS+NFY CPN S++KS V SA++KE RMGASLLRL FHDCFV
Sbjct: 12 IFMCLIGLGS AQLSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFV 68

>gb|ACU22965.1| unknown [Glycine max]
Length = 322

Score = 157 bits (398), Expect = 5e-36
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI+++FA + Q +CP S GD+NLAPLD T FDN YFK+L
Sbjct: 202 QAKCSTFRTRIYNETNIDSSFATSLQANCP--SVGGDSNLAPLDSNQNT-FDNAYFKDLQ 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLH+DQ LFNGGSTDS V GY+++P +F++DFA AM+KMG+ISPLTGS+GEIR NC
Sbjct: 259 SQKGLLHTDQVLFNGGSTDSQVNGYASDPSSFNTDFANAMVKMGNISPLTGSSGEIRTNC 318

Query: 2167 RRIN 2178
+ N
Sbjct: 319 WKTN 322

Score = 134 bits (338), Expect = 5e-29
Identities = 78/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DTSSFTGE+ A N NS RGF VIDNIKS VE +CPGVVSCADIL +AA
Sbjct: 75 VQGCDASVLLNDTSSFTGEQTAAGNVNSIRFGVIDNIKSQVESLCPGVVSCADILTVAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 135 RDSV-----VALGGPSWTVQLG 151

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S+AN+ +P +L QL F GL+T ++VALSG

Sbjct: 152 RRDSTTASLSSANSDLPRFDLSLQQLSDNFQNKGLTTAEMVALSG 196

Score = 76.6 bits (187), Expect = 1e-11
Identities = 40/75 (53%), Positives = 51/75 (68%), Gaps = 5/75 (6%)
Frame = +1

Query: 571 MASFCSRLT-----ICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETR 735
MAS C +T I LF+ G +++QLS++FY +CPN S++KS V SA+S E R
Sbjct: 1 MASSCFSMITPIFKIRFFLFLCFIGISSQLSSDFYSTTCPNALSTIKSAVDSAVSNEAR 60

Query: 736 MGASLLRLFFHDCFV 780
MGASLLRL FHDCFV
Sbjct: 61 MGASLLRLHFHDCFV 75

>ref|XP_002311955.1| predicted protein [Populus trichocarpa]
gb|EEE89322.1| predicted protein [Populus trichocarpa]
Length = 187

Score = 157 bits (398), Expect = 5e-36
Identities = 79/124 (63%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + + LAPLDL TP SFDN YFKNL+
Sbjct: 65 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSN--STLAPLDLVTPNSFDNYYFKNLM 122

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 123 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSAGQIRRIC 182

Query: 2167 RRIN 2178
+N
Sbjct: 183 SAVN 186

Score = 63.2 bits (152), Expect = 2e-07
Identities = 31/57 (54%), Positives = 43/57 (75%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
+GGP++ VKLGRRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 4 VGGPSYAVKLGRRDSTASRTLANAELPAFFESLESISRFAQKKGLTARDMVALSGS 60

>gb|AAM61588.1| peroxidase [Arabidopsis thaliana]

Length = 316

Score = 157 bits (398), Expect = 5e-36
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYN +NI+T+FA +++++CP TSGSGDN A LD+++P FD+ ++K L+
Sbjct: 193 RAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYKQLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLL SDQ LFN G TDS+V YS N F DFA AMIKMGDISPLTGSNG+IR+NC
Sbjct: 253 SKKGLLSDQQLFNGGPTDSLVIAYSHNLNAFYRDFARAMIKMGDISPLTGSNGQIRQNC 312

Query: 2167 RRIN 2178
RR N
Sbjct: 313 RRPN 316

Score = 150 bits (378), Expect = 1e-33
Identities = 85/170 (50%), Positives = 103/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDT SF GEK + P+ NS RGFEVID IK VEK+CPG+VSCADILAI A
Sbjct: 65 VNGCDGSLLDDTSPFLGEKTSGPSNNSVRGFEVIDKIKFKVEKMCPGIVSCADILAITA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 125 RDSVLL-----LGGPGWSVKLG 141

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ +AAN+G IP P + L+ LI+RF A GLST+D+VALSG+ I
Sbjct: 142 RRDSTTANFAAANSVIPPITTLNLINRFKAQGLSTRDMVALSGSHTI 191

Score = 72.8 bits (177), Expect = 2e-10
Identities = 32/62 (51%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+ L + +++ + AQL+ +FY SCP+LF V+ V+ A+++E RMGASLLRLLFFHDCF
Sbjct: 5 VLLMMIMMLASQSEAQLNRDFYKESCPSLFLVVRVVKRAVAREPRMGASLLRLLFFHDCF 64

Query: 778 VN 783
VN
Sbjct: 65 VN 66

>ref|NP_200647.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9LVL2.1|PER67_ARATH RecName: Full=Peroxidase 67; Short=Atperox P67; AltName: Full=ATP44;
Flags: Precursor
dbj|BAA96930.1| peroxidase [Arabidopsis thaliana]
Length = 316

Score = 157 bits (398), Expect = 5e-36
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRSTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYN +NI+T+FA +++++CP TSGSGDN A LD+++P FD+ ++K L+
Sbjct: 193 RAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYKQLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
KKGLL SDQ LFN G TDS+V YS N F DFA AMIKMGDISPLTGSNG+IR+NC
Sbjct: 253 SKKGLLTSQVLFNNGPTDSLVIAYSHNLNAFYRDFARAMIKMGDISPLTGSNGQIRQNC 312

Query: 2167 RRIN 2178
RR N
Sbjct: 313 RRPN 316

Score = 149 bits (377), Expect = 1e-33
Identities = 85/170 (50%), Positives = 102/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAI 1330
+ GCDGS+LLDDT SF GEK + P+ NS RGFEVID IK VEK+CPG+VSCADILAI A
Sbjct: 65 VNGCDGSLLDDTSPFLGEKTSGPSNNSVRGFEVIDKIKFKVEKMCPGIVSCADILAITA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 125 RDSVLL-----LGGPGWSVKLG 141

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ +AAN+G IP P + L+ LI+RF A GLST+D+VALSG I
Sbjct: 142 RRDSTTANFAAANSVIPPPIITLSNLINRFKAQGLSTRDMVALSGAHTI 191

Score = 72.8 bits (177), Expect = 2e-10
Identities = 32/62 (51%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777

+ L + +++ + AQL+ +FY SCP+LF V+ V+ A+++E RMGASLLRLFFHDCF
Sbjct: 5 VLLMMIMMLASQSEAQLNRDFYKESCPSLFLVVRVVKRAVAREPRMGASLLRLFFHDCF 64

Query: 778 VN 783

VN

Sbjct: 65 VN 66

>ref|XP_002460939.1| hypothetical protein SORBIDRAFT_02g037840 [Sorghum bicolor]
gb|EER97460.1| hypothetical protein SORBIDRAFT_02g037840 [Sorghum bicolor]
Length = 325

Score = 157 bits (397), Expect = 7e-36
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C N++ARIYN+ NI AFA + + CP G G N APLD TP +FDN Y+ +LV

Sbjct: 204 QAQCQNYQARIYNDANINAAFAASLRAGCPAGGGGGAN--APLDASTPNAFDNAYYGDLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGST +VR Y+ + FSSDFAAAM+KMG I +TGS+GE+R+NC

Sbjct: 262 AQQGLLHSDQELFNGGSTDGLVRSYAASSARFSSDFAAAMVKMGIGVITGSSGEVRRNC 321

Query: 2167 RRIN 2178
RR+N

Sbjct: 322 RRVN 325

Score = 139 bits (349), Expect = 2e-30
Identities = 76/165 (46%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT +FTGEK+A PN S RGF VID IK+ +E +CP VSCADILA+AA

Sbjct: 77 VQGCDA SVLLDDTGNFTGEKSAGPNAGSLRGFGVIDTIKALLEALCPRTVSCADILAVAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG

Sbjct: 137 RDSV-----VALGGPSWTVQLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S AN +P+P S+L+ L++ F+ GLS+ D+VALSG

Sbjct: 154 RRDSTTASLSTANTDLPSPASSLSTLLAAFARKGLSSTDMVALSG 198

Score = 64.7 bits (156), Expect = 6e-08

Identities = 30/65 (46%), Positives = 43/65 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S+L++ + + +A AQLS FY SCP ++K+ V++A+ + RMGASLLRL F
Sbjct: 13 SKLSVLILALATVVAARAQLSPTFYASSCPAALVTIKTAVRAALVLDRRMGASLLRLHF 72

Query: 766 HDCFV 780
HDCFV
Sbjct: 73 HDCFV 77

>ref|XP_002334018.1| predicted protein [Populus trichocarpa]
gb|EEE77880.1| predicted protein [Populus trichocarpa]
Length = 307

Score = 157 bits (397), Expect = 7e-36
Identities = 79/124 (63%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + LAPLDL TP SFDN YFKNL+
Sbjct: 186 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSNA--TLAPLDLVTPNSFDNYYFKNLM 243

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 244 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSAGQIRRIC 303

Query: 2167 RRIN 2178
+N
Sbjct: 304 SAVN 307

Score = 127 bits (319), Expect = 7e-27
Identities = 74/166 (44%), Positives = 95/166 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLD+T+S EK A N NSARG+ VID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 59 VQGCDASILLDETTSIQSEKTALGNLNSARGYNVIDKAKTEVEKICPGVVSCADIIAVAA 118

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP++ VKLG
Sbjct: 119 RDA-----SAYVGGPSYAVKLG 135

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 136 RRDSTTASRTLANAELPAFFESLESISRFGKKGLTARDMVALSGS 181

Score = 60.5 bits (145), Expect = 1e-06
Identities = 27/50 (54%), Positives = 36/50 (72%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+ AQLS FY SCPN S++ + ++SAI+ + RM ASL+RL FHDCFV
Sbjct: 10 ACQAQLSPAIFYDSSCPNALSAGTAIRSAIASDRRMAASLIRLHFHDCFV 59

>gb|EAY85151.1| hypothetical protein OsI_06506 [Oryza sativa Indica Group]
Length = 335

Score = 157 bits (397), Expect = 7e-36
Identities = 73/123 (59%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 211 AQCQFFRGHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 270

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 271 RRGLLHSDQELFNGGSQDERVKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 330

Query: 2170 RIN 2178
++
Sbjct: 331 VVS 333

Score = 138 bits (347), Expect = 4e-30
Identities = 76/171 (44%), Positives = 95/171 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+AA
Sbjct: 83 VQGCDASILLDDVQGFVGEKTAGPNANSIRGYEVIDKIKANVEAACPGVVSCADILALAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
R+ V + LGGP+W V LG
Sbjct: 143 REGVNL-----LGGPSWEVPLG 159

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHISH 1663
RRD+ TAS+S A++ +P P+S+L LI+ F GL+ +D+ ALSG I +
Sbjct: 160 RRDSTTASKSEADSDLPGPSSSLADLIAAFGKKGLAPRDMTALSGAHTIGY 210

Score = 58.2 bits (139), Expect = 5e-06
Identities = 26/45 (57%), Positives = 34/45 (75%)
Frame = +1

Query: 646 LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
++ ++Y SCP L + V+ T+ SAI E RMGAS+LRLFFHDCFV
Sbjct: 39 MTPSYRKSCPTLEAIVRGTMVSAIKAERRMGASILRLFFHDCFV 83

>emb|CAH10842.1| peroxidase [Picea abies]
Length = 320

Score = 157 bits (397), Expect = 7e-36
Identities = 77/124 (62%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ T FDN Y+ NL
Sbjct: 199 QSRCAFFRTRIYNESNINAAAFATSVKANCP--SAGGDNTLSPLDVVTSIKFDNKYYGNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KLLHSDQQLFNGG TDS V YSTN +F +DFAAAM+KM +ISPLTG++G+IRKNC
Sbjct: 257 IQKGLLHSDQQLFNGGPTDSQVTAYSTNQNSFFTDFAAAMVKMSNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 151 bits (382), Expect = 4e-34
Identities = 88/169 (52%), Positives = 98/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA
Sbjct: 72 VNGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GPTW V LG
Sbjct: 132 RDSV-----VELQGPTWTVM LG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP+P S+L+ LIS F GLSTKDLVALSG I
Sbjct: 149 RRDSTASLSDANNIPASSLSALISSFKHGLSTKDLVALSGAHTI 197

Score = 65.5 bits (158), Expect = 3e-08
Identities = 34/70 (48%), Positives = 43/70 (61%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGSAN-----AQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + + S N QLS+ FY SCP S VK V+ A++KE RMGASL+
Sbjct: 4 RTLLCIGVMAVFVCSININAVSGQLSSTFYDKSCPRAQSIVKRVVQAVAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783
RL FHDCFVN
Sbjct: 64 RLHFHDCFVN 73

>emb|CBI22007.1| unnamed protein product [Vitis vinifera]
Length = 425

Score = 157 bits (396), Expect = 9e-36
Identities = 75/121 (61%), Positives = 97/121 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIRTMNRFDNIYYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGNGEIRSNC 313

Query: 2167 R 2169
R
Sbjct: 314 R 314

Score = 151 bits (381), Expect = 5e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGV-----VQLGGPSWTVPGL 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I

Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 5e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSIISLLACSLNGQLSPNFYASTCPNVQNIVRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|XP_002283995.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 316

Score = 157 bits (396), Expect = 9e-36
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+
Sbjct: 195 KAQCIKFRYRIYNETNVDAFAKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++SPLTG++GEIR NC
Sbjct: 252 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTTFFTDVANAMVKMGNLSPLTGTGEIRTNC 311

Query: 2167 RRIN 2178
R+IN
Sbjct: 312 RKIN 315

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 101/167 (60%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V++GRR
Sbjct: 130 SV-----VALGGPTWTVMGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I
Sbjct: 147 DSTTASLSTANADLPAPTSDDLVLTSLSFNKGFTTQEMVALSGHTI 193

Score = 74.3 bits (181), Expect = 7e-11
Identities = 38/70 (54%), Positives = 48/70 (68%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSFFCMFSFLL--GMAHAQLSPNFYASSCPRALSTIRTAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAN81400.1| hypothetical protein [Vitis vinifera]
Length = 317

Score = 157 bits (396), Expect = 9e-36
Identities = 75/124 (60%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C F +RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFXSRIYNDTNIDPNFAATTRSTCP-VSG-GNSNLAPLDIRTMNRFDNIYYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGNGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 150 bits (380), Expect = 6e-34
Identities = 84/169 (49%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDT IKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W + LG
Sbjct: 129 RDGV-----VQLGGPSWTIPLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I
Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 5e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSIISLLACSINGQLSPNFYASTCPNVQNIVRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>emb|CAN63655.1| hypothetical protein [Vitis vinifera]
Length = 272

Score = 157 bits (396), Expect = 9e-36
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+
Sbjct: 151 KAQCIKFRYRIYNETNVDAAFASKKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 207

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++SPLTG++GEIR NC
Sbjct: 208 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTTFFTDVANAMVKGMLSPLTGTGDEIRTNC 267

Query: 2167 RRIN 2178
R+IN
Sbjct: 268 RKIN 271

Score = 150 bits (379), Expect = 8e-34
Identities = 83/168 (49%), Positives = 102/168 (60%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AAR 1333

QGCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AAR
 Sbjct: 25 QGCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAAAR 84
 Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
 DSV + LGGPTW V++GR
 Sbjct: 85 DSV-----VALGGPTWTVQMGR 101
 Query: 1514 RDARTASQSAANNIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
 RD+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I
 Sbjct: 102 RDSTTASLSTANADLPAPTSDDLVLTSLSNKGFTTQEMVALSGHTI 149

>gb|AAA20472.1| peroxidase [Cenchrus ciliaris]
 Length = 307

Score = 156 bits (395), Expect = 1e-35
 Identities = 75/125 (60%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
 Frame = +1
 Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QARCT FR RIY +TNI+ +FA +QQ+CPR+ G G NLAP+D QTP FDN Y+ NLV
 Sbjct: 188 QARCTTFRGRIYGD TNIDASFAALQQQTCPRSGGDG--NLAPIDAQTPARFDNAYYTNLV 245
 Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSN-GEIRKN 2163
 ++GL HSDQ+LFNGGS D++VR YS++P F+SDF AAMIKMG+I G+N G++R+N
 Sbjct: 246 SRRGLFHSDQELFNGGSQDALVRQYSSSPSQFN SDFVAAMIKMGNI----GANAGQVRRN 301
 Query: 2164 CRRIN 2178
 CR +N
 Sbjct: 302 CRVVN 306

Score = 108 bits (271), Expect = 3e-21
 Identities = 71/168 (42%), Positives = 83/168 (49%)
 Frame = +2
 Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
 +QGCD SIL S GEK+A PN NS RG+EVID IK VE CPGVVSCA I+ +AA
 Sbjct: 68 VQGCASIL----SRSGGEKSAGPNANSVRGYEVIDTIKKNVEAACPGVVSCATIVPLAA 123
 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1510
 R ++ G PTWNV LG
 Sbjct: 124 RPGPNLLGG-----PTWNVPLG 140
 Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSAALGLSTKDLVALSGTKH 1654
 RRD+ TA S AN +P PTS L LIS F LS +D++ALSG H
 Sbjct: 141 RRDSTAMLSTANQNLPPPTS-LGTLISLFGG-RLSARDMIALSGAHH 186

Score = 73.6 bits (179), Expect = 1e-10
Identities = 35/60 (58%), Positives = 44/60 (73%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
CL L+ +A+ AQLST FY SCPNL + V++ + A+S E RMGAS+LRLFFHDCFV
Sbjct: 9 CLLAISLLSFTAHAQLSTTFYASSCPNLQTVVRAAMTQAVSSEPRMGASILRFFHDCFV 68

>gb|ACF08096.1| class III peroxidase [Triticum aestivum]
Length = 313

Score = 156 bits (394), Expect = 1e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL
Sbjct: 188 QAQCQNFRDRLYNETNINSGFATSLKANCPQPTGSGDRNLANLDVSTPYSDNAYYSNLK 247

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R
Sbjct: 248 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKMGNLSPLTGSQGGVRL 307

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 308 SCSKVN 313

Score = 101 bits (252), Expect = 4e-19
Identities = 64/169 (37%), Positives = 83/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGFEVID+IK+ +E +C VSCADIL +AA
Sbjct: 66 VQGCDASVLLSGM-----EQNAFPNVMSLRGFEVIDSIKAKLETMCKQTVSCADILTVAA 120

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 121 RDSV-----VALGGPSWTVPGL 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P P +L L F G + D+VALSG I
Sbjct: 138 RRDSTNANEAVANSDDLPPFFDLVNLTSFGDGKFTVTDMAVALSGAHTI 186

Score = 72.4 bits (176), Expect = 3e-10
Identities = 36/72 (50%), Positives = 50/72 (69%)
Frame = +1

Query: 565 LTMAFCSRLTICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGA 744
+ +S + L +CLA+ +A+AQLS FY +CPN +++KS V +A++KE RMGA
Sbjct: 1 MASSSLSAVLLLCLAV-----AASAQLSPTFYDTTCPNALATIKAHTAAVNKENRMGA 54

Query: 745 SLLRLLFFHDCFV 780
SLLRL FHDCFV
Sbjct: 55 SLLRLHFHDCFV 66

>ref|XP_002461211.1| hypothetical protein SORBIDRAFT_02g042870 [Sorghum bicolor]
gb|EER97732.1| hypothetical protein SORBIDRAFT_02g042870 [Sorghum bicolor]
Length = 321

Score = 156 bits (394), Expect = 1e-35
Identities = 74/125 (59%), Positives = 95/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR IYN+TNI +AFA + Q +CPR +GSGD+ LAPLD +PT+FDN YF NL
Sbjct: 196 QAQCRFFRDHIYNDTNINSAFAASLQANCPRPANGSGDSTLAPLDAASPTAFDNAYFSNL 255

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ KGLLHSDQQLFNGGSTDS VR ++++ FS+ FA AM+ MG+I+P TGS G+IR
Sbjct: 256 MSHKGLLHSDQQLFNGGSTDSTVRSFASSASAFSNAFATAMVMGNIAPKTGSQQGIRVT 315

Query: 2164 CRRIN 2178
C ++N
Sbjct: 316 CSKVN 320

Score = 121 bits (303), Expect = 5e-25
Identities = 71/165 (43%), Positives = 88/165 (53%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD S+LL DT SFTGE+ A PN+NS RGF VID+IK+ VE VC VSCADILA+AA
Sbjct: 69 VDGCDASVLLADTGSFTGEQAIPNKNLSLGRFVIDSIKTQVEAVCNQTVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V +G
Sbjct: 129 RDSV-----VALGGPSWTVLVG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645

RRD+ TAS+ A +P P+ +L L F+ LS D+VALSG
Sbjct: 146 RRDSTTASKDNAERDLPPPSFDLANLTRSFANKNLSVTDMMVALSG 190

Score = 71.2 bits (173), Expect = 6e-10
Identities = 33/66 (50%), Positives = 47/66 (71%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLFF 765
SRL++ + + + +A AQLS+ FY SCP +++KS V +A++ E RMGASLLRL F
Sbjct: 5 SRLSLLVAILALATAATAQLSSTFYDTSCPKALATIKAHTAAVNNEARMGASLLRLHF 64

Query: 766 HDCFVN 783
HDCFV+
Sbjct: 65 HDCFVD 70

>sp|Q02200.1|PERX_NICSY RecName: Full=Lignin-forming anionic peroxidase; Flags: Precursor
gb|AAA34050.1| anionic peroxidase [Nicotiana sylvestris]
Length = 322

Score = 156 bits (394), Expect = 1e-35
Identities = 82/125 (65%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T+I+ FA TR++ CP+ +G NLAPLDL TP FDN YFKNL
Sbjct: 200 QAQCFLFRDRIYSNGTDIDAGFASTRRRQCPQEGENG--NLAPLDLVTPNQFDNYYFKNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LFNGGSTD+IV YS + FSSDFAAAMIKMGDISPL+G NG IRK
Sbjct: 258 IQKKGLLQSDQVLFNGGSTDNIVSEYSNSARAFSSDFAAAMIKMGDISPLSGQNGIIRKV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CGSVN 322

Score = 134 bits (337), Expect = 6e-29
Identities = 76/169 (44%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLD+T S EK A PN SARGF +I++ K VEK+CPGVVSCADIL +AA
Sbjct: 73 VQGCDASILLDETSPSIESEKALPNLGSARGFGIIEDAKREVEKICPGVVSCADILTVA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD+ S +GGP+W VKLG
Sbjct: 133 RDA-----SAAVGGPSWTVKLG 149

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNQLISRFSAALGLSTKDLVALSGTKHI 1657

RRD+ TAS++ A +P P LN+LIS F++ GLST+D+VALSG I

Sbjct: 150 RRDSTTASKTLAETDLPDPFDPLNRLISSFASKGLSTRDMVALSGAHTI 198

Score = 64.7 bits (156), Expect = 6e-08
Identities = 32/68 (47%), Positives = 47/68 (69%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756

SF ++ I +L +L +AQLS FY ++CPN +++++V+ AIS E RM ASL+R

Sbjct: 7 SFRAKAAI-FSLLLLSCMQCHAQLSATFYDNTCPNALNTIRTSVRQAISSERRMAASLIR 65

Query: 757 LFFHDCFV 780

L FHDCFV

Sbjct: 66 LHFHDCFV 73

>ref|XP_002437129.1| hypothetical protein SORBIDRAFT_10g021620 [Sorghum bicolor]
gb|EER88496.1| hypothetical protein SORBIDRAFT_10g021620 [Sorghum bicolor]

Length = 313

Score = 155 bits (393), Expect = 2e-35
Identities = 73/124 (58%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FR+RIY +TNI +FA RQQ+CP++ G G NLA +D QTPT FD Y+ NL+

Sbjct: 191 QARCTTFRSRIYGDTNINASFAALRQQTCPQSGGDG--NLASIDEQTPTRFDTDYTNLM 248

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

++GL HSDQ+LFNGGS D++VR YS + F+SDF AAMIKMG++ LTG+ G+IR+NC

Sbjct: 249 LQRGLFHSDQELFNGGSQDALVRQYSASSSLFNSDFVAAMIKMGNVGVLGTAGQIRRNC 308

Query: 2167 RRIN 2178

R +N

Sbjct: 309 RVVN 312

Score = 128 bits (322), Expect = 3e-27
Identities = 76/169 (44%), Positives = 90/169 (53%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

Sbjct: 66 VQGCDASVLLSGM-----EQNAIPNVMSLRGFEVIDSIKAQLETMCKQTVSCADILTVAA 120

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 121 RDSV-----VALGGPSWTVPLG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++AANN +P P +L L F G + D+VALSG I

Sbjct: 138 RRDSTNANEEAANNEPFPFDLVNLTQSFGDKGFTVTDMVALSGAHTI 186

Score = 72.4 bits (176), Expect = 3e-10
Identities = 36/72 (50%), Positives = 50/72 (69%)
Frame = +1

Query: 565 LTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
+ +S + L +CLA+ +A+AQLS FY +CPN +++KS V +A++KE RMGA

Sbjct: 1 MASSSLSAVLLLCLAV-----AASAQLSPTFYDTTCPNALATIKA VTA AVNKENRMGA 54

Query: 745 SLLRLFFHDCFV 780
SLLRL FHDCFV

Sbjct: 55 SLLRLHFHDCFV 66

>gb|ACI03401.1| peroxidase 1 [Litchi chinensis]
Length = 318

Score = 155 bits (392), Expect = 2e-35
Identities = 87/169 (51%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LLDDTS+F GEK A PN S RGF V+D IK+ +EK CPGVVSCAD+LAI AA

Sbjct: 69 VNGCDGSLLDDTSTFVGEKTAVPNNISVRGFNVVDQIKAKLEKACPGVVSCADLLAI AA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG

Sbjct: 129 RDSV-----VHLGGPSWKVRLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN IP PTSNL+ LIS FSA GLS KDLVALSG+ I

Sbjct: 146 RRDSTTASRALANTSIPPPTSNSALISSFSAQGLSLKDLVALSGSHTI 194

Score = 150 bits (379), Expect = 8e-34
Identities = 70/123 (56%), Positives = 91/123 (73%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT+FR +YN+TNI+++FA++ ++ CPR+ DN LA LD QTP FD Y+ NL++
Sbjct: 197 ARCTSFRGHVYNDTNIDSSFAQLRRKCPRSGN--DNVLANLDRQTPFCFDKLYYDNLLK 254

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKGLLHSDQQLF GGS D V+ Y+ N F DFA AM+KMG+I PLTG G+IR NCR
Sbjct: 255 KKGLLHSDQQLFKGGSadPFVKKYANNTSAFFKDFAGAMVKMGNIKPLTGRAGQIRINCR 314

Query: 2170 RIN 2178
++N
Sbjct: 315 KVN 317

Score = 63.9 bits (154), Expect = 1e-07
Identities = 31/50 (62%), Positives = 34/50 (68%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
AN QL NFY +CP S V V +AI ETR+GASLLRL FHD CFVN
Sbjct: 21 ANGQLCPNFYESTCPQALSIVHKGVAIAIKNETRIGASLLRLHFHDCFVN 70

>ref|XP_002284007.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 316

Score = 155 bits (392), Expect = 2e-35
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C+ FR RIYNETNI+ FA ++Q CP S GD NL+ LD +T T FDN YF NL+
Sbjct: 195 KAQCSKFRDRIYNETNIDATFATSKQAICP--SSGGDENLSDLD-ETTTVFDNVYFTNLI 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQLFNG STDS+V YS + TF +D A+AM+KMG++SPLTG++GEIR NC
Sbjct: 252 EKKGLLHSDQQLYNGNSTDSMVETYSNDSTTFFTDVASAMVKMGNLSPLTGTGDEIRTNC 311

Query: 2167 RRIN 2178
R IN
Sbjct: 312 RAIN 315

Score = 151 bits (381), Expect = 5e-34
Identities = 83/167 (49%), Positives = 102/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTANFTGEKTAGPNNNSVRGYDV IDTIKSMESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V+LGRR
Sbjct: 130 SV-----VALGGPTWTVQLGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V LSGT I
Sbjct: 147 DSTTASFSTANS DLPAPTS DLDALISLFSNKGFTTQEMVVLSGHTI 193

Score = 70.9 bits (172), Expect = 8e-10
Identities = 35/70 (50%), Positives = 50/70 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+++Y SCP+ S++++ V +A++ E+RMGASL
Sbjct: 1 MASLSLFSLFCMFSFLL--GMAHAQLSSDYSSSCPSALSTIQTAVNNAVADES RMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>ref|XP_002323054.1| predicted protein [Populus trichocarpa]
gb|EEF04815.1| predicted protein [Populus trichocarpa]
Length = 317

Score = 155 bits (392), Expect = 2e-35
Identities = 74/124 (59%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT F RI NETNI+++F + Q C T NN PLD+ +PTSFD+ Y++NL+
Sbjct: 199 QARCTTFLTRINNETNIDSSFKTSTQAQCQNT-----NNFVPLDVTSP TSFDSAYYRNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLF+GGSTD+ VR YS+N F +DFA AMIKMG++SPLTG+NG+IR NC
Sbjct: 254 NQKGLLHSDQQLFSGGSTDAQVRAYSSNQAAFRTDFANAMIKMGNLSPLTG TNGQIRTNC 313

Query: 2167 RRIN 2178
R+ N
Sbjct: 314 RKAN 317

Score = 119 bits (297), Expect = 3e-24
Identities = 73/170 (42%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCD S+LLD GEK A N NS RGFEVID+IK+ +E CPGVVSCADIL++AA
Sbjct: 76 VNGCDASVLLDG-----GEKTAPANTNSLRGFEVIDSIKTQLESSCPGVVSCADILSVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 131 RDSV-----VALGGPSWQVQLG 147

Query: 1511 RRDARTA-SQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA S S NN +P+P +++ LIS FS G + K++VALSG+ I
Sbjct: 148 RRDSATAGSVSDVNNVPSPALSVSGLISAFSNGFTAKEMVALSGSHTI 197

Score = 79.0 bits (193), Expect = 3e-12
Identities = 37/57 (64%), Positives = 46/57 (80%)
Frame = +1

Query: 613 FVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
F+L+ G A+AQL++NFY SCP++ S +KS V SA+S E RMGASLLRL FHDCFVN
Sbjct: 21 FLLLVGVAS AQLASNFYGTSCPSVLSVIKSAVDSAVSNEARMGASLLRLHFHDCFVN 77

>gb|EEC82681.1| hypothetical protein OsI_27325 [Oryza sativa Indica Group]
Length = 313

Score = 155 bits (392), Expect = 2e-35
Identities = 70/124 (56%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFD Y+ NL+
Sbjct: 190 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTTPYSFDTAYYSNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PL GS G+IR +C
Sbjct: 250 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLIGSQGQIRLSC 309

Query: 2167 RRIN 2178
++N
Sbjct: 310 SKVN 313

Score = 129 bits (325), Expect = 1e-27

Identities = 73/167 (43%), Positives = 91/167 (54%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AARD

Sbjct: 65 GCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAARD 124

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 125 SV-----VALGGPSWTVGLGRR 141

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 DSTTASMDSANNDLPPPFDDLENLIKAFGDKGFSVTDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 3e-08
Identities = 30/61 (49%), Positives = 43/61 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC

Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTA AVNNEPRMGASLLRLHFHDC 63

Query: 775 F 777

F
Sbjct: 64 F 64

>gb|EAZ01280.1| hypothetical protein OsI_23303 [Oryza sativa Indica Group]
Length = 327

Score = 155 bits (392), Expect = 2e-35
Identities = 73/124 (58%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV

Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNP GTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC

Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RRIN 2178

R++N
Sbjct: 324 RKNV 327

Score = 135 bits (339), Expect = 3e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTPTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANANLPGPASSGASLVAAFAGKGLSAREMTALSG 199

Score = 67.0 bits (162), Expect = 1e-08
Identities = 30/51 (58%), Positives = 39/51 (76%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+A A LST FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSTKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIIRLFFHDCFVN 79

>gb|AAV89058.1| class III peroxidase [Phelipanche ramosa]
Length = 325

Score = 155 bits (392), Expect = 2e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
Q+RC FR+RIY N T+I+ FA TR++ CP+T G DNNLAPLDL TP SFDN YF+NL
Sbjct: 203 QSRCFLFRSRIYSNGTDIDPNFASTRRRRQCPQTGG--DNNLAPLDLVTSPNSFDNNYFRNL 260

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGST+++V YS NP F++DFA+AM++M +I PL GSNG IR+
Sbjct: 261 IQRKGLLESdqVLFNGGSTNALVTSYNNPRLFATDFASAMVRMSEIQPLLGSNGIIRRV 320

Query: 2164 CRRIN 2178
C IN
Sbjct: 321 CNVIN 325

Score = 124 bits (311), Expect = 6e-26
Identities = 70/169 (41%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+ + EK+A PN NS RG++VI+ K VE +CP VSCADI+A+AA
Sbjct: 76 VQGCASILLDDSPTIQSEKSAGPNVNSVRGYDVIETAKREVESICPRNVSCADIVALAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW VKLG
Sbjct: 136 RDA-----SVAVGGPTWTVKLG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ + AN +P+P ++L LI+ F GLS D+VALSG+ I
Sbjct: 153 RRDSTTANPNEANTDLPSPFASLQTLITAFDDKGLSETDMVALSGSHTI 201

Score = 61.2 bits (147), Expect = 6e-07
Identities = 31/71 (43%), Positives = 46/71 (64%), Gaps = 3/71 (4%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGS---ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
S S LT+ ++ +L+ S AQLS FY CPN S++++++ A++ E RM AS
Sbjct: 6 SINSLLTLTISSLILLSLSITPCQAQLSPTFYDSICPNALSTIRTSIRRAVAAERRMAAS 65

Query: 748 LLRLFFHDCFV 780
L+RL FHDCFV
Sbjct: 66 LIRLHFHDCFV 76

>gb|AAW52719.1| peroxidase 5 [Triticum monococcum]
Length = 259

Score = 155 bits (392), Expect = 2e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL
Sbjct: 134 QAQCLNFRDRLYNETNINSGFATSLKANCPQPTGSGDRNLANLDVLTPTSFDNAYYSNLK 193

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R
Sbjct: 194 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKMGNSPLTGSQGGQVRL 253

Query: 2161 NCRRIN 2178
+C ++N

Sbjct: 254 SCSKVN 259

Score = 101 bits (252), Expect = 4e-19
Identities = 64/169 (37%), Positives = 83/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGFVID+IK+ +E +C VSCADIL +AA
Sbjct: 12 VQGCDAVLLSGM-----EQNAFPNVMSLRGFVIDSIKAKLETMCKQTVSCADILTVAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 67 RDSV-----VALGGPSWTVPLG 83

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P P +L L F G + D+VALSG I
Sbjct: 84 RRDSTNANEAVANSDLPPPFDLVNLTSFGDKGFTVTDMVALSGAHTI 132

>gb|AAC49819.1| peroxidase [Oryza sativa Indica Group]
Length = 315

Score = 155 bits (392), Expect = 2e-35
Identities = 70/124 (56%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFD Y+ NL+
Sbjct: 192 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTPYSFDTAYYSNLL 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR ++N FSS F++AM+KM ++ PL GS G+IR +C
Sbjct: 252 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLIGSQGQIRLSC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 132 bits (331), Expect = 3e-28
Identities = 74/169 (43%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AA
Sbjct: 65 VQGCDAVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVGLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSLGLSTKDLVALSGTKHI 1657
RRD+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 RRDSTTASMDSANNDLPPPFDLLENLIKAFGDKGFSVTDMVALSGAHTI 190

Score = 67.0 bits (162), Expect = 1e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTA AVNNEPRMGASLLRLHFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>dbj|BAD97435.1| peroxidase [Pisum sativum]
Length = 318

Score = 155 bits (392), Expect = 2e-35
Identities = 80/125 (64%), Positives = 91/125 (72%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q C FR RIYNETNI+T FA R+ +CP S GD NLAPLD TPT+FDN Y+ +L+
Sbjct: 196 QTECQFFRNRIYNETNIDTNFATLRKSNCP--SSGGDTNLAPLDSVTPTTFDNNYYNDLI 253

Query: 1987 QKKGLLHSDQQLFNG--GSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
KGLLHSDQ LFNG GS S+VR YS N F DFAAAMIK+ ISPLTG+NGEIRKN
Sbjct: 254 ANKGLLHSDQALFNGVGSQVSLVRTYSRNTVAFKRDFAAAMIKLSRISPLTGTNGEIRKN 313

Query: 2164 CRRIN 2178
CR +N
Sbjct: 314 CRLVN 318

Score = 141 bits (355), Expect = 5e-31
Identities = 82/169 (48%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCDGSILLDDT++FTGEK+A PN NSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDGSILLDDTATFTGEKSAGPNINSARGFEVIDTIKTNVEASCNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + ++ GGPTW V LG
Sbjct: 129 RDGIFLL-----GGPTWMVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAAN+ IP P+S+L L + F GL+ DL LSG I
Sbjct: 146 RRDARTASQSAANSQIPGPSSDLATLTMTFRNKGLTLNDLTVLSGAHTI 194

Score = 73.9 bits (180), Expect = 1e-10
Identities = 38/71 (53%), Positives = 52/71 (73%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+F +L + L++ L+ S NAQL NFY +CP+L + V++T+ SAI E R+GAS+
Sbjct: 1 MATFI-KLFVTLSTIIISLLACSTNAQLINNFYATTCPSLQTIVRNTMISAIKTEARIGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|NP_001057821.1| Os06g0547100 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54117.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69329.1| TPA: class III peroxidase 87 precursor [Oryza sativa (japonica
cultivar-group)]
gb|EAZ37289.1| hypothetical protein OsJ_21627 [Oryza sativa Japonica Group]
Length = 327

Score = 155 bits (392), Expect = 2e-35
Identities = 73/124 (58%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV
Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC
Sbjct: 264 AQRGLLHSDQQLFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RRIN 2178
R++N

Sbjct: 324 RKNV 327

Score = 134 bits (338), Expect = 5e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTLTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANLPGPASSGASLVAAFAGKGLSAREMTALSG 199

Score = 64.7 bits (156), Expect = 6e-08
Identities = 29/51 (56%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+A A LS FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSIKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIIRLFFHDCFVN 79

>emb|CBI19220.1| unnamed protein product [Vitis vinifera]
Length = 373

Score = 155 bits (391), Expect = 3e-35
Identities = 85/167 (50%), Positives = 103/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1336
GCD SILLDDT+SFTGEK A PN++S RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTASFTGEKTAGPNKDSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW ++LGR
Sbjct: 130 SV-----VALGGPTWTLQLGR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +P P S+L+ LISRFS G +TK++VALSGT I
Sbjct: 147 DSTTASLSTANSIDLPGPASDLSTLISRFSNKGFTTKEMVALSGTHTI 193

Score = 128 bits (321), Expect = 4e-27
Identities = 64/95 (67%), Positives = 76/95 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR+RIYNETNI+ AFA ++Q+ CP T G DNNL+ LD +T T FDN YF+NL
Sbjct: 195 KARCTSFRRSRIYNETNIDAAFATSKQKICPSTGG--DNNLSLDL-ETTTVFDNVYFRNLK 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSD 2091
KKGLLHSDQQL+NGGSTDSIV YSTN TF +D
Sbjct: 252 AKKGLLHSDQQLYNGGSTDSIVETYSTNSATFFTD 286

Score = 75.1 bits (183), Expect = 4e-11
Identities = 38/70 (54%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSLCVFSFLL--GMAHAQLSSNFYASSCPKALSTIRAAVNNAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>gb|ACN30737.1| unknown [Zea mays]
Length = 260

Score = 155 bits (391), Expect = 3e-35
Identities = 73/127 (57%), Positives = 97/127 (76%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF NL+
Sbjct: 134 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPDADFNDAYFGNLL 193

Query: 1987 QKKGLLHSDQQLF---NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIR 2157
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GEIR
Sbjct: 194 SQRGLLHSDQALFGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGSISPLTGTGDEIR 253

Query: 2158 KNCRIN 2178
NCRR+N
Sbjct: 254 VNCRRVN 260

Score = 145 bits (365), Expect = 3e-32
Identities = 82/164 (50%), Positives = 96/164 (58%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AAR 1333
QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AAR
Sbjct: 8 QGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAV AAR 67

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV LGGP+W V LGR
Sbjct: 68 DSAQ-----LGGPSWAVPLGR 84

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 85 RDATTASASLANSDLPGPTSSLNGLLNAFSNGLSSTDMMVALSG 128

>gb|ACG40622.1| peroxidase 2 precursor [Zea mays]
Length = 342

Score = 155 bits (391), Expect = 3e-35
Identities = 73/127 (57%), Positives = 97/127 (76%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF NL+
Sbjct: 216 RAQCKNCRARIYNDTIDASFAASLRASCPAQAGAGDGALEPLDGSTPDADFNDAYFGNLL 275

Query: 1987 QKKGLLHSDQQLF---NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIR 2157
++GGLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GEIR
Sbjct: 276 SQRGLLHSDQALFGGGGGGATDGLVSAYASNAGQWGADFAAAMVKGMSISPLTGTGDEIR 335

Query: 2158 KNCRRIN 2178
NCRR+N
Sbjct: 336 VNCRRVN 342

Score = 145 bits (366), Expect = 3e-32
Identities = 82/165 (49%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI A 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AA
Sbjct: 89 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAV A 148

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV LGGP+W V LG
Sbjct: 149 RDSVAQ-----LGGPSWAVPLG 165

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 166 RRDATTASASLANSDLPGPTSSLNGLLNAFSNKGLSSTDMDVALSG 210

Score = 57.8 bits (138), Expect = 7e-06
Identities = 32/67 (47%), Positives = 41/67 (61%), Gaps = 1/67 (1%)
Frame = +1

Query: 583 CSRLTICLALFVLIWGSANAQLSTNFYYH-SCPNLFSSVKSTVQSAISKETRMGASLLRL 759
C L + LAL +AQLS+ YY SCP ++++ V +A+ E RMGASLLRL
Sbjct: 24 CGLLVLALALATTA-AVGSAQLSSESYYDASCPAALLTIRTAVSTAVLLEPRMGASLLRL 82

Query: 760 FFHDCFV 780
FFHDCFV
Sbjct: 83 HFHDCFV 89

>emb|CAN83972.1| hypothetical protein [Vitis vinifera]
Length = 290

Score = 154 bits (390), Expect = 4e-35
Identities = 76/124 (61%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C+ FR RIYNETNI+ FA ++Q CP S GD NL+ LD T T FDN YF NL+
Sbjct: 169 KQCSKFRDRIYNETNIDATFATSKQAICP--SSGGDENLSDLXTT-TXFDNVYFTNLI 225

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YS + TF +D A+AM+KMG++SPLTG++GEIR NC
Sbjct: 226 EKKGLLHSDQQLYNGNSTDSMVETYSNDSTTFFTDVASAMVKGNSPLTGTGDEIRTNC 285

Query: 2167 RRIN 2178
R IN
Sbjct: 286 RAIN 289

Score = 135 bits (340), Expect = 3e-29
Identities = 81/186 (43%), Positives = 101/186 (54%), Gaps = 18/186 (9%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFE-----VIDNIKSAVE 1279
QGCD SILLDDT++FTGEK A PN NS RG++ + IKS +E

Sbjct: 25 QGCDASILDDDTANFTGEKTAGPNNNSXRGYDSSNCGSDWYPLCIRVVTCTENTIKSQME 84

Query: 1280 KVC PGV VSCADILAI AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC 1459
+CPGVVSCADI+A+AARDSV

Sbjct: 85 SLCPGVVSCADIVAVAARDSV----- 105

Query: 1460 *F*SI*LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVAL 1639
+ LGGPTW V+LGRRD+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V L

Sbjct: 106 ----VALGGPTWTVQLGRRDSTASFSTANS DLPAPTS DLDALISLFSNKGFTTQEMVVL 161

Query: 1640 SGT KHI 1657
SGT I

Sbjct: 162 SGT HTI 167

>ref|XP_002509737.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus communis]
gb|EEF51124.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus communis]
Length = 322

Score = 154 bits (389), Expect = 6e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ +CP+T G+G NLAPLDL TP +FDN Y+ NL

Sbjct: 200 QAQCVTFRDRIYNNASDIDPDFAATRRGNCPQTGGNG--NLAPLDLVTPNNFDNNYYSNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ K+GLL SDQ LF+GGSTDSIV YST+ +F SDFAAAM+KMG+ISPLTG+ GEIR+

Sbjct: 258 IAKRGLLASDQILFSGGSTDSIVNEYSTDSSSFSDFAAAMVKGNI SPLTGTQGEIRRI 317

Query: 2164 CRRIN 2178
C +N

Sbjct: 318 CSAVN 322

Score = 131 bits (330), Expect = 4e-28
Identities = 75/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI A 1330
+QGCDGS+LL DT +FTGEK+A N NS RG VID+ K+ VE +CPG+VSCADILA+AA

Sbjct: 73 VQGCDGSVLLVDTPFTTGEKSARNNANSIRGENVIDDAKAQVESICPGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GGP+W V LG

Sbjct: 133 RDA-----SVAAGGPSWTVNLG 149

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P + LN+LIS FS GL+ +D+VALSG I

Sbjct: 150 RRDSTTASLAQANSIDLPGFSDPLNRLISLFSKGLNERDMVALSGAHTI 198

Score = 68.9 bits (167), Expect = 3e-09
Identities = 36/73 (49%), Positives = 49/73 (67%), Gaps = 3/73 (4%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSA---NAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMG 741
MAS S + L +F +I S+ AQLS+NFY ++CPN +++KS + +AI E RM
Sbjct: 1 MASRLSFACMILTIFFIINYSSLPCQAQLSSNFYDNTCPNALTTIKSAIDAAIESEQRMA 60

Query: 742 ASLLRLFFHDCFV 780
ASL+RL FHDCFV
Sbjct: 61 ASLIRLHFHDCFV 73

>ref|XP_002268412.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 318

Score = 154 bits (389), Expect = 6e-35
Identities = 75/123 (60%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C F+ RIYNE+NI+ AFAR RQ +CP GD LAPLD T FD YF NLV+
Sbjct: 199 AQC�FFKNRIYNESNIDPAFARARQSTCP--PNGGDTKLAPLD-PTAARFDTGYFTNLVK 255

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGSTD++V+ YSTN G FS+DFA +M+KMG+I PLTG G+IR NCR
Sbjct: 256 RRGLLHSDQALFNGGSTDTLVKTYSTNFGAFSADFAKSMVKMGNIKPLTGKKGQIRVNCR 315

Query: 2170 RIN 2178
++N
Sbjct: 316 KVN 318

Score = 136 bits (343), Expect = 1e-29
Identities = 82/166 (49%), Positives = 97/166 (58%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+ EKNA N NSARGF V+D+IKS V+KVC VVSCADILA+A
Sbjct: 70 VNGCDASILLDATSTIDSEKNAGANANSARGFNVDIKSQVDKVCGRPVVSCADILAVA 129

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 130 ARDSV-----VALGGPSWTVQL 146

Query: 1508 GRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TAS++ ANN IP+P +L LI+RFS GL TKDLVALSG
Sbjct: 147 GRRDSTTASRTDANNIPSPFMDLPALITRFSNQGLDTKDLVALSG 192

Score = 66.6 bits (161), Expect = 2e-08
Identities = 35/69 (50%), Positives = 42/69 (60%), Gaps = 3/69 (4%)
Frame = +1

Query: 586 SRLTICLALFVLI---WGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756
SR +CL FVL +A LS FY CP ++K V++A+ KE RMGASLLR
Sbjct: 3 SRSLLCLYAFVLFLSLATADFSAALSPYFYNKVCPKALPTIKRVVEAAVQKEKRMGASLLR 62

Query: 757 LFFHDCFVN 783
L FHDCFVN
Sbjct: 63 LHFHDCFVN 71

>dbj|BAD36900.1| peroxidase [Lotus japonicus]
Length = 143

Score = 154 bits (389), Expect = 6e-35
Identities = 73/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC+ FR+RIY+E NI+ A+AR+ Q CPRTSG GD+NL+P+D TP FD+ Y++NL+
Sbjct: 21 QSRCSLFRSRIYSEQNIDPAYARSLGGQCPRTSGVGDNLSPIDT-TPNFFDSTYYRNLM 79

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GL HSDQQLFNGGSTDS V Y++NP F DFA AM+KMG++ LTG+ G+IRK C
Sbjct: 80 NKRGLFHSDQQLFNGGSTDSKVSQYASNPLLFRIDFANAMVKMGNLGTLTGTGQGIKVC 139

Query: 2167 RRIN 2178
+N
Sbjct: 140 SSVN 143

>gb|ACN26131.1| unknown [Zea mays]
Length = 323

Score = 154 bits (388), Expect = 7e-35
Identities = 71/124 (57%), Positives = 93/124 (75%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR RIYN+ NI FA RQQ+CP G D LAP+D+QTP +FDN Y+KNL+

Sbjct: 202 QARCATFRNRIYNDGNINATFASLRQQTCPLAGG--DAALAPIDVQTPEAFDNAYYKNLM 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++V+ YS N F++DFA AM++MG ISPLT + GE+R +C

Sbjct: 260 ARQGLFHSDQELFNGGSQDALVKKYSGNAAMFTADFAKAMVRMGASPLTATQGEVRLDC 319

Query: 2167 RRIN 2178

R++N

Sbjct: 320 RKNV 323

Score = 140 bits (353), Expect = 8e-31

Identities = 79/165 (47%), Positives = 94/165 (56%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA

Sbjct: 75 VNGCDASILLDDTATFTGEKNAGPNANSVRGYEVIDAIKARVEASCNATVSCADILALAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LGGP+W V LG

Sbjct: 135 RDAVNL-----LGGPSWTVYLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDARTASQS AN +P P S+L L++ F GLS +D+ ALSG

Sbjct: 152 RRDARTASQSDANANLPGPGSSLATLVMTFGNKGLSARDMTALSG 196

Score = 67.8 bits (164), Expect = 7e-09

Identities = 36/73 (49%), Positives = 47/73 (64%), Gaps = 4/73 (5%)

Frame = +1

Query: 577 SFCSRLTICLALF----VLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGA 744
S S + CL L VL +A LST+FY CP++ S V++ V SA++ E RMGA

Sbjct: 4 SAASSVVRCLQLLTVA AVLAGAAAGGLSTSFYSKKCPDVQSIVRAGVASAVAAE KRMGA 63

Query: 745 SLLRLFFHDCFVN 783

S+LR+FFHDCFVN

Sbjct: 64 SILRMFFHDCFVN 76

>gb|ACF08094.1| class III peroxidase [Triticum aestivum]

Length = 321

Score = 153 bits (387), Expect = 9e-35
Identities = 70/124 (56%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR+R+YNETNI+ AFA + + +CPRT+ SG+++LAPLD TP FDN Y+ NL+
Sbjct: 198 QSQCRFFRSRLYNETNIDAAFATSLKANCPRRTSSGNSSLAPLDTTTPNGFDNAYYSNLM 257

Query: 1987 QKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DFAAAM++MG+ISPLTG+ G+IR +C
Sbjct: 258 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRDFAAAMVRMGNISPLTGAQGGIRLSC 317

Query: 2167 RRIN 2178
R+N
Sbjct: 318 SRVN 321

Score = 132 bits (332), Expect = 2e-28
Identities = 76/165 (46%), Positives = 93/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 71 VQGCDAVLLSDTATFTGEQGAAPNARSIRGMNVIDNIKAQVEAVCRQTVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 131 RDSV-----VALGGPSWTVPPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RRD+ TAS S AN+ +PAP+ +L L + F+A GLS D+VALSG
Sbjct: 148 RRDSTTASLSLANS DLPAPSF DLANLTANFAAKGLSVTDMVALSG 192

Score = 65.5 bits (158), Expect = 3e-08
Identities = 32/63 (50%), Positives = 41/63 (65%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L++ L L + SA+ LS FY SCP +++KS V +A+ E RMGASLLRL FHD
Sbjct: 9 LSVLLLLCLAAAASAPPLSPQFYAKSCPRALATIKSAVTA AVRSEPRMGASLLRLHFHD 68

Query: 772 CFV 780
CFV
Sbjct: 69 CFV 71

>ref|XP_002509733.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF51120.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 321

Score = 153 bits (387), Expect = 9e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ +CP+T G+G NLAPLDL TP +FDN Y+ NL
Sbjct: 199 QAQCVTFRDRIYNNASDIDPDFAATRRGNCPQTGGNG--NLAPLDLVTNNFDNNYYSNL 256

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ K+GLL SDQ LF+GGSTDSIV YST+ +F SDFAAAM+KMG+ISPLTG+ GEIR+
Sbjct: 257 MAKRGLLASDQILFSGGSTDSIVNEYSTDSSSFSDFAAAMVKGNIPLTGTQGEIRRL 316

Query: 2164 CRRIN 2178
C +N
Sbjct: 317 CSAVN 321

Score = 131 bits (330), Expect = 4e-28
Identities = 75/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGS+LL DT +FTGEK+A N NS RG VID+ K+ VE +CPG+VSCADILA+AA
Sbjct: 72 VQGCDGSVLLVDTPFTFTGEKSARNNANSIRGENVIDDAKAQVESICPGIVSCADILAVAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GGP+W V LG
Sbjct: 132 RDA-----SVAAGGPSWTNVLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P + LN+LIS FS GL+ +D+VALSG I
Sbjct: 149 RRDSTTASLAQANSIDLPGFSDPLNRLISLFSKGLNERDMVALSGAHTI 197

Score = 67.4 bits (163), Expect = 9e-09
Identities = 35/72 (48%), Positives = 48/72 (66%), Gaps = 2/72 (2%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGA--NAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGA 744
MAS S + L +F + S+ AQLS+NFY ++CPN +++KS + +AI E RM A

Sbjct: 1 MASHLSFACMILTIFFIPNYSSLCQAQLSSNFYDNTCPNALTTIKSAIDAAIESEQRMAA 60

Query: 745 SLLRLFFHDCFV 780
SL+RL FHDCFV

Sbjct: 61 SLIRLHFHDCFV 72

>ref|XP_002319407.1| predicted protein [Populus trichocarpa]
gb|EEE95330.1| predicted protein [Populus trichocarpa]
Length = 302

Score = 153 bits (387), Expect = 9e-35
Identities = 72/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YNET++++ A + + +CP T D++L+ LD TP +FDN YFKNL
Sbjct: 181 QARCLLFRNRVYNETSLSLSTLTKSNCPNTGS--DDSLSSLDATTPVTFDINSYFKNLA 238

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLF+GG+TDS V+ YS N TF +DFA+AM+KMG ISPLTGS+G+IR NC
Sbjct: 239 NNKGLLHSDQQLFSGGTTDSQVKTYINSATFYADFASAMVKMGISPLTGSQGIRTNC 298

Query: 2167 RRIN 2178
++N
Sbjct: 299 AKVN 302

Score = 147 bits (372), Expect = 5e-33
Identities = 83/180 (46%), Positives = 105/180 (58%)
Frame = +2

Query: 1118 AS*ILSKH*QMCGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV 1297
AS + + H QGCD S+LLDDTSSFTGEK A PN NS RG++VID IKS +E +CPGV
Sbjct: 43 ASLLRLHFHDCFQGCDA SVLLDDTSSFTGEKTAGPNANSLRGYDVIDTIKSQLESICPGV 102

Query: 1298 VSCADILAI AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI* 1477
VSCADILA+AARDSV +
Sbjct: 103 VSCADILAVAARDSV-----VA 119

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
L GP+W V+LGRRD+ TAS AAN+ +P+P +L+ LI+ FS G + K++VALSG+ I
Sbjct: 120 LSGPSWTVQLGRRDSTASLGAANS DLP SPLMDLSDLITSFSNKGFTAKEMVALSGSHTI 179

Score = 65.5 bits (158), Expect = 3e-08
Identities = 30/54 (55%), Positives = 39/54 (72%)

Frame = +1

Query: 616 VLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRRLFHDCF 777
+L+ G +AQLST FY +CP S++++ V A+ KE RMGASLLRL FHDCE
Sbjct: 1 MLLGLVHAQLSTTFYATTCPKALSTIRTAVLKAVVKEHRMGASLLRRLFHDCF 54

>dbj|BAA77388.1| peroxidase 2 [Scutellaria baicalensis]
Length = 325

Score = 153 bits (387), Expect = 9e-35
Identities = 78/126 (61%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
Q++C NFRARIY N ++IE FA TR++ CP+ GSGD+NLAPLDL TP SFDN Y++NL
Sbjct: 201 QSQCGNFRARIYSNGSDIEANFASTRRRQCPQ-DGSGDSNLAPLDLVTPNSFDNYYRNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPL-TGSNGEIRK 2160
V ++GLL SDQ L +GG TD+IV YS+NP TF+SDFA AMIKMG+I PL G NG IR+
Sbjct: 260 VARRGLLQSDQVLLSGGETDAIVTSYSSNPATFASDFANAMIKMGEIQPLQLGQNGIIRR 319

Query: 2161 NCRRIN 2178
C +N
Sbjct: 320 TCGAVN 325

Score = 140 bits (353), Expect = 8e-31
Identities = 75/165 (45%), Positives = 98/165 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLD+TS+ EK A PN S RGF+VID K+AVE++CPGVVSCADIL +AA
Sbjct: 74 VQGCDA SILLDETSTIQSEKTAGPNAGSVRGFQVIDAAKTAVERLCPGVVSCADILTAA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 134 RDA-----SVAVGGPSWTVRLG 150

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TA+++ AN +P PTS L QLI+RF A GL+ +++VALSG
Sbjct: 151 RRDSTTANRAQANTDLPGPTSTLTQLITRFDAKGLNAREMVALSG 195

Score = 63.9 bits (154), Expect = 1e-07
Identities = 30/68 (44%), Positives = 44/68 (64%)
Frame = +1

Query: 577 SFC SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR 756
SF +I + +L + AQLS FY +CPN S++++++ A+S E RM ASL+R
Sbjct: 7 SFRPIFSIAALVLLLTLPSEAQLSATFYDSTCPNAVSTIRTSIRQAVSAERRMAASLIR 66

Query: 757 LFFHDCFV 780
L FHDCFV
Sbjct: 67 LHFHDCFV 74

>gb|ACF08095.1| class III peroxidase [Triticum aestivum]
Length = 321

Score = 153 bits (386), Expect = 1e-34
Identities = 69/124 (55%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
Q++C FR+R+YNETNI+ AFA + + +CPR++GSG+++LAPLD TP FDN Y+ NL+
Sbjct: 198 QSQCRFFRSRLYNETNIDAAFAASLKANCPRSTGSGNSSLAPLDTNTPNGFDNAYYSNLM 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DFA AM++MG+ISPLTG+ G+IR +C
Sbjct: 258 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRFDAVAMVRMGNISPLTGAQGGIRLSC 317

Query: 2167 RRIN 2178
R+N
Sbjct: 318 SRVN 321

Score = 132 bits (332), Expect = 2e-28
Identities = 76/165 (46%), Positives = 93/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 71 VQGCDASVLLSDTATFTGEQGAAPNARSIRGMNVIDNIKAQVEAVCRQTVSCADILAVAA 130

Query: 1331 RDSVQIVSGGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 131 RDSV-----VALGGPSWTVPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S AN+ +PAP+ +L L + F+A GLS D+VALSG
Sbjct: 148 RRDSTTASLSLANS DLPAPSFDLANLTANFAAKGLSVTDMVALSG 192

Score = 67.8 bits (164), Expect = 7e-09
Identities = 33/63 (52%), Positives = 42/63 (66%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L++ L L + SA+ QLS FY SCP +++KS V +A+ E RMGASLLRL FHD
Sbjct: 9 LSVLLLLCLAAAASASPQLSPQFYAKSCPRALATIKSAVTA AVRSEPRMGASLLRLHFHD 68

Query: 772 CFV 780
CFV
Sbjct: 69 CFV 71

>gb|EAZ01279.1| hypothetical protein OsI_23302 [Oryza sativa Indica Group]
Length = 318

Score = 153 bits (386), Expect = 1e-34
Identities = 68/124 (54%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D+ LAP+D+QTP +FDN Y+ NLV
Sbjct: 197 QARCATFRSRIFGDGNVDAFAALRQQACPSGG--DSTLAPIDVQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 255 KKQLFLHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 140 bits (354), Expect = 6e-31
Identities = 78/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW ++LG
Sbjct: 130 RDAVNLL-----GGPTWTMQLG 146

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 147 RRDALTASQAANGNLPGPSDLATLVTFMGKGLSPRDMTALSG 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>ref|NP_001046392.1| Os02g0236600 [Oryza sativa (japonica cultivar-group)]
dbj|BAD27598.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69269.1| TPA: class III peroxidase 27 precursor [Oryza sativa (japonica cultivar-group)]
gb|EAY85140.1| hypothetical protein OsI_06495 [Oryza sativa Indica Group]
gb|EAZ22363.1| hypothetical protein OsJ_06021 [Oryza sativa Japonica Group]
dbj|BAH01530.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 321

Score = 152 bits (385), Expect = 2e-34
Identities = 82/169 (48%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD S+LLDD+S+ TGEKNA PN NS RGFEVID+IKS VE CPG VSCADILA+AA
Sbjct: 73 VNGCDASVLLDDSSSTITGEKNAGPNANSLRGFEVIDSIKSQVEAACPGTVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW V+LG
Sbjct: 133 RDGVNLL-----GGPTWAVQLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD RTASQSAAN+ +P+P+S+ L+S F++ GL ++D+VALSG I
Sbjct: 150 RRDTRTASQSAANSNLPSPSSAAALVSAFASKGLDSRDMVALSGAHTI 198

Score = 151 bits (382), Expect = 4e-34
Identities = 72/123 (58%), Positives = 89/123 (72%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARC FRAR+YN+TNI FA R+Q CP + GD NLAPLD + FDN YF+NL+
Sbjct: 201 ARCATFRARVYNDTNISPGFAVRRRQVCP--ASGGDGNLAPLDALSSVRFDNGYFRNLGM 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+ GLLHSDQ+LFNGG DSI + Y+ N FS DF A++KMG+ISPLTGS+GE+R NCR

Sbjct: 259 RFGLLHSDQELFNGGPVDSIAQQYAANGAASFSDVFTAVVKMGNISPLTGSSGEVRSNCR 318

Query: 2170 RIN 2178
+ N

Sbjct: 319 KPN 321

Score = 68.2 bits (165), Expect = 5e-09
Identities = 33/66 (50%), Positives = 47/66 (71%), Gaps = 1/66 (1%)
Frame = +1

Query: 589 RLTICLALFVLIW-GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFF 765
R+ + +A+ L+ G AQL+ +Y SCP+L S V+S + +A+ +E RMGAS+LRLFF
Sbjct: 9 RMVVVVAIAALVAPGEVAAQLTPTYDGCPSLQSIVRSAMAAVQQEPRMGASILRLFF 68

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 69 HDCFVN 74

>gb|EAZ37287.1| hypothetical protein OsJ_21626 [Oryza sativa Japonica Group]
Length = 309

Score = 152 bits (385), Expect = 2e-34
Identities = 68/124 (54%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D LAP+D+QTP +FDN Y+ NLV
Sbjct: 188 QARCATFRSRIFGDGNVDAAFALRQQACPQSGG--DTLAPIDVQTPDAFDNAYYANLV 245

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 246 KKQGLFHSQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 305

Query: 2167 RRIN 2178
R++N
Sbjct: 306 RKNV 309

Score = 122 bits (307), Expect = 2e-25
Identities = 73/165 (44%), Positives = 87/165 (52%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA

Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RD+V + LG

Sbjct: 130 RDAVNL-----LG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG

Sbjct: 138 RRDAL TASQSAANGNLPGPSDLATLVMTFGNKGLSPRDMTALSG 182

Score = 66.6 bits (161), Expect = 2e-08

Identities = 31/71 (43%), Positives = 46/71 (64%)

Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750

MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+

Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783

LR+FFHDCFVN

Sbjct: 61 LRMFFHDCFVN 71

>gb|ABD47726.1| peroxidase [Eucalyptus globulus subsp. globulus]

Length = 258

Score = 152 bits (385), Expect = 2e-34

Identities = 73/123 (59%), Positives = 92/123 (74%)

Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT+FR RIYN++NI+T+FA Q CP+ D+ L LD+QTPT FDN Y+ NL+Q

Sbjct: 138 ARCTSFRGRIYND SNIDTSFAHKLQNICPKIGN--DSVLQRLDIQTPTFFDNLYYHNLLQ 195

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169

KKGLLHSDQ+LFNG S DS+V+ Y+ + G F DFA AMIKM I P GS+G+IRKNCR

Sbjct: 196 KKGLLHSDQELFNGSSVDSL VKKYACDTGKFFRDFAKAMIKMSKIKPPKGSSGQIRKNCR 255

Query: 2170 RIN 2178

++N

Sbjct: 256 KVN 258

Score = 152 bits (383), Expect = 3e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT SF GEK A PN NS RGFEVID IK+++EK CPGVVSCADI+A+AA
Sbjct: 10 VNGCDASILLDDTPSFVGEKTAAPNNNSVRGFEVIDRIKASLEKECPGVVSCADIVALAA 69

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 70 RDSV-----VHLGGPSWTVSLG 86

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
R+D+ TAS+S AN IP PTSNL+ LI+ F+A GLS K++VALSG+ I
Sbjct: 87 RKDSITASRSLANTSIPPPTSNSALITSFAAQGLSVKNMVALSGSHTI 135

>ref|NP_001057820.1| Os06g0546500 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54114.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69330.1| TPA: class III peroxidase 88 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF19734.1| Os06g0546500 [Oryza sativa Japonica Group]
dbj|BAG93666.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 318

Score = 152 bits (385), Expect = 2e-34
Identities = 68/124 (54%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D LAP+D+QTP +FDN Y+ NLV
Sbjct: 197 QARCATFRSRIFGDGNVDAFAALRQQACPSGG--DTTLAPIDVQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 255 KKQGLFHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 142 bits (357), Expect = 3e-31
Identities = 79/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW V+LG
Sbjct: 130 RDAVNLL-----GGPTWTVQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 147 RRDALTASQSAANGNLPGPSDLATLVMTFGNKGLSPRDMTALSG 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>ref|XP_002438534.1| hypothetical protein SORBIDRAFT_10g021650 [Sorghum bicolor]
gb|EER89901.1| hypothetical protein SORBIDRAFT_10g021650 [Sorghum bicolor]
Length = 325

Score = 152 bits (384), Expect = 2e-34
Identities = 71/124 (57%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+++C FR+RIY E+NI +FA RQ++CPR+ G D LAP D+QTP FDN Y++NLV
Sbjct: 204 RSQCQFFRSRIYTESNINASFAALRQKTCPRSGG--DATLAPFDVQTPDGF DNAYYQNLV 261

Query: 1987 QKKGLLHSDQQLFNNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNNGS D++VR YSTN FS+DF +AMIKMG++ P +G+ E+R NC
Sbjct: 262 AQKGLLHSDQELFNNGSQDALVRQYSTNANQFSADFVSAMIKMGNLMPSSGTPTEVRLNC 321

Query: 2167 RRIN 2178
R+ N
Sbjct: 322 RKTN 325

Score = 143 bits (360), Expect = 1e-31
Identities = 81/169 (47%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEK A PN NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 77 VNGCDGSILLDDTSTFTGEKGAGPNANSVRGFEVIDAIKTKVEASCKATVSCADILALAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW+V LG
Sbjct: 137 RDGVNLL-----GGPTWSVPLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
R+D+RTASQS AN+ +P P S+L LI F GLS +D+ ALSG I
Sbjct: 154 RKDSRTASQSLANSNLPGPGSSLATLIRMFGNQLSARDMTALSGAHTI 202

Score = 68.9 bits (167), Expect = 3e-09
Identities = 39/78 (50%), Positives = 54/78 (69%), Gaps = 7/78 (8%)
Frame = +1

Query: 571 MASFCSR----LTICLALFV--LIWGSANAQ-LSTNFYHSCPNLFSSVKSTVQSAISKE 729
MA+F R L++ A+ V L G+A+AQ LS NFY +CPN+ + V+ + SA++ E
Sbjct: 1 MATFTCRSMAFLSLAAAVLVALLTAGAADAQKLSPNFYSKTCPNVATIVRQQMASAVAAE 60

Query: 730 TRMGASLLRLFFHDCFVN 783
RMGAS+LR+FFHDCFVN
Sbjct: 61 KRMGASILRMFFHDCFVN 78

>ref|NP_001140437.1| hypothetical protein LOC100272496 [Zea mays]
gb|ACF83840.1| unknown [Zea mays]
Length = 263

Score = 152 bits (384), Expect = 2e-34
Identities = 72/129 (55%), Positives = 97/129 (75%), Gaps = 5/129 (3%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF +L+
Sbjct: 135 RAQCKNCRARIYNDTIDASFAASLRASCPAQAGAGDGALEPLDGSTPDADFNDAYFGDLL 194

Query: 1987 QKKGLLHSDQQLF-----NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GE
Sbjct: 195 SQRGLLHSDQALFGGGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGISPLTGTGDE 254

Query: 2152 IRKNCRRIN 2178
IR NCRR+N

Sbjct: 255 IRVNCRRVN 263

Score = 145 bits (366), Expect = 3e-32
Identities = 83/164 (50%), Positives = 96/164 (58%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AAR 1333
QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILAI AAR
Sbjct: 9 QGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAI AAR 68

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV LGGP+W V LGR
Sbjct: 69 DSVAQ-----LGGPSWAVPLGR 85

Query: 1514 RDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 86 RDATTASASLANS DLPGPTSSLNGLLNAFSNKLSSTD MVALSG 129

>gb|ACF82414.1| unknown [Zea mays]
Length = 349

Score = 152 bits (384), Expect = 2e-34
Identities = 72/129 (55%), Positives = 97/129 (75%), Gaps = 5/129 (3%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF +L+
Sbjct: 221 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPD AFDNAYFGDLL 280

Query: 1987 QKKGLLHSDQQLF-----NGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTG SNGE 2151
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GE
Sbjct: 281 SQRGLLHSDQALFGGGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGSI SPLTGT DGE 340

Query: 2152 IRKNCRRIN 2178
IR NCRR+N
Sbjct: 341 IRVNCRRVN 349

Score = 145 bits (367), Expect = 2e-32
Identities = 83/165 (50%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI A 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILAI A
Sbjct: 94 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAI A 153

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV LGGP+W V LG
Sbjct: 154 RDSVAQ-----LGGPSWAVPLG 170

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSAALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 171 RRDATTASASLANSDLPGPTSSLNGLLNAFSNKGLSSTDMDVALSG 215

Score = 57.4 bits (137), Expect = 9e-06
Identities = 36/92 (39%), Positives = 51/92 (55%), Gaps = 1/92 (1%)
Frame = +1

Query: 508 TPFQSNTNT*STKLVLCLSKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYH-SCPNL 684
TP + + +++ LS+ C L + LAL +AQLS+ YY SCP
Sbjct: 4 TPLECDMAPAASRNKHLRSWPLPRCGLLVVLALAATA-AVGSAQLSSEDYYDASCPAA 62

Query: 685 FSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
++++ V +A+ E RMGASLLRL FHDCFV
Sbjct: 63 LLTIRTAVSTAVLLEPRMGASLLRLHFHDCFV 94

>dbj|BAF19735.2| Os06g0547100 [Oryza sativa Japonica Group]
Length = 353

Score = 152 bits (383), Expect = 3e-34
Identities = 72/122 (59%), Positives = 89/122 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV
Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC
Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RR 2172
R+
Sbjct: 324 RK 325

Score = 134 bits (338), Expect = 5e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTLTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANANLPGPASSGASLVAAFAGKLSAREMTALSG 199

Score = 64.7 bits (156), Expect = 6e-08
Identities = 29/51 (56%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+A A LS FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSIKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIIRLFFHDCFVN 79

>ref|XP_002438533.1| hypothetical protein SORBIDRAFT_10g021640 [Sorghum bicolor]
gb|EER89900.1| hypothetical protein SORBIDRAFT_10g021640 [Sorghum bicolor]
Length = 318

Score = 151 bits (382), Expect = 4e-34
Identities = 71/124 (57%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA RQQ+CP+T G G NLAP D QTP +FDN Y+ NLV
Sbjct: 197 RARC VF FR GRIYGE PNINATFAAVRQQTCPQTGGDG--NLAPFDDQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGG+ D++VR YS N F++DFA AM+KMG ++P G+ E+R NC
Sbjct: 255 ARRGLLHSDQELFNGGTQDALVRKYSGNGRMFANDFAKAMVKMGLAPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 136 bits (342), Expect = 2e-29
Identities = 75/165 (45%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IK+ VE C VSCADI+A+A+
Sbjct: 70 VNGCDASILLDDTPTFTGEKNAGANVNSVRGYEVIDAIKTQVEAACKATVSCADIVALAS 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 130 RDAVNLLGG-----PTWNVQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R D+RTASQSAAN +P P S+ L++ F+A GLS +D+ ALSG
Sbjct: 147 RTDSRTASQSAANANLPGPGSSAASLVAAFAAKGLSARDMTALSG 191

Score = 66.2 bits (160), Expect = 2e-08
Identities = 29/63 (46%), Positives = 43/63 (68%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
++ L + + + +LST FY SCP + + V+S A++KE RMGAS++RLFFHDC
Sbjct: 9 SVALLTLLCLLLCHGKLSTKIFYAKSCPGVAAIIVRSVTAQAVAKEPRMGASIIRLFFHDC 68

Query: 775 FVN 783
FVN
Sbjct: 69 FVN 71

>gb|ACE00594.1| lignin biosynthetic peroxidase [Leucaena leucocephala]
Length = 316

Score = 151 bits (382), Expect = 4e-34
Identities = 76/124 (61%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
Q +C FR RIYNE NI+ +FA TR+ +CPRT G NLAPLD TP FDN Y+K+LV
Sbjct: 196 QGQCNNFRNRIYENNIDPSFAATRRATCPRTGGG--INLAPLDF--TPNRF DNYYKDLV 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ FNGGS D+IVR YSTN F DFA AM+KM I+PLTGS GEIRK+C
Sbjct: 253 NRRGLFHSDQVFFNGGSQDAIVRAYSTNSVLFFGDFAFAMVKMSSITPLTGSQGEIRKDC 312

Query: 2167 RRIN 2178
R +N
Sbjct: 313 RVVN 316

Score = 126 bits (317), Expect = 1e-26

Identities = 77/169 (45%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD ILLDDT+SFTGEKNA PN+ SARG+EVID IK+ VE C G VSCADILA+AA
Sbjct: 70 VNGCDAGILLDDTASFTGEKNAGPNQ-SARGYEVIDAIKTNVEAACRGTVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
++ V LGGP L
Sbjct: 129 QEGVTQ-----LGGPHGQYHLA 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQS AN+ IP P+S L+ LIS F+A GL+ +++ LSG I
Sbjct: 146 RRDARTASQSKANSEIPGPSSSELSTLISMFAAKGLNAREMTVLSGAHSI 194

Score = 80.1 bits (196), Expect = 1e-12
Identities = 37/71 (52%), Positives = 52/71 (73%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS + L++ L S+NAQLS NFY SCPN+ + V++T++ A+++E R+GAS+
Sbjct: 1 MASLTHFFLLALSVLSLFASSNAQLSPNFYARSCPNVRAIVRNTMRQALAREARLGASI 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>emb|CBI19221.1| unnamed protein product [Vitis vinifera]
Length = 441

Score = 151 bits (381), Expect = 5e-34
Identities = 83/167 (49%), Positives = 102/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
Sbjct: 68 GCDASILLDDTANFTGEKTAGPNNSVRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 127

Query: 1337 SVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V+LGRR
Sbjct: 128 SV-----VALGGPTWTVQLGR 144

Query: 1517 DARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V LSGT I
Sbjct: 145 DSTTASFSTANS DLPAPTS DLDALISLFSNKGFTTQEMVVLSGHTI 191

Score = 83.2 bits (204), Expect = 2e-13
Identities = 45/84 (53%), Positives = 55/84 (65%)
Frame = +1

Query: 1867 FARTRQQSCPRTS GSGDNNLAPLDLQTPTSF DNYYFKNLVQKKGLLHSDQQLFNGGSTDS 2046
F RT+ + R GD+NL+PLD +T T F YF++L +KKGLLHSDQQL+N GSTDS
Sbjct: 357 FFRTKGITVIRIESGGDDNLSPLD-KTTTVFYAYFRDLKEKKGLLHSDQQLYNDGSTDS 415

Query: 2047 IVRGYSTNPGTFSSDFAAAMIKMG 2118
IV YS N TF D AM+ G
Sbjct: 416 IVESYSINSATFFRDVTNAMVLDG 439

Score = 69.3 bits (168), Expect = 2e-09
Identities = 34/69 (49%), Positives = 49/69 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+++Y SCP+ S++++ V +A++ E+RMGASL
Sbjct: 1 MASLSLFSLFCMFSFLL--GMAHAQLSSDYSSSCPSALSTIQ TAVNNAVADES RMGASL 58

Query: 751 LRLFFHDCF 777
LRL FHDCF
Sbjct: 59 LRLHFHDCF 67

Score = 42.7 bits (99), Expect = 0.23
Identities = 17/30 (56%), Positives = 23/30 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCP 1896
+A+C+ FR RIYNETNI+ FA ++Q CP
Sbjct: 193 KAQCSKFRDRIYNETNIDATFATSKQAICP 222

Score = 38.1 bits (87), Expect = 5.8
Identities = 17/30 (56%), Positives = 22/30 (73%)
Frame = +2

Query: 1556 IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
+P PT NL+QL+S FS G +TK+ V LSG
Sbjct: 302 LPGPTLNLSQLVSAFSNKGFTTKETVVLSG 331

>ref|XP_002451846.1| hypothetical protein SORBIDRAFT_04g008590 [Sorghum bicolor]
gb|EES04822.1| hypothetical protein SORBIDRAFT_04g008590 [Sorghum bicolor]
Length = 325

Score = 151 bits (381), Expect = 5e-34
Identities = 83/169 (49%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDD+++ TGEKNA PN NS RGFEVID IKS VE CPG VSCADILA+AA
Sbjct: 75 VQGCDASVLLDDSATLTGEKNAAPNANSLRGFEVIDAIKSQVEAACPGTVSCADILALAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++S GPTW V+LG
Sbjct: 135 RDGVNLLS-----GPTWAVQLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD RTASQSAAN+ +P+P+S+ L+S F++ GL ++DLVALSG I
Sbjct: 152 RRDTRTASQSAANSNLPSPSSAAALVSAFASKGLDSRDLVALSGAHTI 200

Score = 147 bits (372), Expect = 5e-33
Identities = 70/123 (56%), Positives = 87/123 (70%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC +FR+RIYN++NI FA R+Q C SG D NLAPLD + FDN YF++LV
Sbjct: 203 ARCASFRRSRIYNDNINAGFAAKRKQICGPQSGGTDGNLAPLDAMSSVKFDNGYFRDLVS 262

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+ GLLHSDQ+LF G DS+ Y+ N FSSDF A++KMG+ISPLTGS+GEIR NCR
Sbjct: 263 QFGLLHSDQELFGAGVVDVTARYARNGAAFSSDFVTAIVKMGNISPLTGSSGEIRANCR 322

Query: 2170 RIN 2178
+ N
Sbjct: 323 KPN 325

Score = 66.6 bits (161), Expect = 2e-08
Identities = 34/62 (54%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
T+ +A V + G+ QLS FY SCPNL S V+S + +A+ +E RMGAS+LRLFFHDC
Sbjct: 15 TVAVACVVAL-GAMAQQLSPTFYDASCPNLQSIVRSGMAAAVQQEPRMGASILRLFFHDC 73

Query: 775 FV 780

FV
Sbjct: 74 FV 75

>emb|CAL25299.1| properoxidase [Picea abies]
Length = 341

Score = 151 bits (381), Expect = 5e-34
Identities = 86/169 (50%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCDGSILLDDTSSFTGEK ANPNRNS RGF V+D IKS +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNRNSVRGFGVVDQIKSELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGNSTHTLETKFKRQGLNVVDLVALSGAHTI 208

Score = 122 bits (305), Expect = 3e-25
Identities = 65/132 (49%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGKSDPTLDTTYLKHLRAVCPQT-GTDDNQTTPLDPVTPIKFDID 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SDQ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDQILYSTKGSRTVGLVESYSTSMHAFFKQFAASMIKMGNINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 3e-07
Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYYHSCPRLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS

Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780

LLRL FHDCFV

Sbjct: 73 LLRLHFHDCFV 83

>emb|CBI15847.1| unnamed protein product [Vitis vinifera]

Length = 263

Score = 150 bits (380), Expect = 6e-34

Identities = 73/124 (58%), Positives = 94/124 (75%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986

Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV

Sbjct: 142 QSRCLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC

Sbjct: 200 DNKGLLHSDQELFNNGSTDSQVSSYASSATSFYKDFTAAMVKMGNISPLTGTKGQIRVNC 259

Query: 2167 RRIN 2178

R+IN

Sbjct: 260 RKIN 263

Score = 150 bits (378), Expect = 1e-33

Identities = 85/169 (50%), Positives = 101/169 (59%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330

+ GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AA

Sbjct: 15 VNGCDGSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGPTW V+LG

Sbjct: 75 RDSV-----VALGGPTWTVQLG 91

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I

Sbjct: 92 RRDSTTASISDAETDIPSPALDLDLISAFSDKGFSKEMVALSGSHTI 140

>ref|XP_002451850.1| hypothetical protein SORBIDRAFT_04g008650 [Sorghum bicolor]

gb|EES04826.1| hypothetical protein SORBIDRAFT_04g008650 [Sorghum bicolor]

Length = 323

Score = 150 bits (380), Expect = 6e-34
Identities = 73/124 (58%), Positives = 92/124 (74%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSG-SGDNNLAPLDLQTPTSFDNYYFKNLV 1986
A+C +R+RIY++ NI FA T + +C T G S D NLA LD+QT FDN YF NL+
Sbjct: 200 AQCKTYRSRIYSDANINKQFANTLKGNC SATQGGSTDTNLAGLDVQTQVVDNAYFGNLM 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+LFNGGS D++V+ Y +PG F+S F AMIKMG+ISPLTGS G+IR NC
Sbjct: 260 KKKGLLHSDQELFNGGSQDALVQQYDADPGLFASHFVTAMIKMGNISPLTGSQGGIRANC 319

Query: 2167 RRIN 2178
R+N
Sbjct: 320 GRVN 323

Score = 139 bits (350), Expect = 2e-30
Identities = 77/166 (46%), Positives = 99/166 (59%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDT-SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD SILLDD +F GEKNA PN NS G++VI+NIK+AVE CPGVVSCADI+A+A
Sbjct: 71 VQGC DASILLDDVPGTFVGEKNAGPNANSVLGYDVINNIKTAVEANCPGVVSCADIVALA 130

Query: 1328 ARDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V ++ GGPTW+V L
Sbjct: 131 ARDGVNLL-----GGPTWSVSL 147

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TASQS AN+ +P+P S+L+ LI+ F++ GL+ D+ ALSG
Sbjct: 148 GRRDSTTASQSQANS DLPSPASSLSTLIAAFASKGLNATDMTALSG 193

Score = 64.3 bits (155), Expect = 8e-08
Identities = 33/56 (58%), Positives = 41/56 (73%), Gaps = 1/56 (1%)
Frame = +1

Query: 616 VLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISK-ETRMGASLLRLFFHDCFV 780
+L+ +A QLST+FY SCP+L S+V+S V I+ RMGASLLRLFFHDCFV
Sbjct: 16 ILLSSAAYGQLSTSFYDTSCPSLESTVRSVVGVINNGNRRMGASLLRLFFHDCFV 71

>ref|XP_002276796.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 1225

Score = 150 bits (380), Expect = 6e-34

Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV

Sbjct: 1104 QSRCLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 1161

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC

Sbjct: 1162 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFTAAMVKMGNISPLTGTKGQIRVNC 1221

Query: 2167 RRIN 2178

R+IN

Sbjct: 1222 RKIN 1225

Score = 150 bits (378), Expect = 1e-33
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AA

Sbjct: 977 VNGCDGSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAA 1036

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V+LG

Sbjct: 1037 RDSV-----VALGGPTWTVQLG 1053

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I

Sbjct: 1054 RRDSTTASISDAETDIPSPALDLDLISAFSDKGFSKEMVALSGSHTI 1102

Score = 62.8 bits (151), Expect = 2e-07
Identities = 27/52 (51%), Positives = 37/52 (71%)
Frame = +1

Query: 628 GSANAQLSTNFYYHSCP NFLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783

G ++ LS+ FY CP S++++ V +A++ E RMGASLLRL FHDCFVN

Sbjct: 927 GVVSSGLSSTFYSAKCPKALSTIRTAVNTAVANENRMGASLLRLHFHDCFVN 978

>gb|EAZ22364.1| hypothetical protein OsJ_06022 [Oryza sativa Japonica Group]
Length = 282

Score = 150 bits (380), Expect = 6e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV

Sbjct: 160 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 217

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC

Sbjct: 218 AGAGLLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIPLTGSTGEVRLNC 277

Query: 2167 RRIN 2178

R++N

Sbjct: 278 RKNV 281

Score = 78.6 bits (192), Expect = 4e-12

Identities = 38/65 (58%), Positives = 46/65 (70%), Gaps = 1/65 (1%)

Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333

GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR

Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAVGSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQI 1348

DSV +

Sbjct: 138 DSVNL 142

Score = 61.2 bits (147), Expect = 6e-07

Identities = 28/63 (44%), Positives = 40/63 (63%)

Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771

L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD

Sbjct: 14 LLLLLAVALALAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRLFYHD 73

Query: 772 CFV 780

CFV

Sbjct: 74 CFV 76

>gb|EAY85141.1| hypothetical protein OsI_06496 [Oryza sativa Indica Group]

Length = 326

Score = 150 bits (380), Expect = 6e-34

Identities = 71/124 (57%), Positives = 92/124 (74%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDSVQVLYSSNAAAFSSDFAASMIRLGNIPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 119 bits (298), Expect = 2e-24
Identities = 68/164 (41%), Positives = 89/164 (54%), Gaps = 1/164 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR
Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAIGSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W V LGR
Sbjct: 138 DSVNL-----LGGPSWAVPLGR 154

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 155 RDALSPSRSAVSTDLPGP EADISALVS AFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 6e-07
Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRL F+HD
Sbjct: 14 LLLLLAVALALAAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLR LFFHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>tpe|CAH69268.1| TPA: class III peroxidase 26 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 326

Score = 150 bits (380), Expect = 6e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 112 bits (281), Expect = 2e-22
Identities = 65/166 (39%), Positives = 88/166 (53%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNR--NSARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAIA
Sbjct: 76 VQGCDASVLLDDTPAAPGEKGVGPNAVSTTVFDLVDTIKAQVEAVCPATVSCADVLAIA 135

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
R + + LGGP+W V L
Sbjct: 136 GRR-----RVQLGGPSWAVPL 152

Query: 1508 GRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 153 GRRDALSPRSASVSTDLPGPEADISALVSAFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 6e-07
Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNI FSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALAARARAQLSPGFYSASCTVHGVVRQVMSQAVMNDTRAGAAVLRRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>ref|NP_001046393.1| Os02g0236800 [Oryza sativa (japonica cultivar-group)]
 dbj|BAD27599.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
 dbj|BAD29072.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
 dbj|BAF08307.1| Os02g0236800 [Oryza sativa Japonica Group]
 dbj|BAG91008.1| unnamed protein product [Oryza sativa Japonica Group]
 dbj|BAG94336.1| unnamed protein product [Oryza sativa Japonica Group]
 dbj|BAG96877.1| unnamed protein product [Oryza sativa Japonica Group]
 Length = 326

Score = 150 bits (380), Expect = 6e-34
 Identities = 71/124 (57%), Positives = 92/124 (74%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 +A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
 Sbjet: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
 GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
 Sbjet: 262 AGAGLLHSDQELFNNGPVDVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
 R++N
 Sbjet: 322 RKNV 325

Score = 119 bits (298), Expect = 2e-24
 Identities = 68/164 (41%), Positives = 89/164 (54%), Gaps = 1/164 (0%)
 Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
 GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR
 Sbjet: 78 GCDASVLLDDTPAAPGEKGVGPNAVGSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
 DSV + LGGP+W V LGR
 Sbjet: 138 DSVNL-----LGGPSWAVPLGR 154

Query: 1514 RDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
 RDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
 Sbjet: 155 RDALSPSRSAVSTDLPGEADISALVSAFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 6e-07

Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALALAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>gb|ABK22680.1| unknown [Picea sitchensis]
Length = 341

Score = 150 bits (379), Expect = 8e-34
Identities = 85/169 (50%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
++GCDGSILLDDTSSFTGEK ANPN+NS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNKNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F LGL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGPNSTHQTLTKFKRLGLNVVDLVALSGAHTI 208

Score = 122 bits (305), Expect = 3e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGNHDPDLDTTYLKQLRAVCPQT-GTDDNQTTPLDPVTPIKFDIN 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 3e-07
Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ---LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPQAIIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>emb|CAN61440.1| hypothetical protein [Vitis vinifera]
Length = 262

Score = 150 bits (379), Expect = 8e-34
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV
Sbjct: 141 QSRCLVFRDRIYNDNDIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 198

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC
Sbjct: 199 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFXAAMVKMGNISPLTGTGKQIRVNC 258

Query: 2167 RRIN 2178
R+IN
Sbjct: 259 RKIN 262

Score = 150 bits (378), Expect = 1e-33
Identities = 85/168 (50%), Positives = 101/168 (60%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AAR 1333
+GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AAR
Sbjct: 15 KGCDSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAAR 74

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGPTW V+LGR
Sbjct: 75 DSV-----VALGGPTWTVQLGR 91

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I
Sbjct: 92 RDSTTASISDAETDIPSPALDLDLISAFSDKGFSKEMVALSGSHTI 139

>gb|AAC31550.1| peroxidase PXC2 precursor [Avena sativa]
Length = 313

Score = 150 bits (379), Expect = 8e-34
Identities = 71/126 (56%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKN 1980
QA+C NFR+RIY +TNI AFA + Q +CP+ T GSGD++LAPLD +TP +FDN Y+ N
Sbjct: 187 QAQCKNFRSRIYGGDTNINAAFATSLQANCPQATGGSGDSSLAPLDTKTPNAFDNSYYNN 246

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRK 2160
L+ +KGLLHSDQ LFN G+TD+ VR ++++ F+ F AMIKMG+ISPLTG+ G+IR
Sbjct: 247 LLSQKGLLHSDQVLFNNGTTDNTVRNFASSASAFTGAFTTAMIKMGNISPLTGTQGQIRL 306

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 307 SCSKVN 312

Score = 105 bits (261), Expect = 4e-20
Identities = 69/167 (41%), Positives = 84/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDNIK+ VE VC VSC DILA+AARD
Sbjct: 69 GCDASVLLSGN-----EQNAAPNAGSLRGFSVIDNIKTQVEAVCKQTVSCDDILAVAARD 123

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 124 SV-----VALGGPSWTVPLGRR 140

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ +A+ + + +PAPTS+L QL + FS L T D+VALSG I
Sbjct: 141 DSTSATGNTGD--LPAPTSSLAQLQAASFKNLDTTDMVALSGAHTI 185

Score = 65.5 bits (158), Expect = 3e-08
Identities = 32/64 (50%), Positives = 45/64 (70%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S +++ + L L +A+AQLS+ FY SCP +++KS V +A+S + RMGASLLRL F

Sbjct: 5 SCISLRVMLVALAATAASAQLSSTFYDTSCPKALATIKSGVAAVSSDRRMGASLLRLHF 64

Query: 766 HDCF 777
HDCF

Sbjct: 65 HDCF 68

>gb|AAC31551.1| peroxidase PXC6 precursor [Avena sativa]
Length = 314

Score = 150 bits (379), Expect = 8e-34
Identities = 71/126 (56%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKN 1980
QA+C NFR+RIY +TNI AFA + Q +CP+ T GSGD++LAPLD +TP +FDN Y+ N
Sbjct: 188 QAQCKNFRSRIYGGDTNINAAFATSLQANCPQATGGSGDSSLAPLDTKTPNAFDNSYNN 247

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ +KGLLHSDQ LFN G+TD+ VR ++++ F+ F AMIKMG+ISPLTG+ G+IR
Sbjct: 248 LLSQKGLLHSDQVLFNNGTTDNTVRNFASSASAFTGAFTAMIKMGNISPLTGTQGGQIRL 307

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 308 SCSKVN 313

Score = 94.0 bits (232), Expect = 9e-17
Identities = 68/168 (40%), Positives = 82/168 (48%), Gaps = 1/168 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDNIK+ VE VC VSCADILA+AARD
Sbjct: 69 GCDASVLLSGN-----EQNAAPNAGSLRGFSVIDNIKTQVEAVCKQTVSCADILAVAARD 123

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP-TWNVKLGR 1513
SV + LGGP V LGR
Sbjct: 124 SV-----VALGGPFLEQVPLGR 140

Query: 1514 RDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RD+ +A+ + + +PAPTS+L QL + FS L T +VALSG I
Sbjct: 141 RDSTSATGNTGD--LPAPTSSLAQLQAAFSKKNLDTTGMVALSGAHTI 186

Score = 65.5 bits (158), Expect = 3e-08
Identities = 32/64 (50%), Positives = 45/64 (70%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
S +++ + L L +A+AQLS+ FY SCP +++KS V +A+S + RMGASLLRL F
Sbjct: 5 SCISLRVMLVALAATAASAQLSSTFYDTSCPKALATIKSGVAAVSSDRRMGASLLRLHF 64

Query: 766 HDCF 777
HDCF
Sbjct: 65 HDCF 68

>emb|CAA71492.1| peroxidase [Spinacia oleracea]
Length = 315

Score = 149 bits (375), Expect = 2e-33
Identities = 81/165 (49%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTS+F GEK A PN+NS RGF+ +D+IK+++EK CPGVVSCADILAIA+
Sbjct: 66 VNGCDGSILLDDTSTFRGEKTAIPKNNSVRGFKAVDSIKASLEKACPGVVSCADILAIA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + GGPTW V+LG
Sbjct: 126 RDAV-----VQYGGPTWQVRLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TA++SAAN IPAP+ NL L S F+ +GLS KD+V LSG
Sbjct: 143 RRDSLTANRSAANAFIPAPSFNLRNLTSFTTVGLSFKDMVVL 187

Score = 133 bits (335), Expect = 1e-28
Identities = 66/124 (53%), Positives = 93/124 (75%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT+FR I+N+TNI AFA++ Q+ CP+ SG+G L PLD QT FD+ Y++NL+
Sbjct: 194 ARCTSFRPHIHNDTNINAFAKSLQKKCPQ-SGNG-KVLQPLDYQTKFRFDDKYYQNLLV 251

Query: 1990 KKGLLHSDQQLFNGGST-DSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQL++G + D+ VR Y++ G F +F +MI+MG+I PLTG++G+IR+NC
Sbjct: 252 KKGLLHSDQQLYSGNNNADAYVRKYASKQGEFFQEFGNSMIRMGNIKPLTGTHGQIRRNC 311

Query: 2167 RRIN 2178
R+ N
Sbjct: 312 RKS 315

Score = 64.3 bits (155), Expect = 8e-08
Identities = 29/51 (56%), Positives = 34/51 (66%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
+ N QLS NFY +CPN VK + I KE R+GAS+LRL FHDCFVN
Sbjct: 17 TVNGQLSPNFYSSTCPNALRIVKQGIKRIKKEARVGASILRLHFHDCFVN 67

>ref|NP_001054096.1| Os04g0651000 [Oryza sativa (japonica cultivar-group)]
emb|CAE04507.2| OSJNBb0059K02.17 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69299.1| TPA: class III peroxidase 57 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF16010.1| Os04g0651000 [Oryza sativa Japonica Group]
dbj|BAG98582.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 319

Score = 149 bits (375), Expect = 2e-33
Identities = 82/169 (48%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AA
Sbjct: 70 VNGCDGSVLLDDTAAITGEKNAKPNKNSLRGFEVVDDIKSQLEDACEQVSCADILAVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW+V+LG
Sbjct: 130 RDSV-----VALGGPTWDVELG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 147 RRDGTTASLDAANNLPPPTSDLADLIKSFSKGLTASDMIALSGAHTI 195

Score = 148 bits (373), Expect = 4e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 197 QARCTNFRGRLYNETNLATLATS LKPSCPNPTG-GDDNTAPLDPATSYVFDNFYRNLL 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 256 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 315

Query: 2167 RRIN 2178
R++N

Sbjct: 316 RKNV 319

Score = 74.7 bits (182), Expect = 6e-11
Identities = 34/70 (48%), Positives = 52/70 (74%), Gaps = 1/70 (1%)
Frame = +1

Query: 577 SFC SRLTICLALFVLIW GSA-NAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
++ ++ +C A+ L++ + +AQLST+FY +CP+ ++S V+ A+SKE+RMGASLL
Sbjct: 2 AYSRQIFVCSAMAALLFS AVVSAQLSTDFYDETC PDALDIIESAVRDAVSKESRMGASLL 61

Query: 754 RLFFHDCFVN 783
RL FHDCFVN
Sbjct: 62 RLHFHDCFVN 71

>ref|XP_002308244.1| predicted protein [Populus trichocarpa]
gb|EEE91767.1| predicted protein [Populus trichocarpa]
Length = 321

Score = 149 bits (375), Expect = 2e-33
Identities = 71/123 (57%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C F+ RIYNETNI+ FAR R+ +CPRT G D+NLAPL+ TP+ FD Y+ +L++
Sbjct: 202 AQCFTFKDRIYNETNIDPKFARERKLTCPRTGG--DSNLAPLN-PTPSYFDARYYNDLLK 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GL HSDQ LFNGGSTDS+V+ YS+N F +DFA +M+KMG+I+PLTG G+ R NCR
Sbjct: 259 KRGLFHSDQALFNGGSTDSLKAYSSNAKAFWTFANSMVKMGNIPLTGKQGQTRLNCR 318

Query: 2170 RIN 2178
++N
Sbjct: 319 KVN 321

Score = 135 bits (339), Expect = 3e-29
Identities = 82/166 (49%), Positives = 93/166 (56%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+F EKNANPN NS RGFEVID IK V+K C VVSCADILA+A
Sbjct: 73 VNGCDASILLDSTSAFDSEKNANPNINSIRGFEVIDRIKLEVDKACGRPVVSCADILAVA 132

Query: 1328 ARDSVQIVSGQTNTKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGPTW V+L

Sbjct: 133 ARDSV-----VALGGPTWAVQL 149

Query: 1508 GRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TAS++ ANN IPAP +L LI F GL+ KDLV LSG

Sbjct: 150 GRRDSTTASKTTANNDIPAPFMDLPDLIINFKKHGLNKKDLVVLSG 195

Score = 64.3 bits (155), Expect = 8e-08
Identities = 34/76 (44%), Positives = 47/76 (61%)
Frame = +1

Query: 556 LSKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLSSVKSTVQSAISKETR 735
++ L + S S L + LAL S++ LS N+Y + CP ++K V++A+ E R

Sbjct: 1 MASLGIFSLISTLFLVLALATT--ASSSKGLSPNYYDYVCPKALPTIKRVVEAAVYNERR 58

Query: 736 MGASLLRLFFHDCFVN 783
MGASLLRL FHDCFVN

Sbjct: 59 MGASLLRLHFHDCFVN 74

>emb|CBI19222.1| unnamed protein product [Vitis vinifera]
Length = 255

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 101/167 (60%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD

Sbjct: 17 GCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 76

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V++GRR

Sbjct: 77 SV-----VALGGPTWTVMGR 93

Query: 1517 DARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I

Sbjct: 94 DSTTASLSTANADLPAPTSDDLVLTSLSFNKGFTTQEMVALSGTHTI 140

Score = 126 bits (317), Expect = 1e-26
Identities = 62/106 (58%), Positives = 82/106 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPSFNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+

Sbjct: 142 KAQCIKFRYRIYNETNVDAFAKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 198

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDI 2124
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++
Sbjct: 199 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTTFFTDVANAMVKMGNL 244

>ref|XP_002467656.1| hypothetical protein SORBIDRAFT_01g031740 [Sorghum bicolor]
gb|EER94654.1| hypothetical protein SORBIDRAFT_01g031740 [Sorghum bicolor]
Length = 344

Score = 148 bits (374), Expect = 3e-33
Identities = 83/165 (50%), Positives = 98/165 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AA
Sbjct: 92 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAVAA 151

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV LGGP+W+V LG
Sbjct: 152 RDSVAQ-----LGGPSWSVPLG 168

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTSNLN L++ FS GLS+ D+VALSG
Sbjct: 169 RRDATTASASLANSDLPGPTSNLNGLLNAFSNKGLSSTDMVALSG 213

Score = 143 bits (361), Expect = 1e-31
Identities = 69/126 (54%), Positives = 95/126 (75%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCP-RTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
+A+C N R+RIYN+T+I+ +A + + SCP + G+ D L PLD TP +FDN YF NL
Sbjct: 219 RAQCKNIRSRIYNDTDIDATYAASLRASCPAQAGGASDGALEPLDDATPDADFNDAYFGNL 278

Query: 1984 VQKKGLLHSDQQLFNGG-STDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+ ++GLLHSDQ LF GG +TD +V Y+++ + SDFAAAM+KMG+ISPLTG++GEIR
Sbjct: 279 LSQRGLLHSDQALFGGGGATDGLVSTYASSADQWGSDFAAAMVKMGNISPLTGTGGEIRV 338

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 339 NCRRVN 344

Score = 55.5 bits (132), Expect = 4e-05
Identities = 29/65 (44%), Positives = 42/65 (64%), Gaps = 5/65 (7%)
Frame = +1

Query: 601 CLALFVLIWGSA----NAQLSTNFYYH-SCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
CL + ++ +A +AQLS+ YY SCP +++++ V +A+ + RMGASLLRL F
Sbjct: 28 CLLILIVALAAAAVASAQLSSEDYYDASCPAALFTIRTAVSTAVLLDRRMGASLLRLHF 87

Query: 766 HDCFV 780
HDCFV
Sbjct: 88 HDCFV 92

>gb|EEE61812.1| hypothetical protein OsJ_16433 [Oryza sativa Japonica Group]
Length = 1129

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AARD
Sbjct: 78 GCDGSVLLDDTAAITGEKNAKPNKNSLRGFVVDDIKSQLEDACEQVVSCADILAVAARD 137

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 138 SV-----VALGGPTWDVELGRR 154

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 155 DGTASLDAANNDLPPTS D LADLIKSFSDKGLTASDMIALSGAHTI 201

Score = 134 bits (336), Expect = 8e-29
Identities = 63/115 (54%), Positives = 82/115 (71%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 203 QARCTNFRGRLYNETNLDATLATS LKPSCPNPTG-GDDNTAPLPATSYVFDNFYYRNLL 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G+
Sbjct: 262 RNKGLLHSDQQLFSGGSADAQTTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQ 316

Score = 69.7 bits (169), Expect = 2e-09
Identities = 31/49 (63%), Positives = 40/49 (81%)
Frame = +1

Query: 637 NAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+AQLST+FY +CP+ ++S V+ A+SKE+RMGASLLRL FHDCFVN
Sbjct: 11 SAQLSTDFYDETCPDALDIIESAVRDAVSKE SRMGASLLRLHFHDCFVN 59

>gb|EEC78144.1| hypothetical protein OsI_17703 [Oryza sativa Indica Group]
Length = 325

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGF EV+D+IKS +E C VVSCADILA+AARD
Sbjct: 78 GCDGSVLLDDTAAITGEKNAKPNKNSLRGF EVVDDIKSQLEDACEQVVSCADILAVAARD 137

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 138 SV-----VALGGPTWDVELGRR 154

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 155 DGTASLDAANNDLPPPTS D LADLIKSFS DKGLTASDMIALSGAHTI 201

Score = 148 bits (373), Expect = 4e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 203 QARCTNFRGRLYNETNL DATLATS LKPSCPNPTG-GDDNTAPLDPATSYVFDNFYYRNLL 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GG S D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 262 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 70.1 bits (170), Expect = 1e-09
Identities = 31/49 (63%), Positives = 41/49 (83%)
Frame = +1

Query: 637 NAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783

+AQLST+FY +CP+ ++S V++A+SKE+RMGASLLRL FHDCFVN
Sbjct: 11 SAQLSTDFYDETCPDALDIIESAVRAAVSKESRMGASLLRLHFHDCFVN 59

>emb|CAJ86184.1| H0212B02.16 [Oryza sativa (indica cultivar-group)]
emb|CAJ86323.1| OSIGBa0113E10.6 [Oryza sativa (indica cultivar-group)]
Length = 337

Score = 148 bits (374), Expect = 3e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AARD
Sbjct: 90 GCDGSVLLDDTAAITGEKNAKPNKNSLRGFVVDDIKSQLEDACEQV VSCADILAVAARD 149

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 150 SV-----VALGGPTWDVELGRR 166

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 167 DGTASLDAANNDLPPTSDLADLIKSFSKGLTASDMIALSGAHTI 213

Score = 148 bits (373), Expect = 4e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 215 QARCTNFRGRLYNETNL DATLATS LKPSCPNPTG-GDDNTAPLDPATSYVFDNFYYRNLL 273

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 274 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 333

Query: 2167 RRIN 2178
R++N
Sbjct: 334 RKNV 337

Score = 75.1 bits (183), Expect = 4e-11
Identities = 34/70 (48%), Positives = 53/70 (75%), Gaps = 1/70 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSA-NAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753

++ ++ +C A+ L++ + +AQLST+FY +CP+ ++S V++A+SKE+RMGASLL
Sbjct: 2 AYSRQIFVCSAMAALLFSAVVSAQLSTDFYDETCPDALDIIESAVRAAVSKESRMGASLL 61

Query: 754 RLFFHDCFVN 783

RL FHDCFVN

Sbjct: 62 RLHFHDCFVN 71

>gb|EAZ22372.1| hypothetical protein OsJ_06030 [Oryza sativa Japonica Group]
Length = 257

Score = 148 bits (374), Expect = 3e-33
Identities = 69/123 (56%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989

A CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT +FDN Y+ NL+

Sbjct: 135 ALCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNAFDNAYYGNLLV 194

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169

++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR

Sbjct: 195 RRGLLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 252

Query: 2170 RIN 2178

+N

Sbjct: 253 VVN 255

Score = 93.6 bits (231), Expect = 1e-16
Identities = 46/68 (67%), Positives = 53/68 (77%), Gaps = 2/68 (2%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324

+QGCD SILLDD + F GEK A PN NS RG+EVID IK+ VE VCPGVVSCADI+A+

Sbjct: 69 VQGCDASILLDDVPATGFVGEKTAAPNNNSVRGYEVIDQIKANVEDVCPGVVSCADIVAL 128

Query: 1325 AARDSVQI 1348

AARDS +

Sbjct: 129 AARDSTAL 136

Score = 70.1 bits (170), Expect = 1e-09
Identities = 34/59 (57%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPNISSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

L +F L+ A+ QLST++Y SCP++ V +TV SAI E RMGASL+RLFFHDCFV

Sbjct: 11 LLVFLLSDDASGQLSTSYADSCPSVEKVVHATVASAIQAERRMGASLIRLFFHDCFV 69

>ref|NP_001046401.1| Os02g0240300 [Oryza sativa (japonica cultivar-group)]
dbj|BAD28871.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69271.1| TPA: class III peroxidase 29 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF08315.1| Os02g0240300 [Oryza sativa Japonica Group]
dbj|BAG90221.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96858.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 321

Score = 148 bits (374), Expect = 3e-33
Identities = 68/123 (55%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT +FDN Y+ NL+
Sbjct: 199 SQCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNAFDNAYYGNNLV 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR
Sbjct: 259 RRGLLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 316

Query: 2170 RIN 2178
+N
Sbjct: 317 VVN 319

Score = 137 bits (344), Expect = 9e-30
Identities = 79/168 (47%), Positives = 95/168 (56%), Gaps = 2/168 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD + F GEK A PN NS RG+EVID IK+ VE VCPGVVSCADI+A+
Sbjct: 69 VQGCASILLDDVPATGFVGEKTAAPNNSVRGYEVIDQIKANVEDVCPGVVSCADIVAL 128

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 129 AARDSTAL-----LGGPSWAVP 145

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
LGR D+ TAS+S AN+ +P P SNL LI+RF GLS +D+ ALSG+
Sbjct: 146 LGRCDSTTASRSEANSDLPGPGSNLTMLIARFGNKGLSPRDMTALSGS 193

Score = 70.1 bits (170), Expect = 1e-09
Identities = 34/59 (57%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
L +F L+ A+ QLST++Y SCP++ V +TV SAI E RMGASL+RLFFHDCFV
Sbjct: 11 LLVFLLSDDASGQLSTSYADSCPSVEKVHATVASAIQAERRMGASLIRLFFHDCFV 69

>gb|ABK21983.1| unknown [Picea sitchensis]
Length = 341

Score = 148 bits (373), Expect = 4e-33
Identities = 84/169 (49%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
++GCDGSILLDDTSSFTGEK ANPN+NS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNKNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGNSTHTLETKFQRQLNVVDLVALSGAHTI 208

Score = 121 bits (304), Expect = 4e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGKPDPTLDTTYLKQLRAVCPQT-GTDDNQTPDPVTPIKFDID 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 3e-07

Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYYKSCPKAQAIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>ref|XP_002461210.1| hypothetical protein SORBIDRAFT_02g042860 [Sorghum bicolor]
gb|EER97731.1| hypothetical protein SORBIDRAFT_02g042860 [Sorghum bicolor]
Length = 313

Score = 148 bits (373), Expect = 4e-33
Identities = 70/124 (56%), Positives = 93/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+NF IYN+TNI+ AFA + Q +CP SG +LAPLD TPT+FDN Y+ NL+
Sbjct: 191 QAQCSNFNDHIYNDTNIDAAFATSLQANCP---ASGSTSLAPLDTMTPTTFDNDYYTNLM 247

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFN GSTDS V ++++ F+S F AAM+KMG++SPLTG++GEIR C
Sbjct: 248 SQKGLLHSDQQLFNGGSTDSTVSNFASSASAFTSAFTAAMVKMGNLSPLTGTGEIRLAC 307

Query: 2167 RRIN 2178
+N
Sbjct: 308 GIVN 311

Score = 123 bits (309), Expect = 1e-25
Identities = 76/169 (44%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LL+DTS GE+++ PN+ S R F+VID+IK+ VE VCPGVVSCADILA+AA
Sbjct: 68 VHGCDGSVLLNDTS---GEQSSPPNKGSLRRFDVIDSIKAQVEAVCPGVVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVLLG 141

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + +PAPTS+L QL+S FS L D+VALSG I
Sbjct: 142 RRDS-TASFPSETTDLPAPTSSLQQLLSLFSNKNLDATDMVALSGAHTI 189

Score = 68.2 bits (165), Expect = 5e-09
Identities = 34/63 (53%), Positives = 44/63 (69%), Gaps = 2/63 (3%)
Frame = +1

Query: 601 CLALFVL--IWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
CLA V + A+AQLS+ FY SCPN S++KS V +A+ +E R GASLLR+ FHDC
Sbjct: 7 CLAFLVAAAVASVASAQLSSTFYDTSCPNALSTIKSGVDAAVMQEARTGASLLRMHFHDC 66

Query: 775 FVN 783
FV+
Sbjct: 67 FVH 69

>emb|CBI18065.1| unnamed protein product [Vitis vinifera]
Length = 413

Score = 147 bits (372), Expect = 5e-33
Identities = 83/169 (49%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSTFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RG+EV+D IKS +E CPGVVSCADILA+AA
Sbjct: 15 VNGCDASILLDDTSNFTGEKTAGPNANSVRGYEVVDTIKSQLEASCPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GP+W V+LG
Sbjct: 75 RDSV-----VALRGPSWMVRLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LIS F+ G + +++VALSG+ I
Sbjct: 92 RRDSTTASLSAANSNIPAPTLNLSGLISAFTNKGFNAREMVALSGSHTI 140

Score = 136 bits (343), Expect = 1e-29
Identities = 66/101 (65%), Positives = 77/101 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT FR RIYNE NI+ +F + Q +CP S GDN L+PLD QTPT+FDN Y+ NLV
Sbjct: 142 QARCTTFRTRIYNEANIDASFKTSLQANCP--SSGGDNTLSPLDTQTPTTFDNAYYTNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI 2109
KKGLLHSDQQLFNGGST++V YST TF +DFA AM+
Sbjct: 200 NKKGLLHSDQQLFNGGSTDAVVNTYSTRSTTFFTFDFANAMM 240

Score = 106 bits (265), Expect = 1e-20
Identities = 64/139 (46%), Positives = 77/139 (55%), Gaps = 1/139 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+ EKNA N NSARGF V+D+IKS V+KVC VVSCADILA+A
Sbjct: 309 VNGCDASILLDATSTIDSEKNAGANANSARGFNVVDDIKSQVDKVCGRPVVSCADILAVA 368

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 369 ARDSV-----VALGGPSWTVQL 385

Query: 1508 GRRDARTASQSAANNGIPA 1564
GRRD+ TAS++ ANN IP+
Sbjct: 386 GRRDSTTASRTDANNIPS 404

Score = 68.2 bits (165), Expect = 5e-09
Identities = 40/89 (44%), Positives = 49/89 (55%), Gaps = 4/89 (4%)
Frame = +1

Query: 529 NT*STKLVL-SKLTMASFCSRLTICLALFVLI---WGSANAQLSTNFYYHSCPRLFSSV 696
NT ST+ + A SR +CL FVL +A LS FY CP ++
Sbjct: 222 NTYSTRSTTFFTFDFANAMMASRLLCLYAFVLFSLATADFSAAALSPYFYNKVC PKALPTI 281

Query: 697 KSTVQSAISKETRMGASLLRLFFHDCFVN 783
K V++A+ KE RMGASLLRL FHDCFVN
Sbjct: 282 KRVVEAAVQKEKRMGASLLRLHFHDCFVN 310

>gb|ACF08091.1| class III peroxidase [Triticum aestivum]
Length = 316

Score = 147 bits (372), Expect = 5e-33
Identities = 69/125 (55%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL
Sbjct: 191 QACSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTGGQIRLS 310

Query: 2164 CRRIN 2178

C R+N
Sbjct: 311 CSRVN 315

Score = 94.4 bits (233), Expect = 7e-17
Identities = 63/170 (37%), Positives = 85/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 68 VQGCDA SVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VA SG I
Sbjct: 140 RRDSIDANEAEANS DLPGFNSSRSELEAAFLRKGGLNTVDMVAPSGAHTI 189

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/62 (53%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L VL+ +A+ QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAASGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|EAY85149.1| hypothetical protein OsI_06504 [Oryza sativa Indica Group]
Length = 135

Score = 147 bits (372), Expect = 5e-33
Identities = 69/123 (56%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT FDN Y+ NL+
Sbjct: 13 SQCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNLFDNAYYGNLLV 72

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR

Sbjct: 73 RRGLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 130

Query: 2170 RIN 2178

IN

Sbjct: 131 FIN 133

>gb|AAW52716.1| peroxidase 2 [Triticum monococcum]

Length = 316

Score = 147 bits (372), Expect = 5e-33

Identities = 69/125 (55%), Positives = 94/125 (75%), Gaps = 1/125 (0%)

Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983

QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL

Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163

+ ++GLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +

Sbjct: 251 MSQRGLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTQQQIRLS 310

Query: 2164 CRRIN 2178

C R+N

Sbjct: 311 CSRVN 315

Score = 97.1 bits (240), Expect = 1e-17

Identities = 64/170 (37%), Positives = 86/170 (50%), Gaps = 1/170 (0%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330

+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA

Sbjct: 68 VQGCDA SVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGP+W V LG

Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNLISRFSAL-GLSTKDLVALSGTKHI 1657

RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VALSG I

Sbjct: 140 RRDSIDANEAEANS DLPGFNSSRSELEAAFLRKGLNTVDMVALSGAHTI 189

Score = 66.6 bits (161), Expect = 2e-08

Identities = 33/62 (53%), Positives = 44/62 (70%), Gaps = 2/62 (3%)

Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L VL+ +A+ QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAASGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|AAA32972.1| peroxidase [Hordeum vulgare]
Length = 315

Score = 147 bits (372), Expect = 5e-33
Identities = 70/125 (56%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI TA+A + + +CP+T GSGD +LA LD T +FDN Y+ NL
Sbjct: 190 QAQCSTFRARIYGGDTNINTAYAASLRANCPQTVGSGDGLANLDTTANTFDNAYYTNL 249

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKN 2163
+ +KGLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 250 MSQKGLLHSDQVLFNDDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTQQGIRLS 309

Query: 2164 CRRIN 2178
C R+N
Sbjct: 310 CSRVN 314

Score = 95.9 bits (237), Expect = 2e-17
Identities = 64/170 (37%), Positives = 84/170 (49%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 67 VQGCDA SVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 122 RDSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRF-SALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN +P S+ +L + F GL+T D+VALSG I
Sbjct: 139 RRDSIDANENEANTDLPGFNSSRAEEAFLKKGGLNTVDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 3e-08
Identities = 31/59 (52%), Positives = 42/59 (71%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
L + V + +A+AQLS FY SCP +++KS V +A++ + RMGASLLRL FHDCFV
Sbjct: 9 LLVLVALVTAASAQLSPTFYDTSCPRLATIKSGVMAAVTSDPRMGASLLRLHFHDCFV 67

>emb|CBI22008.1| unnamed protein product [*Vitis vinifera*]
Length = 154

Score = 147 bits (371), Expect = 7e-33
Identities = 82/163 (50%), Positives = 97/163 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 25 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACKATVSCADILALAA 84

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 85 RDGVVL-----LGGPSWTVPLG 101

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVAL 1639
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ AL
Sbjct: 102 RRDARTANQSAANNLPPAPFANLSALISGFAAKGLNADDMTAL 144

Score = 43.5 bits (101), Expect = 0.14
Identities = 18/23 (78%), Positives = 21/23 (91%)
Frame = +1

Query: 715 AISKETRMGASLLRLFFHDCFVN 783
A+ +E RMGAS+LRLFFHDCFVN
Sbjct: 4 AVIREPRMGASILRLFFHDCFVN 26

>gb|ACD70388.1| class III peroxidase [*Triticum aestivum*]
Length = 316

Score = 147 bits (371), Expect = 7e-33
Identities = 70/124 (56%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR RIYNETNI+TAF + + +CPR+ G DN+LAPLD TP FDN Y+ NL+
Sbjct: 194 QSQCRFFRDRIYNETNIDTAFATSLRANCPRSGG--DNSLAPLDTGTPNGFDNAYYTLM 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ LFNGG D+ VR +S++ TF+S F AMI MG+I+P TG+ G+IR C
Sbjct: 252 SQKGLLHSDQVLFNGGGADNTVRSFSSSAATFNSAFTTAMINMGNIAPKTGTQGQIRLVC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 127 bits (320), Expect = 6e-27
Identities = 76/169 (44%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LL DT SF GE+ A PN NS RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 67 VDGCDGSVLLADTGSFIGEQGAAPNNNSIRGMNVIDNIKTQVEAVCKQTVSCADILAVAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 127 RDSV-----VALGGPTWTVLLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ A N +P PT +L L + F LS D+VALSG I
Sbjct: 144 RRDSTTASKTNAENDLPPPTFDLQNLTTLFGNKQLSMTDMVALSGAHTI 192

Score = 70.1 bits (170), Expect = 1e-09
Identities = 34/63 (53%), Positives = 46/63 (73%), Gaps = 2/63 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
CL L VL+ +A+AQLS+ FY SCPN +++K+ V +A+ E RMGASL+RL FHDC
Sbjct: 6 CLGLVVLVAMASAASAQLSSTFYDTSCPNALATIKAGVTAAVQNEARMGASLVRLHFHDC 65

Query: 775 FVN 783
FV+
Sbjct: 66 FVD 68

>gb|ABF48527.1| cell wall peroxidase [Capsicum annuum]
gb|ABG73021.1| cell wall peroxidase [Capsicum annuum]
Length = 322

Score = 147 bits (370), Expect = 9e-33
Identities = 79/125 (63%), Positives = 91/125 (72%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
 QA+C FR RIY N T+I+ FA TR++ CP+ +G NLAPLDL TP DN YFKNL
 Sbjct: 200 QACFLFRDRIYSNGTDIDAGFASTRRRRCQEDQNG--NLAPLDLVTPNQLDNNYFKNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
 Q+KGLL SDQ L +GGSTD IV YS +P F+SDFAAAMI+MGDISPLTGSNG IR
 Sbjct: 258 RQRKGLLQSDQVLLSGGSTDDIVLEYSNSPRAFASDFAAAMIRMGDISPLTGSNGIIRTV 317

Query: 2164 CRRIN 2178
 C IN
 Sbjct: 318 CGAIN 322

Score = 127 bits (320), Expect = 6e-27
 Identities = 71/169 (42%), Positives = 92/169 (54%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAI AA 1330
 +QGCD SILLD+T + EK A PN S RG+ +I++ K +EK CPG+VSCADILA+AA
 Sbjct: 73 VQGCDASILLDETPTIVSEKTALPNLGSVRGYIIEDAKRELEKTC PGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RD+ +V GGP+W VKLG
 Sbjct: 133 RDASTLV-----GGPSWTVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TAS + A +P P L +LIS F+ GLST+D+VALSG+ I
 Sbjct: 150 RRDSTTASHTLAETDLP GPFDP LTRLISGFAKKGLSTRDMVALSGSHSI 198

Score = 62.8 bits (151), Expect = 2e-07
 Identities = 28/58 (48%), Positives = 41/58 (70%)
 Frame = +1

Query: 607 ALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
 +L +L +AQLS+ FY +CPN ++++ +V+ A+S E RM ASL+RL FHDCFV
 Sbjct: 16 SLVLLCSMQCHAQLSSTFYDRACPNALNTIRKSVRQAVSAERRMAASLIRLHFHDCFV 73

>gb|ACF08092.1| class III peroxidase [Triticum aestivum]
 Length = 316

Score = 146 bits (369), Expect = 1e-32
 Identities = 68/125 (54%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
 Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL
Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FS+ F AMIKMG+I+P TG+ G+IR +
Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSNAFTTAMIKMGNIAPKTGTQGQIRLS 310

Query: 2164 CRRIN 2178
C R+N
Sbjct: 311 CSRVN 315

Score = 97.1 bits (240), Expect = 1e-17
Identities = 64/170 (37%), Positives = 86/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 68 VQGCDA SVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQT VSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VALSG I
Sbjct: 140 RRDSIDANEAEANS DLPGFNSSRSELEAAFLRKGLNTVDMVALSGAHTI 189

Score = 65.5 bits (158), Expect = 3e-08
Identities = 33/62 (53%), Positives = 43/62 (69%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L VL+ +A QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAAAGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|ACN37032.1| unknown [Zea mays]
Length = 314

Score = 146 bits (369), Expect = 1e-32

Identities = 68/124 (54%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C +F IYN+TNI AFA + + +CP SG ++LAPLD TPT+FDN Y+ NL+

Sbjct: 193 QAQCLSFNDHIYNDTNINPAFAMSLRTNCP---ASGSSSLAPLDAMTPTAFDNAYYTLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGBISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFN GS DS V ++ N F+S FA AM+KMG++SPLTGS G++R NC

Sbjct: 250 SQRGLLHSDQELFNNGSADSTVSSFAANAAFTSAFATAMVKMGNLSPLTGSQGGVRINC 309

Query: 2167 RRIN 2178

R+N

Sbjct: 310 WRVN 313

Score = 115 bits (287), Expect = 4e-23
Identities = 72/170 (42%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD S+LL+DTS GE+N PN+ + RGF+V D+IK+ VE VCPG+VSCADILA+A

Sbjct: 69 VQGCDAVLLNDTS---GEQNQIPNQTNLNPRGFDVFDSIKAQVEAVCPGIVSCADILAVA 125

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V + LGGP+W V L

Sbjct: 126 ARDGV-----VALGGPSWTVAL 142

Query: 1508 GRRDARTASQAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

GRRD+ TAS A + +P PTS+L QL+ +S L+ D+VALSG I

Sbjct: 143 GRRDS-TASFPAQTSDLPPPTSSLQQLLRAYSKKNLNQDTMVALSGAHTI 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 35/70 (50%), Positives = 50/70 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MA+ S L + L + V++ A+AQLS+ FY SCP+ S++ S V +A+++E R+GASL

Sbjct: 1 MAASASCL-LSLLVVVLAALASAQLSSTFYDTSCPSALSTISSGVTAAVAQEARVGASL 59

Query: 751 LRLFFHDCFV 780

LRL FHDCFV

Sbjct: 60 LRLHFHDCFV 69

>sp|P27337.1|PER1_HORVU RecName: Full=Peroxidase 1; Flags: Precursor

emb|CAA41294.1| peroxidase [Hordeum vulgare]
Length = 315

Score = 146 bits (369), Expect = 1e-32
Identities = 69/125 (55%), Positives = 93/125 (74%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD T +FDN Y+ NL
Sbjct: 190 QACSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGSANLDTTANTFDNAYYTNL 249

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ +KGLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 250 MSQKGLLHSDQVLFNDDTTDNTVRNFASNPAAFSSSFTTAMIKMGNIAPKTGTQQGIRLS 309

Query: 2164 CRRIN 2178
C R+N
Sbjct: 310 CSRVN 314

Score = 95.9 bits (237), Expect = 2e-17
Identities = 64/170 (37%), Positives = 84/170 (49%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 67 VQGCDASVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 122 RDSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRF-SALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN +P S+ +L + F GL+T D+VALSG I
Sbjct: 139 RRDSIDANENEANTDLPGFNSSRAELEAAFLKKGGLNTVDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 3e-08
Identities = 31/59 (52%), Positives = 42/59 (71%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
L + V + +A+AQLS FY SCP +++KS V +A++ + RMGASLLRL FHDCFV
Sbjct: 9 LLVLVALVTAASAQLSPTFYDTSCPRALATIKSGVMAAVTSDPRMGASLLRLHFHDCFV 67

>gb|ABV24961.1| peroxidase [Catharanthus roseus]

Length = 135

Score = 146 bits (368), Expect = 2e-32
Identities = 82/170 (48%), Positives = 98/170 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDTSSFTGEKNA PN+ S RGFEVID IKS +E +CPGVVSCADILA+AA
Sbjct: 8 VNGCDGSVLLDDTSSFTGEKNARPNKGLRGFEVIDTIKSQLETICPGVVSCADILAVAA 67

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W V+LG
Sbjct: 68 RDSV-----VALGGPAWIVELG 84

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHIS 1660
RRD+ TAS S A IP P +L +++ FS G S K++VALSG I+
Sbjct: 85 RRDSTTASLSDAEANIPFPRMDLTDILTAFSNKGFSKEMVALSGAHTIT 134

>emb|CAL25298.1| properoxidase [Picea abies]
Length = 341

Score = 146 bits (368), Expect = 2e-32
Identities = 84/169 (49%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
++GCDGSILLDDTSSFT EK ANPNRNS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTREKTANPNRNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGPNSTHTLETKFQRQLNVVDLVALSGAHTI 208

Score = 121 bits (303), Expect = 5e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFKARLYNQTVNGKPDPTLDTTYLKLHRAVCPQT-GTDDNQTTPLDPVTPIRFDIN 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142

Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGNNINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N

Sbjct: 330 HGEIRKNCRRMN 341

Score = 59.7 bits (143), Expect = 2e-06
Identities = 36/71 (50%), Positives = 44/71 (61%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE M AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEAGMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>gb|ACF08089.1| class III peroxidase [Triticum aestivum]
Length = 149

Score = 146 bits (368), Expect = 2e-32
Identities = 70/124 (56%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR RIYNETNI TAFa + + +CPR+ G DN+LAPLD TPT+FDN Y+ NL+
Sbjct: 27 QSQCRFFRDRIYNETNIGTAFATSLRANCPRSGG--DNSLAPLDGTPTAFDNAYYTNLN 84

Query: 1987 QKKGLLHSDQQLFNNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ LFNGG D+ V ++++ TF+S F AMI MG+I+P TG+ G+IR C
Sbjct: 85 SKKGLLHSDQVLFNNGGADNTVMSFASSAATFNSAFTTAMINMGNIAPKTGTQGGIRLVC 144

Query: 2167 RRIN 2178
++N
Sbjct: 145 SKVN 148

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Feb 13, 2010 7:16 AM
Number of letters in database: 3,559,509,877
Number of sequences in database: 10,432,217

Lambda K H
0.318 0.134 0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 10432217

Number of Hits to DB: 15,045,157,324

Number of extensions: 301983811

Number of successful extensions: 641055

Number of sequences better than 10.0: 1970

Number of HSP's gapped: 638318

Number of HSP's successfully gapped: 6610

Length of query: 910

Length of database: 3,559,509,877

Length adjustment: 146

Effective length of query: 764

Effective length of database: 2,036,406,195

Effective search space: 1555814332980

Effective search space used: 1555814332980

Neighboring words threshold: 12

Window for multiple hits: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 33 (17.3 bits)

BLASTn Output of the 3' Border Sequences Flanking the Insert in Soybean Event DAS-68416-4 against GenBank Nucleotide Collection (nt/nr)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 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.

Query= 68416_3_border
(1082 letters)

Database: /usr/local/blast/db/blastlibs/nt
10,930,266 sequences; 30,212,464,392 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
gb AC235472.1	Glycine max strain Williams 82 clone GM_WBc0099F2...	64	2e-06
emb AM473070.1	Vitis vinifera contig VV78X025151.6, whole genom...	48	0.11
gb AC233130.7	Solanum lycopersicum strain Heinz 1706 chromosome...	46	0.42
gb CP001633.1	Francisella tularensis subsp. tularensis NE061598...	46	0.42
ref XM_002426020.1	Pediculus humanus corporis synaptonemal comp...	46	0.42
emb AJ749949.2	Francisella tularensis subsp. tularensis SCHU S4...	46	0.42
gb AC235129.1	Glycine max strain Williams 82 clone GM_WBa0052I0...	46	0.42
tpg BK006741.1	TPA: TPA_reasm: Francisella tularensis subsp. ho...	46	0.42
ref XM_001336009.2	PREDICTED: Danio rerio hypothetical LOC10000...	46	0.42
gb CP000915.1	Francisella tularensis subsp. mediasiatica FSC147...	46	0.42
gb AC206008.3	Pongo abelii BAC clone CH276-282M20 from chromoso...	46	0.42
gb AC216474.1	Populus trichocarpa clone POP081-J22, complete se...	46	0.42
ref XM_001713455.1	Guillardia theta hypothetical protein (orf43...	46	0.42
gb CP000803.1	Francisella tularensis subsp. holarctica FTNF002-...	46	0.42
ref XM_001479242.1	PREDICTED: Mus musculus similar to MK-5 type...	46	0.42
emb AM457942.2	Vitis vinifera contig VV78X124814.1, whole genom...	46	0.42
emb AM446264.2	Vitis vinifera contig VV78X146694.5, whole genom...	46	0.42
gb CP000608.1	Francisella tularensis subsp. tularensis WY96-341...	46	0.42
ref NM_001110031.1	Danio rerio zgc:136903 (zgc:136903), mRNA >g...	46	0.42
emb AM485714.1	Vitis vinifera, whole genome shotgun sequence, c...	46	0.42
gb CP000439.1	Francisella tularensis subsp. novicida U112, comp...	46	0.42
emb CT027756.10	Zebrafish DNA sequence from clone DKEY-95F11 in...	46	0.42
gb CP000437.1	Francisella tularensis subsp. holarctica OSU18, c...	46	0.42
emb AM286280.1	Francisella tularensis subsp. tularensis strain ...	46	0.42
gb DQ681941.1	Synthetic construct Francisella tularensis clone ...	46	0.42

gb AC151347.2	Xenopus (Silurana) tropicalis clone ISB-394A6, co...	46	0.42
gb AC125096.3	Mus musculus BAC clone RP24-181K19 from chromosom...	46	0.42
gb AC131109.3	Mus musculus BAC clone RP23-362M7 from chromosome...	46	0.42
dbj AK137657.1	Mus musculus adult female vagina cDNA, RIKEN ful...	46	0.42
emb CR690313.2	Tetraodon nigroviridis full-length cDNA	46	0.42
gb AC026100.19	Homo sapiens 3 BAC RP11-449F7 (Roswell Park Canc...	46	0.42
gb AF165818.4	Guillardia theta nucleomorph chromosome 1, comple...	46	0.42
emb BX548071.7	Zebrafish DNA sequence from clone DKEY-25L23 in ...	46	0.42
emb BX537275.8	Zebrafish DNA sequence from clone DKEYP-120E12 i...	46	0.42
emb BX537269.8	Zebrafish DNA sequence from clone DKEY-181H1 in ...	46	0.42
dbj AP005846.2	Oryza sativa Japonica Group genomic DNA, chromos...	46	0.42
emb AM233362.1	Francisella tularensis subsp. holarctica LVS com...	46	0.42
gb AC151343.2	Xenopus (Silurana) tropicalis clone ISB-373E17, c...	46	0.42
gb AC155316.6	Mus musculus BAC clone RP23-181P9 from chromosome...	46	0.42
ref XM_733026.1	Plasmodium chabaudi chabaudi hypothetical prote...	46	0.42
emb AL935040.6	Zebrafish DNA sequence from clone CH211-176L21, ...	46	0.42
emb FP236458.5	Zebrafish DNA sequence from clone CH73-374P12, c...	44	1.7
emb AL844509.2	Plasmodium falciparum 3D7 chromosome 13	44	1.7
emb AL844508.1	Plasmodium falciparum 3D7 chromosome 9	44	1.7
dbj AP010895.1	Solanum lycopersicum DNA, chromosome 8, clone: C...	44	1.7
gb CP001110.1	Pelodictyon phaeoclathratiforme BU-1, complete ge...	44	1.7
ref XM_001740672.1	Entamoeba dispar SAW760 F-box/leucine rich r...	44	1.7
ref XM_001712135.1	Hemiselmis andersenii hypothetical protein (...)	44	1.7
gb CP000881.1	Hemiselmis andersenii chromosome 1, complete sequ...	44	1.7
dbj AB270792.1	Malus x domestica MdSFB9-alpha, S9-RNase, MdSFB...	44	1.7
ref XM_001350114.1	Plasmodium falciparum 3D7 hypothetical prote...	44	1.7
ref XM_001349842.1	Plasmodium falciparum 3D7 hypothetical prote...	44	1.7
gb AC187618.3	Pan troglodytes BAC clone CH251-584I16 from chrom...	44	1.7
gb AC192762.3	Pan troglodytes BAC clone CH251-676O11 from chrom...	44	1.7
emb CT961058.16	M. truncatula DNA sequence from clone MTH2-80N17...	44	1.7
ref XM_001032614.1	Tetrahymena thermophila conserved hypothetic...	44	1.7
emb CT827810.6	Zebrafish DNA sequence from clone DKEY-120E24 in...	44	1.7
emb AM231674.1	Prunus dulcis partial s-RNase gene for ribonucle...	44	1.7
gb AC154194.2	Mus musculus BAC clone RP24-401L2 from chromosome...	44	1.7
gb AC091473.2	Mus musculus chromosome X clones RP21-114F21, RP2...	44	1.7
gb AC006353.3	Homo sapiens PAC clone RP5-1062J16 from 7, comple...	44	1.7
gb AC132451.3	Mus musculus BAC clone RP23-194C20 from chromosom...	44	1.7
ref XM_651154.1	Entamoeba histolytica HM-1:IMSS hypothetical pr...	44	1.7
gb AC113349.2	Homo sapiens chromosome 5 clone CTD-2544H17, comp...	44	1.7
emb AL353592.9	Human DNA sequence from clone RP11-569012 on chr...	44	1.7
emb AL031297.4	Human DNA sequence from clone RP1-97P20 on chrom...	44	1.7
emb BX571852.20	Zebrafish DNA sequence from clone DKEY-175N6 in...	44	1.7
emb BX936441.6	Zebrafish DNA sequence from clone CH211-234M15 i...	44	1.7
emb BX511195.5	Zebrafish DNA sequence from clone DKEYP-57D12 in...	44	1.7
emb BX255948.4	Zebrafish DNA sequence from clone CH211-250J1, c...	44	1.7
gb AC108005.8	Homo sapiens chromosome 11, clone CTD-2515M10, co...	44	1.7
emb AL445564.1	Mycoplasma pulmonis (strain UAB CTIP) complete g...	44	1.7
gb AC008436.5	AC008436 Homo sapiens chromosome 5 clone CTC-327B1...	44	1.7
gb AC149381.2	Phakopsora pachyrhizi clone JGIAFNA-5A7, complete...	44	1.7

emb	AL928731.11	Mouse DNA sequence from clone RP23-171N20 on ch...	44	1.7
gb	AC238432.1	Mus musculus BAC clone RP24-76M8 from chromosome ...	42	6.6
gb	CP001701.1	Cyanothece sp. PCC 8802, complete genome	42	6.6
ref	NW_003033920.1	Schistosoma mansoni genome sequence supercon...	42	6.6
emb	FN409584.1	Equus caballus microsatellite DNA, locus ABGe15567	42	6.6
ref	XM_002445459.1	Sorghum bicolor hypothetical protein, mRNA	42	6.6
ref	XM_002444559.1	Sorghum bicolor hypothetical protein, mRNA	42	6.6
ref	XM_002450673.1	Sorghum bicolor hypothetical protein, mRNA	42	6.6
emb	FN357601.1	Schistosoma mansoni genome sequence supercontig ...	42	6.6
emb	FN368115.1	Schistosoma mansoni genome sequence supercontig ...	42	6.6
gb	AC202790.4	Gallus gallus BAC clone CH261-161K24 from chromos...	42	6.6
gb	AC235243.1	Glycine max strain Williams 82 clone GM_WBb0032L2...	42	6.6
gb	AC235153.1	Glycine max strain Williams 82 clone GM_WBa0085L0...	42	6.6
gb	AC235140.1	Glycine max strain Williams 82 clone GM_WBa0068I0...	42	6.6
emb	AL844502.1	Plasmodium falciparum 3D7 chromosome 3	42	6.6
gb	CP000857.1	Salmonella enterica subsp. enterica serovar Parat...	42	6.6
emb	FM992689.1	Candida dubliniensis CD36 chromosome 2, complete...	42	6.6
gb	FJ581043.1	Oryza punctata clone OP_Ba0017E18, complete sequence	42	6.6
ref	XM_002166130.1	PREDICTED: Hydra magnipapillata similar to p...	42	6.6
gb	CP001176.1	Bacillus cereus B4264, complete genome	42	6.6
emb	CU855905.8	Zebrafish DNA sequence from clone CH73-190M24 in...	42	6.6
ref	NG_008899.1	Homo sapiens sarcoglycan zeta (SGCZ) on chromos...	42	6.6
ref	NM_001135888.1	Bombyx mori osiris 9 (Osi9), mRNA >gi 207339...	42	6.6
emb	CU914133.2	Medicago truncatula chromosome 5 clone mth2-150o...	42	6.6
gb	CP001120.1	Salmonella enterica subsp. enterica serovar Heide...	42	6.6
emb	AM910991.1	Plasmodium knowlesi strain H chromosome 9, compl...	42	6.6
gb	AC198044.3	Pongo abelii BAC clone CH276-446K19 from chromoso...	42	6.6
gb	AC216598.1	Populus trichocarpa clone POP037-D13, complete se...	42	6.6
gb	AC205959.4	Canis familiaris, clone XX-180015, complete sequence	42	6.6
gb	AC213090.1	Populus trichocarpa clone POP118-019, complete se...	42	6.6
gb	AC212636.1	Solanum lycopersicum chromosome 7 clone C07HBa017...	42	6.6
gb	CP000409.1	Rickettsia canadensis str. McKiel, complete genome	42	6.6
gb	AC198093.4	Pongo abelii BAC clone CH276-31L11 from chromosom...	42	6.6
emb	CU329671.1	Schizosaccharomyces pombe chromosome II	42	6.6
ref	XM_001645942.1	Vanderwaltozyma polyspora DSM 70294 hypothet...	42	6.6
gb	AC209107.1	Populus trichocarpa clone POP088-K16, complete se...	42	6.6
ref	XM_001638933.1	Nematostella vectensis predicted protein (NE...	42	6.6
gb	AC174335.10	Medicago truncatula clone mth2-155122, complete ...	42	6.6
gb	CP000721.1	Clostridium beijerinckii NCIMB 8052, complete genome	42	6.6
gb	AC202303.8	Medicago truncatula clone mth2-155j9, complete se...	42	6.6
gb	EF533700.1	Glycine max clone BAC GM_WBb080D08, complete sequ...	42	6.6
gb	DQ914719.1	Fungal sp. EXP0495F 18S ribosomal RNA gene, parti...	42	6.6
emb	AM473707.2	Vitis vinifera contig VV78X111932.6, whole genom...	42	6.6
emb	AM483283.2	Vitis vinifera contig VV78X178586.8, whole genom...	42	6.6
emb	AM481633.2	Vitis vinifera contig VV78X190383.5, whole genom...	42	6.6
emb	AM479192.2	Vitis vinifera contig VV78X197549.13, whole geno...	42	6.6
emb	AM425055.2	Vitis vinifera contig VV78X086233.8, whole genom...	42	6.6
emb	AM463129.2	Vitis vinifera contig VV78X099343.8, whole genom...	42	6.6
emb	AM453496.2	Vitis vinifera contig VV78X099343.7, whole genom...	42	6.6

emb	AM433228.2	Vitis vinifera contig VV78X071247.4, whole genom...	42	6.6
emb	AM432606.2	Vitis vinifera contig VV78X032134.1, whole genom...	42	6.6
emb	AM436044.2	Vitis vinifera contig VV78X143044.4, whole genom...	42	6.6
gb	BC140581.1	Bos taurus cDNA clone IMAGE:8238248	42	6.6
ref	XM_001017552.2	Tetrahymena thermophila hypothetical protein...	42	6.6
emb	CU210926.7	Mouse DNA sequence from clone CH29-115D7 on chro...	42	6.6
ref	XM_001351252.1	Plasmodium falciparum 3D7 hypothetical prote...	42	6.6
gb	AC197607.1	Pongo abelii BAC clone CH276-100H12 from chromoso...	42	6.6
emb	CT583646.5	Zebrafish DNA sequence from clone DKEYP-72G6 in ...	42	6.6
emb	AM471960.1	Vitis vinifera contig VV78X029428.17, whole geno...	42	6.6
emb	AM458894.1	Vitis vinifera, whole genome shotgun sequence, c...	42	6.6
gb	AC192717.3	Gallus gallus BAC clone CH261-36N8 from chromosom...	42	6.6
dbj	AP009289.1	Solanum lycopersicum genomic DNA, chromosome 8, ...	42	6.6
emb	CT573243.6	Zebrafish DNA sequence from clone CH73-365J20 in...	42	6.6
emb	CU024879.5	M.truncatula DNA sequence from clone MTH2-70F3 o...	42	6.6
emb	CR790361.11	Zebrafish DNA sequence from clone DKEY-29N19, c...	42	6.6
gb	AE014297.2	Drosophila melanogaster chromosome 3R, complete s...	42	6.6
ref	XM_392161.3	PREDICTED: Apis mellifera similar to CG2931-PA,...	42	6.6
emb	CR627495.19	Zebrafish DNA sequence from clone DKEY-58G10 in...	42	6.6
emb	CR533579.7	Zebrafish DNA sequence from clone CH211-232J20 i...	42	6.6
emb	CT573422.5	Mouse DNA sequence from clone RP24-76M8 on chrom...	42	6.6
emb	CR848045.10	Zebrafish DNA sequence from clone DKEY-8K3 in l...	42	6.6
gb	CP000153.1	Sulfurimonas denitrificans DSM 1251, complete genome	42	6.6
gb	AC164170.7	Mus musculus 10 BAC RP24-419C12 (Roswell Park Can...	42	6.6
gb	AC102324.9	Mus musculus chromosome 1, clone RP24-476A18, com...	42	6.6
gb	AC158641.12	Mus musculus 10 BAC RP23-461E22 (Roswell Park Ca...	42	6.6
gb	AC150800.3	Medicago truncatula chromosome 7 clone mth2-77m9,...	42	6.6
gb	AY018508.1	Oryza sativa microsatellite MRG0833 containing (A...	42	6.6
gb	U23181.2	Caenorhabditis elegans cosmid ZK84, complete sequence	42	6.6
gb	AY330624.1	Galleria mellonella inducible metalloproteinase i...	42	6.6
gb	AC146790.16	Medicago truncatula clone mth2-123b21, complete ...	42	6.6
gb	AC137078.24	Medicago truncatula clone mth2-10e12, complete s...	42	6.6
gb	AC108876.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	42	6.6
gb	AC117265.2	Oryza sativa Japonica Group chromosome 5 clone OJ...	42	6.6
gb	AC142111.3	Mus musculus BAC clone RP24-63G9 from chromosome ...	42	6.6
gb	AC139290.15	Medicago truncatula clone mth2-23f4, complete se...	42	6.6
gb	AC124558.4	Mus musculus BAC clone RP23-24808 from chromosome...	42	6.6
gb	AC123865.5	Mus musculus BAC clone RP23-365C14 from chromosom...	42	6.6
gb	AC123714.6	Mus musculus chromosome 9, clone RP23-393E20, com...	42	6.6
gb	AC110169.7	Mus musculus chromosome 9, clone RP23-233D3, comp...	42	6.6
gb	AE017245.1	Mycoplasma synoviae 53, complete genome	42	6.6
dbj	AP008983.1	Clostridium phage c-st genomic DNA, complete genome	42	6.6
gb	AC164090.3	Mus musculus BAC clone RP23-403F3 from chromosome...	42	6.6
gb	AC157542.11	Mus musculus chromosome 1, clone RP23-115I1, com...	42	6.6
emb	CR450724.10	Zebrafish DNA sequence from clone DKEY-168I4 in...	42	6.6
ref	XM_805808.1	Trypanosoma cruzi strain CL Brener hypothetical...	42	6.6
ref	XM_803717.1	Trypanosoma cruzi strain CL Brener hypothetical...	42	6.6
gb	DQ075075.1	Scirtothrips astrictus isolate PA-04-009 18S ribo...	42	6.6
gb	AC163647.3	Mus musculus BAC clone RP23-214L4 from chromosome...	42	6.6

emb	CR931715.1	Streptococcus pneumoniae strain 198/71 (serotype...	42	6.6
emb	CR931706.1	Streptococcus pneumoniae strain 7765/43 (serotyp...	42	6.6
emb	CR931704.1	Streptococcus pneumoniae strain 1936/39 (serotyp...	42	6.6
ref	NM_001021038.1	Schizosaccharomyces pombe transcription fact...	42	6.6
gb	AC157474.2	Mus musculus BAC clone RP24-565B5 from chromosome...	42	6.6
emb	CR352233.9	Zebrafish DNA sequence from clone CH211-193J5 in...	42	6.6
gb	AC143340.4	Medicago truncatula clone mth2-7f4, complete sequ...	42	6.6
dbj	AK054176.1	Mus musculus 2 days pregnant adult female oviduc...	42	6.6
dbj	AK053595.1	Mus musculus 0 day neonate eyeball cDNA, RIKEN f...	42	6.6
gb	AC044781.12	Homo sapiens chromosome 10 clone RP11-142M10, co...	42	6.6
gb	AC117398.3	Homo sapiens 3 BAC RP11-715A9 (Roswell Park Cance...	42	6.6
gb	AC002505.3	Arabidopsis thaliana chromosome 2 clone T9J22 map...	42	6.6
gb	AC096687.5	Oryza sativa chromosome 3 BAC OSJNBa0010E04 genom...	42	6.6
gb	AC020992.10	Homo sapiens chromosome 8, clone RP11-23H1, comp...	42	6.6
emb	AL365496.15	Human DNA sequence from clone RP11-449J3 on chr...	42	6.6
gb	AY060392.1	Drosophila melanogaster LD29917 full length cDNA	42	6.6
gb	AC034205.4	Homo sapiens chromosome 5 clone CTB-23I7, complet...	42	6.6
gb	AC091045.3	Homo sapiens chromosome 15 clone RP11-111A22 map ...	42	6.6
emb	AL137855.10	Human DNA sequence from clone RP5-1064J9 on chr...	42	6.6
emb	AL096771.11	Human DNA sequence from clone RP1-238D15 on chr...	42	6.6
emb	Z92813.1	Caenorhabditis elegans Cosmid T28A8, complete sequ...	42	6.6
emb	Z81139.1	Caenorhabditis elegans Cosmid W05H5, complete sequ...	42	6.6
gb	S74768.1	16S progenitor toxin: cha 33=hemagglutinin...cha-70...	42	6.6
emb	BX957329.9	Zebrafish DNA sequence from clone CH211-130P21 i...	42	6.6
dbj	AP005800.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP005000.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
emb	BX511180.7	Zebrafish DNA sequence from clone CH211-221H1 in...	42	6.6
dbj	AP005884.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP006164.2	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
emb	BX294435.5	Zebrafish DNA sequence from clone DKEYP-32G6 in ...	42	6.6
emb	BX890568.8	Zebrafish DNA sequence from clone DKEY-208J2 in ...	42	6.6
dbj	AP004462.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP003909.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP005249.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
dbj	AP004384.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
gb	AF476953.1	Vaucheria geminata ribulose-1,5-bisphosphate carb...	42	6.6
gb	AF476952.1	Vaucheria geminata ribulose-1,5-bisphosphate carb...	42	6.6
gb	AC091530.4	Papio anubis clone RP41-444A14, complete sequence	42	6.6
gb	AC098584.2	Homo sapiens BAC clone RP11-10L11 from 4, complet...	42	6.6
gb	AC091619.3	Papio anubis clone RP41-139B7, complete sequence	42	6.6
dbj	AP003209.3	Oryza sativa Japonica Group genomic DNA, chromos...	42	6.6
emb	AL604063.4	Mouse DNA sequence from clone RP23-467J12 on chr...	42	6.6
gb	AC010884.11	Homo sapiens BAC clone RP11-350B7 from 2, comple...	42	6.6
gb	AC093759.3	Homo sapiens BAC clone RP11-67M1 from 4, complete...	42	6.6
gb	AC091247.4	Oryza sativa chromosome 3 BAC OJ1111_B11 genomic ...	42	6.6
gb	AC007755.6	AC007755 Drosophila melanogaster, chromosome 3R, r...	42	6.6
gb	AC007726.7	AC007726 Drosophila melanogaster, chromosome 3R, r...	42	6.6
gb	AC073166.7	Oryza sativa chromosome 10 BAC OSJNBb0064P21 geno...	42	6.6
gb	AC009232.3	Homo sapiens BAC clone RP11-352J11 from 2, comple...	42	6.6

gb AC019215.4 AC019215 Homo sapiens BAC clone RP11-480M18 from 8...	42	6.6
gb AC007404.4 Homo sapiens BAC clone RP11-547I5 from 2, complet...	42	6.6
emb X87946.1 O. sativa ZB8 gene	42	6.6
emb X62389.1 Botulinum bacteriophage genes for HA-17, HA-33, no...	42	6.6
emb X72793.1 Clostridium botulinum C phage BONT/C1, ANTP-139, A...	42	6.6
emb X66433.1 Clostridium botulinum phage 1C, CHn-14, CHn-33, Ch...	42	6.6
ref XM_672717.1 Plasmodium berghei strain ANKA hypothetical pro...	42	6.6
ref XM_668682.1 Plasmodium berghei strain ANKA hypothetical pro...	42	6.6
gb AE017220.1 Salmonella enterica subsp. enterica serovar Chole...	42	6.6
gb AC118672.3 Genomic sequence for Oryza sativa, Nipponbare str...	42	6.6
gb AC132258.3 Mus musculus BAC clone RP24-361F13 from 1, comple...	42	6.6
emb AL954656.9 Zebrafish DNA sequence from clone CH211-67N10 in...	42	6.6
emb BX120013.5 Zebrafish DNA sequence from clone DKEY-76H10, co...	42	6.6
emb BX005215.13 Mouse DNA sequence from clone RP23-280F9 on chr...	42	6.6
emb AL844857.5 Mouse DNA sequence from clone RP23-74L17 on chro...	42	6.6
emb BX247951.11 Zebrafish DNA sequence from clone DKEY-246A16 i...	42	6.6
gb AE016830.1 Enterococcus faecalis V583, complete genome	42	6.6
emb AL929523.5 Zebrafish DNA sequence from clone CH211-250I3, c...	42	6.6
emb AL773566.6 Mouse DNA sequence from clone RP23-181C9 on chro...	42	6.6
emb AL669898.17 Mouse DNA sequence from clone RP23-6C3 on chrom...	42	6.6
gb AE008384.1 Methanosarcina mazei strain Goel, complete genome	42	6.6
emb AL391158.5 Human chromosome 14 DNA sequence BAC R-560013 of...	42	6.6
dbj AB061780.1 Clostridium botulinum orf-22, ha-70, ha-17, ha-3...	42	6.6
emb AL132951.3 Caenorhabditis elegans YAC Y67H2A, complete sequ...	42	6.6
dbj AB012112.1 Clostridium botulinum D phage gene for ORF-22, H...	42	6.6
dbj AB012111.1 Clostridium botulinum D phage gene for ORF-22, H...	42	6.6
gb AC005548.1 AC005548 Homo sapiens chromosome 17, clone hRPK.75...	42	6.6
gb L22534.1 GALLHP82Z Galleria mellonella hexamerin (Lhp82) gene...	42	6.6

>gb|AC235472.1| Glycine max strain Williams 82 clone GM_WBc0099F23, complete sequence
Length = 134971

Score = 63.9 bits (32), Expect = 2e-06
Identities = 47/52 (90%)
Strand = Plus / Plus

Query: 212 tatcttttgtttcatttactttatgtgagggatataatagtaataaacatt 263
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 77662 tatcttttgtatcatttgcattatgttagggatataatagttataaaacatt 77713

Score = 42.1 bits (21), Expect = 6.6
Identities = 36/41 (87%)
Strand = Plus / Minus

Query: 216 ttttgtttcatttactttatgtgagggatataatagtaata 256

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 78023 ttttatttcatttagttaatgtaggatataatagaaata 77983

>emb|AM473070.1| Vitis vinifera contig VV78X025151.6, whole genome shotgun sequence
Length = 4985

Score = 48.1 bits (24), Expect = 0.11
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 4 aacaatcaatatattttaattcttaaactttatt 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 4576 aacaataaatattttaattgttaaactttatt 4607

>gb|AC233130.7| Solanum lycopersicum strain Heinz 1706 chromosome 10 clone hba-256116 map
10, complete sequence
Length = 159015

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 738 agaaattaactttttgttttttaaaaa 764
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 155094 agaaattaactttttcttttttaaaaa 155068

>gb|CP001633.1| Francisella tularensis subsp. tularensis NE061598, complete genome
Length = 1892681

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 971539 tatgtctttctctaattgatgaa 971561

>ref|XM_002426020.1| Pediculus humanus corporis synaptonemal complex protein ZIP1,
putative, mRNA
Length = 4083

Score = 46.1 bits (23), Expect = 0.42

Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 274 aaagaaaataaaaaagttaattt 296
|||||||
Sbjct: 1237 aaagaaaataaaaaagttaattt 1259

>emb|AJ749949.2| Francisella tularensis subsp. tularensis SCHU S4 complete genome
Length = 1892775

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
|||||||
Sbjct: 971474 tatgtctttctctaattgatgaa 971496

>gb|AC235129.1| Glycine max strain Williams 82 clone GM_WBa0052I05, complete sequence
Length = 119088

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataataaattcttatattat 1075
||||||| ||| |||
Sbjct: 53261 ttagagaaaaataataaattcatatattat 53291

>tpg|BK006741.1| TPA: TPA_reasm: Francisella tularensis subsp. holarctica OSU18, complete genome
Length = 1895727

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
|||||||
Sbjct: 1193421 tatgtctttctctaattgatgaa 1193399

>ref|XM_001336009.2| PREDICTED: Danio rerio hypothetical LOC100000153 (LOC100000153), mRNA
Length = 2316

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataataaaattcttatattatgt 1079
|||||||
Sbjct: 1739 agaaaaataataaaatcttatcttatatgt 1709

>gb|CP000915.1| Francisella tularensis subsp. mediasiatica FSC147, complete genome
Length = 1893886

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
|||||||
Sbjct: 1072991 tatgtctttctctaattgatgaa 1072969

>gb|AC206008.3| Pongo abelii BAC clone CH276-282M20 from chromosome unknown, complete
sequence
Length = 222278

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 276 agaaaaataaaaaagttaatttct 298
|||||||
Sbjct: 203364 agaaaaataaaaaagttaatttct 203386

>gb|AC216474.1| Populus trichocarpa clone POP081-J22, complete sequence
Length = 126068

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 738 agaaattaactttttgttttttaaaaactaa 768

|||||
Sbjct: 76109 agaaattaattttttgtttcttaaaaactaa 76139

>ref|XM_001713455.1| Guillardia theta hypothetical protein (orf433) mRNA, complete cds
Length = 1302

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 271 ttttaagaaaataaaaaagttaatttc 297
|||||
Sbjct: 838 ttttaagaaaatacaaaaagttaatttc 864

>gb|CP000803.1| Francisella tularensis subsp. holarctica FTNF002-00, complete genome
Length = 1890909

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 1189845 tatgtctttctctaattgatgaa 1189823

>ref|XM_001479242.1| PREDICTED: Mus musculus similar to MK-5 type 2 (LOC100047833), mRNA
Length = 4795

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaaac 765
|||||
Sbjct: 1815 ttaactttttgttttttaaaaac 1837

>emb|AM457942.2| Vitis vinifera contig VV78X124814.1, whole genome shotgun sequence
Length = 1077

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 734 tgagagaaattaactttttgttttta 760
 |||||
Sbjct: 502 tgagagaaattaactttttgttttta 476

>emb|AM446264.2| Vitis vinifera contig VV78X146694.5, whole genome shotgun sequence
Length = 3788

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 734 tgagagaaattaactttttgttttta 760
 |||||
Sbjct: 353 tgagagaaattaactttttgttttta 379

>gb|CP000608.1| Francisella tularensis subsp. tularensis WY96-3418, complete genome
Length = 1898476

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
 |||||
Sbjct: 832314 tatgtctttctctaattgatgaa 832336

>ref|NM_001110031.1| Danio rerio zgc:136903 (zgc:136903), mRNA
 >gi|133777836|gb|BC115322.1| Danio rerio zgc:136903, mRNA
 (cDNA clone MGC:136903 IMAGE:7993315), complete cds
Length = 2326

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataaataaatcttatattatgt 1079
 |||||
Sbjct: 1739 agaaaaataaataaatcttatattatgt 1709

>emb|AM485714.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X224594.16,

clone ENTAV 115
Length = 13699

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 734 tgagagaaattaactttttgttttta 760
|||||||
Sbjct: 4853 tgagagaaattaaattttgttttta 4879

>gb|CP000439.1| Francisella tularensis subsp. novicida U112, complete genome
Length = 1910031

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
|||||||
Sbjct: 894874 tatgtctttctctaattgatgaa 894896

>emb|CT027756.10| Zebrafish DNA sequence from clone DKEY-95F11 in linkage group 23,
complete sequence
Length = 112354

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 265 agtttatttaaagaaaataaaaa 287
|||||||
Sbjct: 78389 agtttatttaaagaaaataaaaa 78367

>gb|CP000437.1| Francisella tularensis subsp. holarctica OSU18, complete genome
Length = 1895727

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972

|||||
Sbjct: 1193421 tatgtctttctctaattgatgaa 1193399

>emb|AM286280.1| Francisella tularensis subsp. tularensis strain FSC 198 complete genome
Length = 1892616

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 971427 tatgtctttctctaattgatgaa 971449

>gb|DQ681941.1| Synthetic construct Francisella tularensis clone FLH231418.01X xthA
gene, complete sequence
Length = 789

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
|||||
Sbjct: 144 tatgtctttctctaattgatgaa 122

>gb|AC151347.2| Xenopus (Silurana) tropicalis clone ISB-394A6, complete sequence
Length = 78040

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1047 agagaaaaataataaattctta 1069
|||||
Sbjct: 2861 agagaaaaataataaattctta 2839

>gb|AC125096.3| Mus musculus BAC clone RP24-181K19 from chromosome 18, complete
sequence
Length = 154941

Score = 46.1 bits (23), Expect = 0.42

Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1047 agagaaaaataataaattctta 1069
|||||||
Sbjct: 89959 agagaaaaataataaattctta 89937

>gb|AC131109.3| Mus musculus BAC clone RP23-362M7 from chromosome 18, complete
sequence
Length = 177690

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1047 agagaaaaataataaattctta 1069
|||||||
Sbjct: 635 agagaaaaataataaattctta 613

>dbj|AK137657.1| Mus musculus adult female vagina cDNA, RIKEN full-length enriched
library, clone:9930013M24 product:MAP kinase-activated
protein kinase 5, full insert sequence
Length = 4783

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaaac 765
|||||||
Sbjct: 1842 ttaactttttgttttttaaaaac 1864

>emb|CR690313.2| Tetraodon nigroviridis full-length cDNA
Length = 1591

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaagtta 292
|||||||
Sbjct: 372 atttaaagaaaataaaaagtta 394

>gb|AC026100.19| Homo sapiens 3 BAC RP11-449F7 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length = 209521

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 276 agaaaataaaaaagttaatttct 298
|||||||
Sbjct: 28950 agaaaataaaaaagttaatttct 28972

>gb|AF165818.4| Guillardia theta nucleomorph chromosome 1, complete sequence
Length = 196216

Score = 46.1 bits (23), Expect = 0.42
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 271 ttttaagaaaataaaaaagttaatttc 297
||||||| |||||
Sbjct: 23610 ttttaagaaaatacaaaagttaatttc 23584

>emb|BX548071.7| Zebrafish DNA sequence from clone DKEY-25L23 in linkage group 9
Contains the 3' end of the gli2a gene for GLI-Kruppel family member GLI2a, the slc15a2 gene for solute carrier family 15 (H+/peptide transporter) member 2, the gene for a novel protein similar to vertebrate HSPB (heat shock 27kDa) associated protein 1 (HSPBAP1, zgc:100975) and the 5' end of the gene for a novel protein similar to vertebrate disrupted in renal carcinoma 2 (DIRC2, zgc:92095), complete sequence
Length = 223099

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 264 tagtttatttaaagaaaataaaa 286
|||||||
Sbjct: 48437 tagtttatttaaagaaaataaaa 48415

>emb|BX537275.8| Zebrafish DNA sequence from clone DKEYP-120E12 in linkage group 11,
complete sequence
Length = 173631

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataaataaattcttatattatatgt 1079
|||||||
Sbjct: 38891 agaaaaataaataaattcttatattatatgt 38861

>emb|BX537269.8| Zebrafish DNA sequence from clone DKEY-181H1 in linkage group 11,
complete sequence
Length = 73125

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataaataaattcttatattatatgt 1079
|||||||
Sbjct: 62729 agaaaaataaataaattcttatattatatgt 62699

>dbj|AP005846.2| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:B1307A11
Length = 131538

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaact 766
|||||||
Sbjct: 74560 taactttttgttttttaaaaact 74538

>emb|AM233362.1| Francisella tularensis subsp. holarctica LVS complete genome
Length = 1895994

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 950 tatgtctttctctaattgatgaa 972
 |||||
Sbjct: 1189937 tatgtctttctctaattgatgaa 1189915

>gb|AC151343.2| Xenopus (Silurana) tropicalis clone ISB-373E17, complete sequence
 Length = 88775

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1047 agagaaaaataataaattctta 1069
 |||||
Sbjct: 74842 agagaaaaataataaattctta 74820

>gb|AC155316.6| Mus musculus BAC clone RP23-181P9 from chromosome 5, complete sequence
 Length = 204809

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 743 ttaactttttgttttttaaaaac 765
 |||||
Sbjct: 115185 ttaactttttgttttttaaaaac 115163

>ref|XM_733026.1| Plasmodium chabaudi chabaudi hypothetical protein (PC102772.00.0)
 partial mRNA
 Length = 402

Score = 46.1 bits (23), Expect = 0.42
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaaagtta 292
 |||||
Sbjct: 393 atttaaagaaaataaaaaagtta 371

>emb|AL935040.6| Zebrafish DNA sequence from clone CH211-176L21, complete sequence
 Length = 159468

Score = 46.1 bits (23), Expect = 0.42
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1049 agaaaaataaataaattcttatattatatgt 1079
|||||||
Sbjct: 40419 agaaaaataaataaattcttatattatatgt 40389

>emb|FP236458.5| Zebrafish DNA sequence from clone CH73-374P12, complete sequence
Length = 95700

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 266 gtttatttaaagaaaataaaaa 287
|||||||
Sbjct: 65875 gtttatttaaagaaaataaaaa 65854

>emb|AL844509.2| Plasmodium falciparum 3D7 chromosome 13
Length = 2895605

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 269 tatttaaagaaaataaaaaagt 290
|||||||
Sbjct: 611898 tatttaaagaaaataaaaaagt 611919

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 263 ttagtttatttaaagaaaataaaaa 288
|||||||
Sbjct: 1691677 ttagtttatttaaagataataaaaa 1691652

>emb|AL844508.1| Plasmodium falciparum 3D7 chromosome 9

Length = 1541723

Score = 44.1 bits (22), Expect = 1.7

Identities = 22/22 (100%)

Strand = Plus / Minus

Query: 267 tttattttaaagaaaataaaaaa 288

||||||||||||||||

Sbjct: 968625 tttattttaaagaaaataaaaaa 968604

>dbj|AP010895.1| Solanum lycopersicum DNA, chromosome 8, clone: C08HBa0121P10, complete
sequence

Length = 73815

Score = 44.1 bits (22), Expect = 1.7

Identities = 25/26 (96%)

Strand = Plus / Plus

Query: 1052 aaaataaataaattcttatattatat 1077

|||||||||||||||| |||||

Sbjct: 27713 aaaataaataaattcttaattatat 27738

>gb|CP001110.1| Pelodictyon phaeoclathratiforme BU-1, complete genome

Length = 3018238

Score = 44.1 bits (22), Expect = 1.7

Identities = 22/22 (100%)

Strand = Plus / Minus

Query: 934 ttcaaaaaatattttttatgtc 955

||||||||||||||||

Sbjct: 437150 ttcaaaaaatattttttatgtc 437129

>ref|XM_001740672.1| Entamoeba dispar SAW760 F-box/leucine rich repeat protein, putative
EDI_037960 mRNA, complete cds

Length = 1980

Score = 44.1 bits (22), Expect = 1.7

Identities = 22/22 (100%)

Strand = Plus / Plus

Query: 1008 acaaaagtgactgataaatcta 1029

|||||
Sbjct: 1735 acaaaagtgactgataaatcta 1756

>ref|XM_001712135.1| Hemiselmis andersenii hypothetical protein (HAN_lg14) mRNA, complete
cds
Length = 5982

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 267 tttattttaagaaaataaaaaa 288
|||||
Sbjct: 4655 tttattttaagaaaataaaaaa 4676

>gb|CP000881.1| Hemiselmis andersenii chromosome 1, complete sequence; nucleomorph
Length = 207524

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 267 tttattttaagaaaataaaaaa 288
|||||
Sbjct: 17839 tttattttaagaaaataaaaaa 17860

>dbj|AB270792.1| Malus x domestica MdSFBB9-alpha, S9-RNase, MdSFBB9-beta genes, complete
cds, Psi-SFBB9-alpha, Psi-SFBB9-beta pseudogenes
Length = 317412

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 833 tataaaaaatttctcaccatatttat 858
|||||
Sbjct: 160165 tataaaaaatttctcaccatctttat 160140

>ref|XM_001350114.1| Plasmodium falciparum 3D7 hypothetical protein (PF13_0235) partial
mRNA
Length = 11547

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 263 ttagttttatttaaagaaaataaaaaa 288
|||||||
Sbjct: 2324 ttagttttatttaaagataataaaaaa 2349

>ref|XM_001349842.1| Plasmodium falciparum 3D7 hypothetical protein (PF13_0080) partial
mRNA
Length = 7557

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 269 tatttaaagaaaataaaaaagt 290
|||||||
Sbjct: 365 tatttaaagaaaataaaaaagt 386

>gb|AC187618.3| Pan troglodytes BAC clone CH251-584I16 from chromosome 7, complete
sequence
Length = 216311

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1038 tctaccattagagaaaaataaa 1059
|||||||
Sbjct: 199684 tctaccattagagaaaaataaa 199705

>gb|AC192762.3| Pan troglodytes BAC clone CH251-676011 from chromosome 7, complete
sequence
Length = 190460

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1038 tctaccattagagaaaaataaa 1059
|||||||

Sbjct: 108656 tctaccattagagaaaaataaa 108635

>emb|CT961058.16| *M. truncatula* DNA sequence from clone MTH2-80N17 on chromosome 3,
complete sequence
Length = 127385

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 263 ttagttttatTTAAAGAAAATAAAAAA 288
|||||
Sbjct: 52446 ttagttttatTTAAAAAATAAAAAA 52421

>ref|XM_001032614.1| *Tetrahymena thermophila* conserved hypothetical protein, mRNA
Length = 1491

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 255 tataacatttagttttatTTAAAGAAA 280
|||||
Sbjct: 829 tataacttttagttttatTTAAAGAAA 804

>emb|CT827810.6| Zebrafish DNA sequence from clone DKEY-120E24 in linkage group 21,
complete sequence
Length = 97913

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1051 aaaaataaataaattcttatat 1072
|||||
Sbjct: 62570 aaaaataaataaattcttatat 62549

>emb|AM231674.1| *Prunus dulcis* partial s-RNase gene for ribonuclease S26 precursor,
exons 1-3, allele S26, cultivar Avellanera Gruesa
Length = 3717

Score = 44.1 bits (22), Expect = 1.7

Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagt 290
|||||||
Sbjct: 3365 tatttaaagaaaataaaaaagt 3344

>gb|AC154194.2| Mus musculus BAC clone RP24-401L2 from chromosome 17, complete sequence
Length = 196871

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 276 agaaaataaaaaagttaatttc 297
|||||||
Sbjct: 135298 agaaaataaaaaagttaatttc 135277

>gb|AC091473.2| Mus musculus chromosome X clones RP21-114F21, RP21-430D6 complete
sequence
Length = 221860

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataataaatttc 1066
|||||||
Sbjct: 81683 ttagagaaaaataataaatttc 81704

>gb|AC006353.3| Homo sapiens PAC clone RP5-1062J16 from 7, complete sequence
Length = 158090

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1038 tctaccattagagaaaaataaa 1059
|||||||
Sbjct: 103497 tctaccattagagaaaaataaa 103518

>gb|AC132451.3| Mus musculus BAC clone RP23-194C20 from chromosome 8, complete sequence
Length = 188539

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 7 aatcaatatattttaattcttaaa 28
 |||||
Sbjct: 102628 aatcaatatattttaattcttaaa 102649

>ref|XM_651154.1| Entamoeba histolytica HM-1:IMSS hypothetical protein, mRNA
Length = 2685

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 279 aaataaaaaagttaatttctct 300
 |||||
Sbjct: 256 aaataaaaaagttaatttctct 235

>gb|AC113349.2| Homo sapiens chromosome 5 clone CTD-2544H17, complete sequence
Length = 163806

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 255 tataacatttagtttatttaaa 276
 |||||
Sbjct: 110207 tataacatttagtttatttaaa 110186

>emb|AL353592.9| Human DNA sequence from clone RP11-569012 on chromosome 13, complete
sequence
Length = 63325

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttatTTaaagaaaataaaaaa 288

|||||
Sbjct: 25137 tttattttaagaaaataaaaaa 25116

>emb|AL031297.4| Human DNA sequence from clone RP1-97P20 on chromosome 1q23.2-24.3
Contains the 3' end of a novel gene (FLJ45155 FLJ10706
FLJ39174) and the gene for ezrin-binding partner PACE-1
(PACE-1), complete sequence
Length = 103181

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 284 aaaaagttaatttctctttctg 305
|||||
Sbjct: 57119 aaaaagttaatttctctttctg 57140

>emb|BX571852.20| Zebrafish DNA sequence from clone DKEY-175N6 in linkage group 10,
complete sequence
Length = 178333

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 976 tatctatttaagtatatatttat 997
|||||
Sbjct: 3227 tatctatttaagtatatatttat 3206

>emb|BX936441.6| Zebrafish DNA sequence from clone CH211-234M15 in linkage group 18,
complete sequence
Length = 75388

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1051 aaaaataaataaattcttatat 1072
|||||
Sbjct: 72839 aaaaataaataaattcttatat 72818

>emb|BX511195.5| Zebrafish DNA sequence from clone DKEYP-57D12 in linkage group 17,

complete sequence
Length = 79527

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1053 aaataaataaattcttatatta 1074
|||||||
Sbjct: 76946 aaataaataaattcttatatta 76967

>emb|BX255948.4| Zebrafish DNA sequence from clone CH211-250J1, complete sequence
Length = 194257

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1051 aaaaataaataaattcttatat 1072
|||||||
Sbjct: 7443 aaaaataaataaattcttatat 7422

>gb|AC108005.8| Homo sapiens chromosome 11, clone CTD-2515M10, complete sequence
Length = 165443

Score = 44.1 bits (22), Expect = 1.7
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 266 gtttatttaaagaaaaataaaaaagtt 291
|||||||
Sbjct: 16008 gtttatttaaagaaaaataaaaaagtt 15983

>emb|AL445564.1| Mycoplasma pulmonis (strain UAB CTIP) complete genome; segment 2/3
Length = 321250

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 267 tttatttaaagaaaaataaaaaa 288
|||||||

Sbjct: 42091 tttattttaagaaaaataaaaaa 42112

>gb|AC008436.5|AC008436 Homo sapiens chromosome 5 clone CTC-327B12, complete sequence
Length = 118533

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 255 tataacatttagtttattttaa 276
|||||||
Sbjct: 34013 tataacatttagtttattttaa 34034

>gb|AC149381.2| Phakopsora pachyrhizi clone JGIAFNA-5A7, complete sequence
Length = 35166

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 1050 gaaaaataaataaattccttata 1071
|||||||
Sbjct: 17774 gaaaaataaataaattccttata 17753

>emb|AL928731.11| Mouse DNA sequence from clone RP23-171N20 on chromosome X Contains the
Opnlmw gene for opsin 1, medium-wave-sensitive, a
heterogeneous nuclear ribonucleoprotein A3 (Hnrpa3)
pseudogene, the gene for possible ortholog of human
chromosome X open reading frame 2 (CXorf2), a ribosomal
protein L3 (Rpl3) pseudogene and the Tktl1 gene for
transketolase-like 1, complete sequence
Length = 114243

Score = 44.1 bits (22), Expect = 1.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataaataaattc 1066
|||||||
Sbjct: 55099 ttagagaaaaataaataaattc 55120

>gb|AC238432.1| Mus musculus BAC clone RP24-76M8 from chromosome 9, complete sequence

Length = 193025

Score = 42.1 bits (21), Expect = 6.6

Identities = 27/29 (93%)

Strand = Plus / Minus

Query: 260 catttagttttatttaaagaaaataaaaaa 288

|||||

Sbjct: 188172 catttagttttatttaaagaaaataaaaaa 188144

>gb|CP001701.1| Cyanothece sp. PCC 8802, complete genome

Length = 4669813

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 960 tctaattgatgaataatatct 980

|||||

Sbjct: 1091336 tctaattgatgaataatatct 1091316

>ref|NW_003033920.1| Schistosoma mansoni genome sequence supercontig Smp_scaff010824

Length = 3015

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 842 tttctcaccatatttattatt 862

|||||

Sbjct: 396 tttctcaccatatttattatt 416

>emb|FN409584.1| Equus caballus microsatellite DNA, locus ABGe15567

Length = 856

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 290 ttaatttctctttctgccact 310

|||||

Sbjct: 484 ttaatttctctttctgccact 464

>ref|XM_002445459.1| Sorghum bicolor hypothetical protein, mRNA
Length = 3087

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
|||||
Sbjct: 707 aatatctatttaagtatattt 727

>ref|XM_002444559.1| Sorghum bicolor hypothetical protein, mRNA
Length = 3558

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
|||||
Sbjct: 1484 aatatctatttaagtatattt 1504

>ref|XM_002450673.1| Sorghum bicolor hypothetical protein, mRNA
Length = 2985

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
|||||
Sbjct: 605 aatatctatttaagtatattt 625

>emb|FN357601.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000310
Length = 439186

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 921 aaattattcctatttcaaaaaatattttt 949
||||| ||||||||| |||||||||
Sbjct: 244992 aaattgttcctatttcaaaaaatattttt 245020

>emb|FN368115.1| Schistosoma mansoni genome sequence supercontig Smp_scaff010824
Length = 3015

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 842 tttctcaccatatttattatt 862
|||||||
Sbjct: 396 tttctcaccatatttattatt 416

>gb|AC202790.4| Gallus gallus BAC clone CH261-161K24 from chromosome z, complete
sequence
Length = 251539

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 926 attcctatttcaaaaaatattttt 950
||||| ||||||||| |||||||||
Sbjct: 3071 attcgtatttcaaaaaatattttt 3047

>gb|AC235243.1| Glycine max strain Williams 82 clone GM_WBb0032L23, complete sequence
Length = 149341

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 920 aaaattattcctatttcaaaa 940
|||||||
Sbjct: 40182 aaaattattcctatttcaaaa 40162

>gb|AC235153.1| Glycine max strain Williams 82 clone GM_WBa0085L07, complete sequence
Length = 99314

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 60 ctaattcttaaacttcaataa 80
 |||||
Sbjct: 90459 ctaattcttaaacttcaataa 90439

>gb|AC235140.1| Glycine max strain Williams 82 clone GM_WBa0068I04, complete sequence
Length = 138531

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 60 ctaattcttaaacttcaataa 80
 |||||
Sbjct: 102190 ctaattcttaaacttcaataa 102210

>emb|AL844502.1| Plasmodium falciparum 3D7 chromosome 3
Length = 1060087

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 843 ttctcaccatatttattattatata 867
 ||||| |||||
Sbjct: 912945 ttctcacaatatttattattatata 912921

>gb|CP000857.1| Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594,
complete genome
Length = 4833080

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 448 acgtaattgctaccgccgtcaacgg 472
 ||||| |||||
Sbjct: 1614993 acgtaattgctcccgccgtcaacgg 1614969

>emb|FM992689.1| *Candida dubliniensis* CD36 chromosome 2, complete sequence
Length = 2289089

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 919 aaaaattattcctatttcaaa 939
 |||||
Sbjct: 1754450 aaaaattattcctatttcaaa 1754470

>gb|FJ581043.1| *Oryza punctata* clone OP_Ba0017E18, complete sequence
Length = 167491

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 277 gaaaataaaaaagtaatttctctt 301
 |||||
Sbjct: 62747 gaaaataaaaaagctaatttctctt 62723

>ref|XM_002166130.1| PREDICTED: *Hydra magnipapillata* similar to putative mediator of RNA
polymerase II transcription subunit 6 homolog
(LOC100200798), mRNA
Length = 942

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 146 ttcttacctatttttccattgaaat 170
 |||||
Sbjct: 791 ttcttaactatttttccattgaaat 767

>gb|CP001176.1| *Bacillus cereus* B4264, complete genome
Length = 5419036

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 269 tattttaagaaaaataaaaaag 289
 ||||||||||||||||||
Sbjct: 2481986 tattttaagaaaaataaaaaag 2482006

>emb|CU855905.8| Zebrafish DNA sequence from clone CH73-190M24 in linkage group 13,
 complete sequence
 Length = 41814

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 930 ctattttcaaaaaatatttttt 950
 ||||||||||||||||||
Sbjct: 25952 ctattttcaaaaaatatttttt 25932

>ref|NG_008899.1| Homo sapiens sarcoglycan zeta (SGCZ) on chromosome 8
 Length = 1155420

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 735 gagagaaattaactttttgttttt 759
 |||||||||||||||||| |||||
Sbjct: 56971 gagagaaattaacttttttttttt 56995

>ref|NM_001135888.1| Bombyx mori osiris 9 (Osi9), mRNA >gi|207339261|gb|FJ176298.1| Bombyx
 mori osiris 9 mRNA, complete cds
 Length = 1375

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994
 ||||||||||||||||||
Sbjct: 1201 aatatctatttaagtatattt 1221

>emb|CU914133.2| Medicago truncatula chromosome 5 clone mth2-150o3, COMPLETE SEQUENCE
 Length = 130287

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 740 aaattaactttttgttttttaaaaa 764
||||||| |||||||||||||||||
Sbjct: 21545 aaattaattttttgttttttaaaaa 21569

>gb|CP001120.1| Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete
genome
Length = 4888768

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 738 agaaattaactttttgttttttaaa 762
||||||||||||||||| |||||
Sbjct: 1916878 agaaattaactttttgttttttaa 1916902

>emb|AM910991.1| Plasmodium knowlesi strain H chromosome 9, complete genome
Length = 2147124

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttattttaagaaaaataaaaaa 288
|||||||||||||||||
Sbjct: 283639 ttattttaagaaaaataaaaaa 283659

>gb|AC198044.3| Pongo abelii BAC clone CH276-446K19 from chromosome unknown, complete
sequence
Length = 193379

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
|||||||||||||||||
Sbjct: 97735 tatttcaaaaaatatttttta 97755

>gb|AC216598.1| Populus trichocarpa clone POP037-D13, complete sequence
Length = 86619

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 278 aaaataaaaaagttaatttct 298
 |||||
Sbjct: 10003 aaaataaaaaagttaatttct 9983

>gb|AC205959.4| Canis familiaris, clone XX-180015, complete sequence
Length = 191292

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttattttaagaaaaataaaaaa 288
 |||||
Sbjct: 129514 ttattttaagaaaaataaaaaa 129534

>gb|AC213090.1| Populus trichocarpa clone POP118-019, complete sequence
Length = 119882

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 17 ttaattcttaaaccttatttaaact 41
 |||||
Sbjct: 89074 ttaattcttaaaccttatttaaact 89050

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 17 ttaattcttaaaccttatttaaact 41
 |||||

Sbjct: 113171 ttaattcttaaacttaattaaatct 113147

>gb|AC212636.1| Solanum lycopersicum chromosome 7 clone C07HBa0174J08, complete
sequence
Length = 36680

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 962 taattgatgaataatatctat 982
|||||||
Sbjct: 26965 taattgatgaataatatctat 26945

>gb|CP000409.1| Rickettsia canadensis str. McKiel, complete genome
Length = 1159772

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 922 aattattcctatttcaaaaaa 942
|||||||
Sbjct: 891128 aattattcctatttcaaaaaa 891108

>gb|AC198093.4| Pongo abelii BAC clone CH276-31L11 from chromosome unknown, complete
sequence
Length = 203750

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 262 tttagtttatttaaagaaaat 282
|||||||
Sbjct: 13576 tttagtttatttaaagaaaat 13596

>emb|CU329671.1| Schizosaccharomyces pombe chromosome II
Length = 4539804

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)

Strand = Plus / Minus

Query: 928 tcctattttcaaaaaatattttttat 952
 |||||
Sbjct: 318999 tcctattttcaaaaaatatttggtat 318975

>ref|XM_001645942.1| Vanderwaltozyma polyspora DSM 70294 hypothetical protein
 (Kpo1_1031p38) partial mRNA
 Length = 1161

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttattttaagaaaataaaaa 287
 |||||
Sbjct: 756 tttattttaagaaaataaaaa 776

>gb|AC209107.1| Populus trichocarpa clone POP088-K16, complete sequence
 Length = 93454

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 937 aaaaaatattttttatgtcct 957
 |||||
Sbjct: 61180 aaaaaatattttttatgtcct 61200

>ref|XM_001638933.1| Nematostella vectensis predicted protein (NEMVEDRAFT_v1g199871) mRNA,
 complete cds
 Length = 3138

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 269 tatttaagaaaataaaaaag 289
 |||||
Sbjct: 1630 tatttaagaaaataaaaaag 1610

>gb|AC174335.10| Medicago truncatula clone mth2-155122, complete sequence
Length = 87546

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 261 atttagtttatttaagaaaataaaaaag 289
|||||||
Sbjct: 81934 atttagtttatttcaagaaaacaaaaaag 81962

>gb|CP000721.1| Clostridium beijerinckii NCIMB 8052, complete genome
Length = 6000632

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1055 ataaataaattcttatattat 1075
|||||||
Sbjct: 1804335 ataaataaattcttatattat 1804315

>gb|AC202303.8| Medicago truncatula clone mth2-155j9, complete sequence
Length = 103788

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 1047 agagaaaaataaataaattcttata 1071
|||||||
Sbjct: 41726 agagaaaaataaattaattcttata 41702

>gb|EF533700.1| Glycine max clone BAC GM_WBb080D08, complete sequence
Length = 154087

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagttaat 294
|||||||

Sbjct: 136309 atttaaaaaataaaaaagttaat 136333

>gb|DQ914719.1| Fungal sp. EXP0495F 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and
28S ribosomal RNA gene, partial sequence
Length = 606

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 991 attttattgtgaaatccacaa 1011
|||||||
Sbjct: 207 attttattgtgaaatccacaa 227

>emb|AM473707.2| Vitis vinifera contig VV78X111932.6, whole genome shotgun sequence
Length = 4998

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1045 ttagagaaaaataataaatt 1065
|||||||
Sbjct: 539 ttagagaaaaataataaatt 519

>emb|AM483283.2| Vitis vinifera contig VV78X178586.8, whole genome shotgun sequence
Length = 1891

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 740 aaattaactttttgttttttaaaaa 764
||||||| |||||
Sbjct: 968 aaattaacttttttttttaaaaa 944

>emb|AM481633.2| Vitis vinifera contig VV78X190383.5, whole genome shotgun sequence
Length = 5812

Score = 42.1 bits (21), Expect = 6.6

Identities = 22/23 (95%)
Strand = Plus / Plus

Query: 740 aaattaactttttgttttttaa 762
 ||||||| |||||||||||||
Sbjct: 1121 aaattaayttttgttttttaa 1143

>emb|AM479192.2| Vitis vinifera contig VV78X197549.13, whole genome shotgun sequence
Length = 17080

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1044 attagagaaaataaataaat 1064
 |||||||||||||||||||
Sbjct: 11010 attagagaaaataaataaat 10990

>emb|AM425055.2| Vitis vinifera contig VV78X086233.8, whole genome shotgun sequence
Length = 10725

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 748 tttttgttttttaaaaactaa 768
 |||||||||||||||||||
Sbjct: 10704 tttttgttttttaaaaactaa 10684

>emb|AM463129.2| Vitis vinifera contig VV78X099343.8, whole genome shotgun sequence
Length = 3031

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 748 tttttgttttttaaaaactaa 768
 |||||||||||||||||||
Sbjct: 2255 tttttgttttttaaaaactaa 2275

>emb|AM453496.2| Vitis vinifera contig VV78X099343.7, whole genome shotgun sequence

Length = 3607

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 748 tttttgttttttaaaaactaa 768

|||||||

Sbjct: 2185 tttttgttttttaaaaactaa 2165

>emb|AM433228.2| Vitis vinifera contig VV78X071247.4, whole genome shotgun sequence

Length = 6173

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 748 tttttgttttttaaaaactaa 768

|||||||

Sbjct: 473 tttttgttttttaaaaactaa 453

>emb|AM432606.2| Vitis vinifera contig VV78X032134.1, whole genome shotgun sequence

Length = 1047

Score = 42.1 bits (21), Expect = 6.6

Identities = 24/25 (96%)

Strand = Plus / Plus

Query: 11 aatattttaattcttaactttatt 35

||||||| |||||

Sbjct: 627 aatattttaatttttaactttatt 651

>emb|AM436044.2| Vitis vinifera contig VV78X143044.4, whole genome shotgun sequence

Length = 38850

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 1049 agaaaaataaataattctta 1069

|||||||

Sbjct: 26978 agaaaaataaataattctta 26998

>gb|BC140581.1| Bos taurus cDNA clone IMAGE:8238248
Length = 3140

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttattttaagaaaataaaaa 287
|||||||
Sbjct: 2105 tttattttaagaaaataaaaa 2125

>ref|XM_001017552.2| Tetrahymena thermophila hypothetical protein, mRNA
Length = 1332

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
|||||||
Sbjct: 1276 tatttcaaaaaatatttttta 1296

>emb|CU210926.7| Mouse DNA sequence from clone CH29-115D7 on chromosome 6 Contains the
5' end of the Bcd1 gene for bicaudal D homolog 1
(Drosophila), an MRT4, mRNA turnover 4, homolog (S.
cerevisiae) (Mrto4) pseudogene, the Bcd1 gene for
bicaudal D homolog 1 (Drosophila), a DnaJ (Hsp40) homolog,
subfamily B, member 6 (Dnajb6) pseudogene, and an
adaptor-related protein complex AP-1 and sigma 3 (Apls3)
pseudogene, complete sequence
Length = 87584

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 278 aaaataaaaaagttaatttct 298
|||||||
Sbjct: 26238 aaaataaaaaagttaatttct 26218

>ref|XM_001351252.1| Plasmodium falciparum 3D7 hypothetical protein (MAL3P7.22) partial

mRNA
Length = 8121

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 843 ttctcaccatatttattattatata 867
||||||| |||||||||||||||||
Sbjct: 3359 ttctcacaatatttattattatata 3335

>gb|AC197607.1| Pongo abelii BAC clone CH276-100H12 from chromosome unknown, complete
sequence
Length = 199991

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 748 tttttgttttttaaaaactaa 768
|||||||||||||||||||
Sbjct: 56604 tttttgttttttaaaaactaa 56584

>emb|CT583646.5| Zebrafish DNA sequence from clone DKEYP-72G6 in linkage group 1,
complete sequence
Length = 39926

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 1046 tagagaaaaataaataattcttat 1070
||||||||||||||||||| |||||
Sbjct: 5219 tagagaaaaataaataataacttat 5195

>emb|AM471960.1| Vitis vinifera contig VV78X029428.17, whole genome shotgun sequence
Length = 18189

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 931 tatttcaaaaaatatttttta 951
 |||||
Sbjct: 14133 tatttcaaaaaatatttttta 14113

>emb|AM458894.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X000850.16,
 clone ENTAV 115
 Length = 55294

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 734 tgagagaaattaactttttgttttt 758
 |||||
Sbjct: 16240 tgagagaaattaactttttgttttt 16264

>gb|AC192717.3| Gallus gallus BAC clone CH261-36N8 from chromosome z, complete sequence
 Length = 217438

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 926 attcctatttcaaaaaatatttttt 950
 |||| |||||
Sbjct: 112379 attcgtatttcaaaaaatatttttt 112355

>dbj|AP009289.1| Solanum lycopersicum genomic DNA, chromosome 8, clone: C08HBa0294K15,
 complete sequence
 Length = 72577

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
 |||||
Sbjct: 52866 tatttcaaaaaatatttttta 52886

>emb|CT573243.6| Zebrafish DNA sequence from clone CH73-365J20 in linkage group 1,
 complete sequence
 Length = 19888

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 1046 tagagaaaaataaataaattcttat 1070
|||||
Sbjct: 14596 tagagaaaaataaataaatacttat 14620

>emb|CU024879.5| M. truncatula DNA sequence from clone MTH2-70F3 on chromosome 3,
complete sequence
Length = 66861

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 262 tttagtttatttaaagaaaataaaa 286
|||||
Sbjct: 56908 tttagtttattcaaagaaaataaaa 56932

>emb|CR790361.11| Zebrafish DNA sequence from clone DKEY-29N19, complete sequence
Length = 140025

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 847 caccatatttattattatata 867
|||||
Sbjct: 17770 caccatatttattattatata 17790

>gb|AE014297.2| Drosophila melanogaster chromosome 3R, complete sequence
Length = 27905053

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaaagt 290
|||||
Sbjct: 11830374 atttaaagaaaataaaaaagt 11830354

>ref|XM_392161.3| PREDICTED: Apis mellifera similar to CG2931-PA, transcript variant 1
(LOC408620), mRNA
Length = 1381

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1057 aaataaattcttatattatat 1077
|||||||
Sbjct: 1361 aaataaattcttatattatat 1381

>emb|CR627495.19| Zebrafish DNA sequence from clone DKEY-58G10 in linkage group 14,
complete sequence
Length = 110289

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 215 cttttgtttcatttactttat 235
|||||||
Sbjct: 6302 cttttgtttcatttactttat 6282

>emb|CR533579.7| Zebrafish DNA sequence from clone CH211-232J20 in linkage group 6,
complete sequence
Length = 199327

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataataaatt 1065
|||||||
Sbjct: 154257 ttagagaaaaataataaatt 154277

>emb|CT573422.5| Mouse DNA sequence from clone RP24-76M8 on chromosome 9, complete
sequence
Length = 193236

Score = 42.1 bits (21), Expect = 6.6

Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 260 catttagttttatttaaagaaaataaaaaa 288
 |||||
Sbjct: 188383 catttagttttatttaaagaaaataaaaaa 188355

>emb|CR848045.10| Zebrafish DNA sequence from clone DKEY-8K3 in linkage group 16,
 complete sequence
 Length = 104737

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 156 tttttccattgaaatatgtta 176
 |||||
Sbjct: 78404 tttttccattgaaatatgtta 78384

>gb|CP000153.1| Sulfurimonas denitrificans DSM 1251, complete genome
 Length = 2201561

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 932 atttcaaaaaatattttttat 952
 |||||
Sbjct: 1368329 atttcaaaaaatattttttat 1368349

>gb|AC164170.7| Mus musculus 10 BAC RP24-419C12 (Roswell Park Cancer Institute
 (C57BL/6J Male) Mouse BAC Library) complete sequence
 Length = 158496

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 932 atttcaaaaaatattttttat 952
 |||||
Sbjct: 35072 atttcaaaaaatattttttat 35092

>gb|AC102324.9| Mus musculus chromosome 1, clone RP24-476A18, complete sequence
Length = 129634

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 957 ttctctaattgatgaataata 977
 ||||||||||||||||||||
Sbjct: 105079 ttctctaattgatgaataata 105059

>gb|AC158641.12| Mus musculus 10 BAC RP23-461E22 (Roswell Park Cancer Institute
(C57BL/6J Female) Mouse BAC Library) complete sequence
Length = 186390

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 932 atttcaaaaaatattttttat 952
 ||||||||||||||||||||
Sbjct: 35658 atttcaaaaaatattttttat 35638

>gb|AC150800.3| Medicago truncatula chromosome 7 clone mth2-77m9, complete sequence
Length = 116865

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 740 aaattaactttttgttttttaaaaa 764
 ||||||| ||||||||||||||||
Sbjct: 11958 aaattaactttttgttttttaaaaa 11982

>gb|AY018508.1| Oryza sativa microsatellite MRG0833 containing (AT)X17, genomic
sequence
Length = 234

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
 |||||||
Sbjct: 81 taactttttgttttttaaaaa 61

>gb|U23181.2| Caenorhabditis elegans cosmid ZK84, complete sequence
 Length = 26759

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 277 gaaaataaaaaagttaatttc 297
 |||||||
Sbjct: 12138 gaaaataaaaaagttaatttc 12158

>gb|AY330624.1| Galleria mellonella inducible metalloproteinase inhibitor (IMPI)
 mRNA, complete cds
 Length = 878

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 930 ctatttcaaaaaatatttttt 950
 |||||||
Sbjct: 755 ctatttcaaaaaatatttttt 735

>gb|AC146790.16| Medicago truncatula clone mth2-123b21, complete sequence
 Length = 114449

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 261 athtagtttatttaagaaaataaaaaag 289
 ||||||| ||||| |||||
Sbjct: 108866 athtagtttatttcaagaaacaaaaag 108838

>gb|AC137078.24| Medicago truncatula clone mth2-10e12, complete sequence
 Length = 144306

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 1047 agagaaaaataataaattcttata 1071
|||||||
Sbjct: 109171 agagaaaaataaattaattcttata 109195

>gb|AC108876.2| Oryza sativa Japonica Group chromosome 5 clone OJ1525_A02, complete
sequence
Length = 93826

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
|||||||
Sbjct: 37355 taactttttgttttttaaaaa 37335

>gb|AC117265.2| Oryza sativa Japonica Group chromosome 5 clone OJ1281_H05, complete
sequence
Length = 163130

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
|||||||
Sbjct: 131712 taactttttgttttttaaaaa 131692

>gb|AC142111.3| Mus musculus BAC clone RP24-63G9 from chromosome 9, complete sequence
Length = 185361

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 926 attcctatttcaaaaaatatttttt 950
|||||
Sbjct: 61984 attcctttttcaaaaaatatttttt 62008

>gb|AC139290.15| Medicago truncatula clone mth2-23f4, complete sequence
Length = 127701

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataataaatt 1065
|||||
Sbjct: 23952 ttagagaaaaataataaatt 23972

>gb|AC124558.4| Mus musculus BAC clone RP23-24808 from chromosome 10, complete sequence
Length = 199938

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatatttta 951
|||||
Sbjct: 183212 tatttcaaaaaatatatttta 183232

>gb|AC123865.5| Mus musculus BAC clone RP23-365C14 from chromosome 10, complete sequence
Length = 212994

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 931 tatttcaaaaaatatatttta 951
|||||
Sbjct: 187954 tatttcaaaaaatatatttta 187934

>gb|AC123714.6| Mus musculus chromosome 9, clone RP23-393E20, complete sequence
Length = 217860

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 920 aaaattattcctatttcaaaa 940
 |||||
Sbjct: 70799 aaaattattcctatttcaaaa 70819

>gb|AC110169.7| Mus musculus chromosome 9, clone RP23-233D3, complete sequence
 Length = 193041

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 740 aaattaactttttgttttttaaaaa 764
 |||| |
Sbjct: 158008 aatgaactttttgttttttaaaaa 157984

>gb|AE017245.1| Mycoplasma synoviae 53, complete genome
 Length = 799476

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 15 ttttaattcttaaaactttattaaat 39
 |||||
Sbjct: 365410 ttttaattctaaaactttattaaat 365386

>dbj|AP008983.1| Clostridium phage c-st genomic DNA, complete genome
 Length = 185683

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatatgt 1079
 |||||
Sbjct: 70595 ataaattcttatattatatgt 70575

>gb|AC164090.3| Mus musculus BAC clone RP23-403F3 from chromosome 6, complete sequence
 Length = 189441

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)

Strand = Plus / Plus

```
Query: 278      aaaataaaaaagttaatttct 298
              |||
Sbjct: 149086 aaaataaaaaagttaatttct 149106
```

>gb|AC157542.11| Mus musculus chromosome 1, clone RP23-115I1, complete sequence
Length = 211677

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 957      ttctctaattgatgaataata 977
              |||
Sbjct: 157507 ttctctaattgatgaataata 157487
```

>emb|CR450724.10| Zebrafish DNA sequence from clone DKEY-168I4 in linkage group 18,
complete sequence
Length = 197565

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 930      ctattttcaaaaaatatttttt 950
              |||
Sbjct: 68918 ctattttcaaaaaatatttttt 68898
```

>ref|XM_805808.1| Trypanosoma cruzi strain CL Brener hypothetical protein partial mRNA
Length = 4338

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 319      atggtggagagatccgatgca 339
              |||
Sbjct: 1283 atggtggagagatccgatgca 1263
```

>ref|XM_803717.1| Trypanosoma cruzi strain CL Brener hypothetical protein partial mRNA

Length = 4338

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 319 atggtggagatccgatgca 339

||||||||||||||||

Sbjct: 1283 atggtggagatccgatgca 1263

>gb|DQ075075.1| Scirtothrips astrictus isolate PA-04-009 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1,
complete sequence; and 5.8S ribosomal RNA gene, partial
sequence

Length = 1419

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 932 atttcaaaaaatattttttat 952

||||||||||||||||

Sbjct: 89 atttcaaaaaatattttttat 69

>gb|AC163647.3| Mus musculus BAC clone RP23-214L4 from chromosome 6, complete sequence

Length = 197408

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 278 aaaataaaaaagttaatttct 298

||||||||||||||||

Sbjct: 39336 aaaataaaaaagttaatttct 39356

>emb|CR931715.1| Streptococcus pneumoniae strain 198/71 (serotype 42)

Length = 19403

Score = 42.1 bits (21), Expect = 6.6

Identities = 24/25 (96%)

Strand = Plus / Plus

Query: 975 atatctatttaagtatattttattg 999
||||||| |||||||||
Sbjct: 7307 atatctattaaagtatattttattg 7331

>emb|CR931706.1| Streptococcus pneumoniae strain 7765/43 (serotype 35c)
Length = 19741

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 975 atatctatttaagtatattttattg 999
||||||| |||||||||
Sbjct: 7438 atatctattaaagtatattttattg 7462

>emb|CR931704.1| Streptococcus pneumoniae strain 1936/39 (serotype 35a)
Length = 21463

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 975 atatctatttaagtatattttattg 999
||||||| |||||||||
Sbjct: 7100 atatctattaaagtatattttattg 7124

>ref|NM_001021038.1| Schizosaccharomyces pombe transcription factor (predicted)
(SPBC1773.16c) partial mRNA
Length = 1788

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 928 tcctatttcaaaaaatatttttat 952
||||||| |||||||||
Sbjct: 1482 tcctatttcaaaaaatattgttat 1506

>gb|AC157474.2| Mus musculus BAC clone RP24-565B5 from chromosome 9, complete sequence
Length = 192701

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 920 aaaattattcctatttcaaaa 940
 |||||||
Sbjct: 52223 aaaattattcctatttcaaaa 52203

>emb|CR352233.9| Zebrafish DNA sequence from clone CH211-193J5 in linkage group 13,
 complete sequence
 Length = 149899

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 930 ctattttcaaaaaatatttttt 950
 |||||||
Sbjct: 91402 ctattttcaaaaaatatttttt 91422

>gb|AC143340.4| Medicago truncatula clone mth2-7f4, complete sequence
 Length = 114535

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1045 ttagagaaaaataataaatt 1065
 |||||||
Sbjct: 58432 ttagagaaaaataataaatt 58452

>dbj|AK054176.1| Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN
 full-length enriched library, clone:E230025E05
 product:unclassifiable, full insert sequence
 Length = 3790

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 278 aaaataaaaaagttaatttct 298
 |||||||
Sbjct: 2424 aaaataaaaaagttaatttct 2404

>dbj|AK053595.1| Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched
library, clone:E130112N04 product:unclassifiable, full
insert sequence
Length = 3686

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 278 aaaataaaaaagttaatttct 298
|||||||
Sbjct: 442 aaaataaaaaagttaatttct 422

>gb|AC044781.12| Homo sapiens chromosome 10 clone RP11-142M10, complete sequence
Length = 177448

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 736 agagaaattaactttttgttt 756
|||||||
Sbjct: 144613 agagaaattaactttttgttt 144593

>gb|AC117398.3| Homo sapiens 3 BAC RP11-715A9 (Roswell Park Cancer Institute Human BAC
Library) complete sequence
Length = 109182

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 740 aaattaactttttgttttttaaaaa 764
||||||| |||||
Sbjct: 60250 aaattaacttttttttttaaaaa 60226

>gb|AC002505.3| Arabidopsis thaliana chromosome 2 clone T9J22 map B68, complete
sequence
Length = 115851

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1057 aaataaattcttatattatat 1077
 |||||
Sbjct: 88379 aaataaattcttatattatat 88359

>gb|AC096687.5| Oryza sativa chromosome 3 BAC OSJNBa0010E04 genomic sequence, complete
 sequence
 Length = 117505

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 108186 taactttttgttttttaaaaa 108206

>gb|AC020992.10| Homo sapiens chromosome 8, clone RP11-23H1, complete sequence
 Length = 129413

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 735 gagagaaattaactttttgtttttt 759
 |||||
Sbjct: 26314 gagagaaattaacttttttttttt 26290

>emb|AL365496.15| Human DNA sequence from clone RP11-449J3 on chromosome 10 Contains the
 3' end of the PCDH15 gene for protocadherin 15 and a novel
 gene, complete sequence
 Length = 173728

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 262 tttagtttatTTaaagaaaat 282
 |||||
Sbjct: 92667 tttagtttatTTaaagaaaat 92687

>gb|AY060392.1| Drosophila melanogaster LD29917 full length cDNA
Length = 2146

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
|||||||
Sbjct: 2098 atttaaagaaaataaaaaagt 2118

>gb|AC034205.4| Homo sapiens chromosome 5 clone CTB-23I7, complete sequence
Length = 159562

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttatttaagaaaataaaaa 287
|||||||
Sbjct: 49356 tttatttaagaaaataaaaa 49376

>gb|AC091045.3| Homo sapiens chromosome 15 clone RP11-111A22 map 15q14, complete
sequence
Length = 171947

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 156 tttttccattgaaatatgtta 176
|||||||
Sbjct: 73166 tttttccattgaaatatgtta 73186

>emb|AL137855.10| Human DNA sequence from clone RP5-1064J9 on chromosome 1p32.2-33,
complete sequence
Length = 106970

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1045 ttagagaaaaataataaatt 1065
|||||||
Sbjct: 89059 ttagagaaaaataataaatt 89039

>emb|AL096771.11| Human DNA sequence from clone RP1-238D15 on chromosome 6q12-14.3
Contains 3' end of COL12A1 gene for collagen, type XII,
alpha 1, complete sequence
Length = 112292

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 839 aaatttctcaccatatttattattatata 867
|||||||
Sbjct: 46476 aaatttctcaccatataatattttatata 46448

>emb|Z92813.1| Caenorhabditis elegans Cosmid T28A8, complete sequence
Length = 34388

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 931 tattttcaaaaaatatttttta 951
|||||||
Sbjct: 19536 tattttcaaaaaatatttttta 19516

>emb|Z81139.1| Caenorhabditis elegans Cosmid W05H5, complete sequence
Length = 14770

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 277 gaaaataaaaaagttaatttc 297
|||||||
Sbjct: 483 gaaaataaaaaagttaatttc 463

>gb|S74768.1| 16S progenitor toxin: cha 33=hemagglutinin...cha-70=hemagglutinin 70

[Clostridium botulinum, type C, Genomic, 3 genes, 2636
nt]
Length = 2636

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1059 ataaattcttatattatatgt 1079
|||||||
Sbjct: 400 ataaattcttatattatatgt 420

>emb|BX957329.9| Zebrafish DNA sequence from clone CH211-130P21 in linkage group 23,
complete sequence
Length = 76351

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 259 acatttagtttatttaaagaaaataaaaa 287
|||||||
Sbjct: 2458 acatttagtttctttaataaaataaaaa 2430

>dbj|AP005800.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, BAC
clone:OSJNBa0016D04
Length = 147313

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
|||||||
Sbjct: 92509 taactttttgttttttaaaaa 92529

>dbj|AP005000.3| Oryza sativa Japonica Group genomic DNA, chromosome 2, PAC
clone:P0042D01
Length = 148305

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 41741 taactttttgttttttaaaaa 41721

>emb|BX511180.7| Zebrafish DNA sequence from clone CH211-221H1 in linkage group 3,
 complete sequence
 Length = 155448

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 62 aattcttaaaattcaataaacaata 86
 |||||
Sbjct: 153095 aattcttaaaattcaataaacaata 153119

>dbj|AP005884.3| Oryza sativa Japonica Group genomic DNA, chromosome 9, PAC clone:P0598D02
 Length = 155238

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 138870 taactttttgttttttaaaaa 138890

>dbj|AP006164.2| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC
 clone:B1386G10
 Length = 121827

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 945 ttttttatgtctttctctaat 965
 |||||
Sbjct: 27229 ttttttatgtctttctctaat 27249

>emb|BX294435.5| Zebrafish DNA sequence from clone DKEYP-32G6 in linkage group 25,

complete sequence
Length = 128861

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 1051 aaaaataaataaattcttatattat 1075
|||||||
Sbjct: 4297 aaaaataaataaataacttatattat 4321

>emb|BX890568.8| Zebrafish DNA sequence from clone DKEY-208J2 in linkage group 20 Contains
the ches1 gene for checkpoint suppressor 1, a novel gene
(wu:fc15h02) (general transcription factor IIA, 1,
19/37kDa) and a CpG island, complete sequence
Length = 188167

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 30 tttattaaatctaacaataaactgt 54
|||||
Sbjct: 130161 tttataaaatctaacaataaactgt 130185

>dbj|AP004462.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, PAC
clone:P0450B04
Length = 153268

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
|||||||
Sbjct: 19568 taactttttgttttttaaaaa 19548

>dbj|AP003909.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
clone:OJ1300_E01
Length = 103022

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 76480 taactttttgttttttaaaaa 76460

>dbj|AP005249.3| Oryza sativa Japonica Group genomic DNA, chromosome 8, BAC
 clone:OSJNBa0087F21
 Length = 187401

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 168637 taactttttgttttttaaaaa 168617

>dbj|AP004384.3| Oryza sativa Japonica Group genomic DNA, chromosome 7, PAC
 clone:P0506C07
 Length = 123451

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaa 763
 |||||
Sbjct: 80250 ttaactttttgttttttaaaa 80270

>gb|AF476953.1| Vaucheria geminata ribulose-1,5-bisphosphate carboxylase/oxygenase
 large subunit (rbcL) gene, complete cds; chloroplast
 gene for chloroplast product
 Length = 1980

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 18 taattcttaactttatataa 38
 |||||
Sbjct: 110 taattcttaactttatataa 130

>gb|AF476952.1| *Vaucheria geminata* ribulose-1,5-bisphosphate carboxylase/oxygenase
large subunit (rbcL) gene, complete cds; chloroplast
gene for chloroplast product
Length = 1983

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 18 taattcttaaactttattaaa 38
|||||
Sbjct: 114 taattcttaaactttattaaa 134

>gb|AC091530.4| *Papio anubis* clone RP41-444A14, complete sequence
Length = 162413

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 264 tagttttatttaaagaaaaataaaaaa 288
|||||
Sbjct: 12255 tagttttatttaaagaaaaataaaaaa 12279

>gb|AC098584.2| *Homo sapiens* BAC clone RP11-10L11 from 4, complete sequence
Length = 159206

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 261 atttagttttatttaaagaaaaataaa 285
|||||
Sbjct: 23374 atttagttttatttaaagaaaaataaa 23350

>gb|AC091619.3| *Papio anubis* clone RP41-139B7, complete sequence
Length = 181302

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 264 tagttttatttaaagaaaaataaaaaa 288
|||||||
Sbjct: 174048 tagttttatttaaagaaaaaaaaa 174072

>dbj|AP003209.3| Oryza sativa Japonica Group genomic DNA, chromosome 1, BAC clone:B1189A09
Length = 167761

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
|||||||
Sbjct: 127755 taactttttgttttttaaaaa 127775

>emb|AL604063.4| Mouse DNA sequence from clone RP23-467J12 on chromosome 11, complete
sequence
Length = 146759

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaaa 763
|||||||
Sbjct: 46882 ttaactttttgttttttaaaaa 46902

>gb|AC010884.11| Homo sapiens BAC clone RP11-350B7 from 2, complete sequence
Length = 137172

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 934 ttcaaaaaatattttttatgtcttt 958
|||||||
Sbjct: 70408 ttcaaaaaatattttttatgtcttt 70384

>gb|AC093759.3| Homo sapiens BAC clone RP11-67M1 from 4, complete sequence
Length = 177807

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 21 ttcttaaactttattaaatct 41
 |||||
Sbjct: 121174 ttcttaaactttattaaatct 121194

>gb|AC091247.4| Oryza sativa chromosome 3 BAC OJ1111_B11 genomic sequence, complete
 sequence
 Length = 115393

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 31713 taactttttgttttttaaaaa 31733

>gb|AC007755.6|AC007755 Drosophila melanogaster, chromosome 3R, region 89A-89B, BAC clone
 BACR04C07, complete sequence
 Length = 173660

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
 |||||
Sbjct: 48147 atttaaagaaaataaaaaagt 48167

>gb|AC007726.7|AC007726 Drosophila melanogaster, chromosome 3R, region 89B-89B, BAC clone
 BACR05C20, complete sequence
 Length = 177278

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaaagt 290

|||||
Sbjct: 33586 atttaaagaaaataaaaaagt 33566

>gb|AC073166.7| Oryza sativa chromosome 10 BAC OSJNBb0064P21 genomic sequence, complete
sequence
Length = 142114

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaa 764
|||||
Sbjct: 92239 taactttttgttttttaaaaa 92219

>gb|AC009232.3| Homo sapiens BAC clone RP11-352J11 from 2, complete sequence
Length = 139885

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 425 tgacaggttgatgggtggagaagac 449
|||||
Sbjct: 103613 tgacaggttgatgggtggagcagac 103589

>gb|AC019215.4|AC019215 Homo sapiens BAC clone RP11-480M18 from 8, complete sequence
Length = 192579

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 735 gagagaaattaactttttgtttttt 759
|||||
Sbjct: 152163 gagagaaattaacttttttttttt 152139

>gb|AC007404.4| Homo sapiens BAC clone RP11-547I5 from 2, complete sequence
Length = 168506

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)

Strand = Plus / Plus

```
Query: 748   tttttgttttttaaaaactaa 768
          |||||||
Sbjct: 59454 tttttgttttttaaaaactaa 59474
```

>emb|X87946.1| O. sativa ZB8 gene
Length = 4660

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

```
Query: 744   taactttttgttttttaaaaa 764
          |||||||
Sbjct: 1051 taactttttgttttttaaaaa 1071
```

>emb|X62389.1| Botulinum bacteriophage genes for HA-17, HA-33, nontoxic components
and C1 toxin
Length = 9613

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 1059 ataaattcttatattatatgt 1079
          |||||||
Sbjct: 272   ataaattcttatattatatgt 252
```

>emb|X72793.1| Clostridium botulinum C phage BONT/C1, ANTP-139, ANTP-33, ANTP-17,
ANTP-70 genes and ORF-22
Length = 12297

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 1059 ataaattcttatattatatgt 1079
          |||||||
Sbjct: 2962 ataaattcttatattatatgt 2942
```

>emb|X66433.1| Clostridium botulinum phage 1C, CHn-14, CHn-33, Chn-138 and BoNT/C1
genes
Length = 9689

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatatgt 1079
|||||||
Sbjct: 354 ataaattcttatattatatgt 334

>ref|XM_672717.1| Plasmodium berghei strain ANKA hypothetical protein (PB108599.00.0)
partial mRNA
Length = 213

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaaagttaat 294
|||||||
Sbjct: 133 atttaaagaaaataaaaaagataat 109

>ref|XM_668682.1| Plasmodium berghei strain ANKA hypothetical protein (PB300464.00.0)
partial mRNA
Length = 579

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
|||||||
Sbjct: 139 ttatttaaagaaaataaaaaa 159

>gb|AE017220.1| Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67,
complete genome
Length = 4755700

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 448 acgtaattgctaccgccggtcaacgg 472
 |||||
Sbjct: 2278219 acgtaattgctcccgccggtcaacgg 2278243

>gb|AC118672.3| Genomic sequence for Oryza sativa, Nipponbare strain, clone
 OSJNBb0078P24, from chromosome 3, complete sequence
 Length = 146930

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 744 taactttttgttttttaaaaa 764
 |||||
Sbjct: 52650 taactttttgttttttaaaaa 52670

>gb|AC132258.3| Mus musculus BAC clone RP24-361F13 from 1, complete sequence
 Length = 130493

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 1008 acaaaagtgactgataaatctaatt 1032
 |||||
Sbjct: 40309 acaaaagtgactgataaatgtaatt 40333

>emb|AL954656.9| Zebrafish DNA sequence from clone CH211-67N10 in linkage group 23,
 complete sequence
 Length = 180590

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 259 acatttagttttatttaaagaaaataaaaa 287
 |||||
Sbjct: 122350 acatttagttttctttaataaaaataaaaa 122378

>emb|BX120013.5| Zebrafish DNA sequence from clone DKEY-76H10, complete sequence

Length = 170264

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 847 caccatatttattattatata 867

|||||

Sbjct: 29453 caccatatttattattatata 29433

>emb|BX005215.13| Mouse DNA sequence from clone RP23-280F9 on chromosome X Contains the 5' end of the Cask gene for calcium/calmodulin-dependent serine protein kinase (MAGUK family), a makorin, ring finger protein, 2 (Mkrn2) pseudogene and one CpG island, complete sequence

Length = 189900

Score = 42.1 bits (21), Expect = 6.6

Identities = 27/29 (93%)

Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagttaatttct 298

||||| ||||| |||||||

Sbjct: 28440 atttaaagaaaaaaaacgtaatttct 28468

>emb|AL844857.5| Mouse DNA sequence from clone RP23-74L17 on chromosome X, complete sequence

Length = 209399

Score = 42.1 bits (21), Expect = 6.6

Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 1045 ttagagaaaaataataaatt 1065

|||||

Sbjct: 42758 ttagagaaaaataataaatt 42778

>emb|BX247951.11| Zebrafish DNA sequence from clone DKEY-246A16 in linkage group 18 Contains the 5' end of the gene for a novel protein similar to vertebrate protein inhibitor of activated STAT, 1 (PIAS1), three novel genes and two CpG islands, complete sequence

Length = 189723

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 930 ctattttcaaaaaatatttttt 950
|||||||
Sbjct: 101732 ctattttcaaaaaatatttttt 101752

>gb|AE016830.1| Enterococcus faecalis V583, complete genome
Length = 3218031

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttattttaagaaaataaaaaa 288
|||||||
Sbjct: 2933665 ttattttaagaaaataaaaaa 2933685

>emb|AL929523.5| Zebrafish DNA sequence from clone CH211-250I3, complete sequence
Length = 133678

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 262 tttagtttattttaagaaaataaaa 286
|||||||
Sbjct: 29372 tttagtttattttaaaaaataaaa 29396

>emb|AL773566.6| Mouse DNA sequence from clone RP23-181C9 on chromosome 2 Contains a
pseudogene similar to part of ring finger and WD repeat
domain 2 (Rfwd2) and the 5' end of a novel gene, complete
sequence
Length = 184254

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 266 gtttattttaagaaaataaaa 286

|||||
Sbjct: 56693 gtttatttaaagaaaataaaa 56713

>emb|AL669898.17| Mouse DNA sequence from clone RP23-6C3 on chromosome X Contains a novel
pseudogene, the 5' end of a novel gene, a heat shock
protein 9A (Hspa9a) pseudogene, a ribosomal protein L7a
(Rpl7a) pseudogene, a farnesyl diphosphate synthetase
(Fdps) pseudogene and one CpG island, complete sequence
Length = 220201

Score = 42.1 bits (21), Expect = 6.6
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 263 ttagtttatttaaagaaaataaaaaagtt 291
|||||
Sbjct: 102002 ttagtttatttaaagaaaataaaaaagtt 101974

>gb|AE008384.1| Methanosarcina mazei strain Goel, complete genome
Length = 4096345

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 1964887 tatttcaaaaaatatttttta 1964907

>emb|AL391158.5| Human chromosome 14 DNA sequence BAC R-560013 of library RPCI-11 from
chromosome 14 of Homo sapiens (Human), complete sequence
Length = 202792

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 939 aaaatattttttatgtctttc 959
|||||
Sbjct: 141390 aaaatattttttatgtctttc 141370

>dbj|AB061780.1| Clostridium botulinum orf-22, ha-70, ha-17, ha-33, ntnha, nt genes

for ORF-22, HA-70, HA-17, HA-33, NTNHA, neurotoxin,
complete cds
Length = 11747

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatatgt 1079
|||||||
Sbjct: 2666 ataaattcttatattatatgt 2646

>emb|AL132951.3| Caenorhabditis elegans YAC Y67H2A, complete sequence
Length = 57745

Score = 42.1 bits (21), Expect = 6.6
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 15 ttttaattcttaaactttattaaat 39
|||||||
Sbjct: 12667 ttttaattcttaaactttattaaat 12691

>dbj|AB012112.1| Clostridium botulinum D phage gene for ORF-22, HA3, HA2, HA1, NTNH,
NTX, complete and partial sequence
Length = 11584

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatatgt 1079
|||||||
Sbjct: 2688 ataaattcttatattatatgt 2668

>dbj|AB012111.1| Clostridium botulinum D phage gene for ORF-22, HA3, HA2, HA1, NTNH,
complete and partial sequence
Length = 4525

Score = 42.1 bits (21), Expect = 6.6
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1059 ataaattcttatattatatgt 1079

|||||||

Sbjct: 2791 ataaattcttatattatatgt 2771

>gb|AC005548.1|AC005548 Homo sapiens chromosome 17, clone hRPK.756_K_11, complete sequence
Length = 156811

Score = 42.1 bits (21), Expect = 6.6

Identities = 24/25 (96%)

Strand = Plus / Plus

Query: 737 gagaaattaacttttggtttttaa 761

||||| |||||||

Sbjct: 101272 gagaaaataacttttggtttttaa 101296

>gb|L22534.1|GALLHP82Z Galleria mellonella hexamerin (Lhp82) gene, exons 1-6
Length = 9420

Score = 42.1 bits (21), Expect = 6.6

Identities = 24/25 (96%)

Strand = Plus / Plus

Query: 917 taaaaaattattcctatttcaaaaa 941

||||||| |||||||

Sbjct: 6455 taaaaaatattcctatttcaaaaa 6479

Database: /usr/local/blast/db/blastlibs/nt

Posted date: Feb 13, 2010 7:27 AM

Number of letters in database: 30,212,464,392

Number of sequences in database: 10,930,266

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 10930266

Number of Hits to DB: 418,746,764

Number of extensions: 32796916
Number of successful extensions: 1090417
Number of sequences better than 10.0: 251
Number of HSP's gapped: 1090417
Number of HSP's successfully gapped: 254
Length of query: 1082
Length of database: 30,212,464,392
Length adjustment: 23
Effective length of query: 1059
Effective length of database: 29,961,068,274
Effective search space: 31728771302166
Effective search space used: 31728771302166
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 14 (28.2 bits)
S2: 21 (42.1 bits)

BLASTn Output of the 3' Border Sequences Flanking the Insert in Soybean Event DAS-68416-4 against GeneBank No_human and No_mouse ESTs (est_others)

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 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.

Query= 68416_3_border
(1082 letters)

Database: /usr/local/blast/db/blastlibs/est_others
51,680,690 sequences; 29,218,461,503 total letters

Searching.....done

Sequences producing significant alignments:			Score	E
			(bits)	Value
emb FM898080.1	FM898080 MS (sb101) Brachionus plicatilis cDNA c...	48	0.10	
emb FM898359.1	FM898359 MS (sb101) Brachionus plicatilis cDNA c...	48	0.10	
emb FM927614.1	FM927614 REH (sb103) Brachionus plicatilis cDNA ...	48	0.10	
emb FM924849.1	FM924849 REH (sb103) Brachionus plicatilis cDNA ...	48	0.10	
emb FM913370.1	FM913370 RE (sb102) Brachionus plicatilis cDNA c...	48	0.10	
gb FD053629.1	CBP02606.b1 CBP0: Normalized channel catfish cDNA...	46	0.40	
gb ES577805.1	FPS016.C7_I22 LSG10-01 Lymnaea stagnalis cDNA clo...	46	0.40	
gb EH469861.1	FDR103-P00035-DEPE-R_A05 FDR103 Danio rerio cDNA ...	46	0.40	
gb GW128346.1	CABF3044.b1 CABF Amphimedon queenslandica release...	44	1.6	
gb GR579840.1	CBZY2359.b1 CBZY Dictyostelium purpureum 18 hr st...	44	1.6	
gb GR571694.1	CBTG2131.g1 CBTG Dictyostelium purpureum 12 hr ve...	44	1.6	
gb GR569517.1	CBTF493.g1 CBTF Dictyostelium purpureum 12 hr veg...	44	1.6	
emb FM898411.1	FM898411 MS (sb101) Brachionus plicatilis cDNA c...	44	1.6	
gb EG296472.1	MSAM275665_3153_3889 LCM-dissected maize inbred l...	44	1.6	
gb FC660687.1	CAXW1786.fwd CAXW Lottia gigantea from female gon...	44	1.6	
gb EY322309.1	CAWX8378.fwd CAWX Helobdella robusta Primary Earl...	44	1.6	
gb EL503163.1	F09_PFLAB1-M-PLATE11B.AB1 Blood stage Plasmodium ...	44	1.6	
gb EE473560.1	BNYS2DCT_UP_002_G01_27FEB2005_003 Brassica napus ...	44	1.6	
gb DW737772.1	MSAM049071_0042_0724 LCM-dissected maize shoot ap...	44	1.6	
gb DW273902.1	UI-S-GS1-acu-g-13-0-UI.s1 UI-S-GS1 Euprymna scolo...	44	1.6	
gb BE682501.1	180577 MARC 4BOV Bos taurus cDNA 5', mRNA sequence	44	1.6	
gb GW128347.1	CABF3044.g1 CABF Amphimedon queenslandica release...	42	6.2	
gb GT905149.1	CBWA5555.b1 CBWA Piromyces sp. E2 fungal mat and ...	42	6.2	
gb GT905946.1	CBWA6101.b1 CBWA Piromyces sp. E2 fungal mat and ...	42	6.2	
gb GT899067.1	CBWA1102.b1 CBWA Piromyces sp. E2 fungal mat and ...	42	6.2	

gb G0898162.1	hsxao_0013_A09.ab1 cucumber stamen suppression su...	42	6.2
gb G0632170.1	EST_afim_evh_929871 afimevh mixed_tissue Anoplopo...	42	6.2
gb G0632169.1	EST_afim_evh_929103 afimevh mixed_tissue Anoplopo...	42	6.2
gb G0619033.1	EST_afim_evh_744874 afimevh mixed_tissue Anoplopo...	42	6.2
gb G0616757.1	EST_afim_evh_740424 afimevh mixed_tissue Anoplopo...	42	6.2
gb G0290381.1	CAXN8486.rev CAXN Teleopsis dalmanni Late larval ...	42	6.2
gb GE815430.1	EST_scau_evk_976152 scauevk mixed_tissue Sebastes...	42	6.2
gb FE945836.1	Sma-USC-EA-2734 S. maximus Aeromonas cDNA library...	42	6.2
emb FM141483.1	FM141483 etnokid Rattus norvegicus cDNA clone et...	42	6.2
dbj DC436761.1	DC436761 epM- Bombyx mori cDNA clone E_FL_epM-_1...	42	6.2
gb FD375664.1	CBPN7243.g1 CBPN: Subtracted channel catfish cDNA...	42	6.2
dbj DC567981.1	DC567981 wd-- Bombyx mori cDNA clone E_FL_wd--_1...	42	6.2
gb FK484441.1	454GmaGlobSeed219073 Soybean Seeds Containing Glo...	42	6.2
gb FG146004.1	AGN_RPC010xgl7f1.ab1 AGN_RPC Nicotiana tabacum cD...	42	6.2
dbj DK032256.1	DK032256 OLBR Oryzias latipes cDNA clone olbr29a...	42	6.2
dbj DK030432.1	DK030432 OLBR Oryzias latipes cDNA clone olbr23m...	42	6.2
gb FD480788.1	NADI-aaa35b01.g1 Rhodnius prolixus_EST_NADI_5th_i...	42	6.2
gb FC800453.1	CBGC3708.fwd CBGC Lottia gigantea 15h 18h embryos...	42	6.2
gb FC796037.1	CBGC23939.fwd CBGC Lottia gigantea 15h 18h embryo...	42	6.2
gb FC796036.1	CBGC23939.rev CBGC Lottia gigantea 15h 18h embryo...	42	6.2
gb FC782133.1	CBGC13519.rev CBGC Lottia gigantea 15h 18h embryo...	42	6.2
gb FC777700.1	CBGC10606.fwd CBGC Lottia gigantea 15h 18h embryo...	42	6.2
gb FC766135.1	CBBN2940.rev CBBN Lottia gigantea 3, 4, 5, 6.5d Larv...	42	6.2
gb FC753028.1	CBBI6751.rev CBBI Lottia gigantea 26h, 37h, 61h Lar...	42	6.2
gb FC756058.1	CBBI9130.rev CBBI Lottia gigantea 26h, 37h, 61h Lar...	42	6.2
gb FC735597.1	CBBG9775.rev CBBG Lottia gigantea 12, 15, 18h embry...	42	6.2
gb FC731985.1	CBBG6977.rev CBBG Lottia gigantea 12, 15, 18h embry...	42	6.2
gb EY387612.1	CAXA6853.fwd CAXA Helobdella robusta Subtracted L...	42	6.2
gb EY381443.1	CAXA3466.fwd CAXA Helobdella robusta Subtracted L...	42	6.2
gb EY369837.1	CAXA12577.fwd CAXA Helobdella robusta Subtracted ...	42	6.2
gb EL503377.1	G09_PFLAB1-LARGE-PLATE11B.AB1 Blood stage Plasmod...	42	6.2
gb ES451332.1	26302 Myzus persicae 2001-12 (red), Fenton Myzus ...	42	6.2
gb ES389027.1	MUS07-B22.yld-s SHGC-MUS Mytilus californianus cD...	42	6.2
gb EB332296.1	CNSN01-F-138072-501 Normalized CNS library (juven...	42	6.2
gb EB304551.1	CNSN01-F-064136-501 Normalized CNS library (juven...	42	6.2
gb EB293882.1	CNSN01-F-043505-501 Normalized CNS library (juven...	42	6.2
gb EH367395.1	D04_j001_plate_103 j001 Nicotiana benthamiana cDN...	42	6.2
dbj DC106228.1	DC106228 Yamamoto/Hyodo-Miura NIBB/NBRP Xenopus ...	42	6.2
dbj DC006569.1	DC006569 Osada Taira anterior endomesoderm (AEM)...	42	6.2
gb DW756131.1	MSAM097773_1318_0782 LCM-dissected maize shoot ap...	42	6.2
emb CU072018.1	CU072018 AGENAE Rainbow trout multi-tissues libr...	42	6.2
dbj DB762915.1	DB762915 RIKEN full-length enriched honey bee cD...	42	6.2
dbj DB767567.1	DB767567 RIKEN full-length enriched honey bee cD...	42	6.2
dbj BB982965.1	BB982965 ovS3 Bombyx mori cDNA clone ovS3014B06r...	42	6.2
dbj BB982491.1	BB982491 ovS3 Bombyx mori cDNA clone ovS3007D09r...	42	6.2
gb EC327493.1	GUTF089549D10 POSSUM_01-POSSUM-GUT-2KB Trichosuru...	42	6.2
gb EC272309.1	TT1BV58TV Tetrahymena thermophila SB210 cDNA libr...	42	6.2
gb EC226765.1	410398 CK01 Drosophila melanogaster cDNA clone 15...	42	6.2
gb EC215214.1	410484 CK01 Drosophila melanogaster cDNA clone 15...	42	6.2

dbj DB393193.1	DB393193 APE Asterina pectinifera unfertilized e...	42	6.2
dbj BY919518.1	BY919518 fcP8 Bombyx mori cDNA clone E_EL_fcP8_1...	42	6.2
gb DY231459.1	EST02214 BmP Bombyx mori cDNA clone BmpM13_E09 3'...	42	6.2
gb DY230884.1	EST01628 BmP Bombyx mori cDNA clone BmpC_C53R_200...	42	6.2
gb DY227165.1	ID0AAK10YF21CM1 ApHL3SD Acyrthosiphon pisum cDNA ...	42	6.2
gb DV791356.1	Hw_liver_61_050822_A05 Bos taurus CF-24-HW liver ...	42	6.2
gb DV691543.1	CGN-35248 Leaf Coffea canephora cDNA clone cccl15...	42	6.2
gb DV280402.1	NAAGL61TF Aedes aegypti - Fat Bodies Normalized (...)	42	6.2
gb DT954953.1	CFW136-D04.yld-s SHGC-CFW Gasterosteus aculeatus ...	42	6.2
gb DT280951.1	JGI_CAAV9522.rev CAAV Pimephales promelas testis ...	42	6.2
gb DR769667.1	ILLUMIGEN_MCQ_63477 Katze_MMTE Macaca mulatta cDN...	42	6.2
emb AJ926041.1	AJ926041 Theileria annulata merozoite Theileria ...	42	6.2
gb CV503593.1	70065.1 Mixed Floral Solanum tuberosum cDNA clone...	42	6.2
gb C0315764.1	EK262410.5prime Exelixis FlyTag CK01 pCDNA-SK+ Dr...	42	6.2
gb C0284895.1	EK167420.5prime Exelixis FlyTag CK01 pCDNA-SK+ Dr...	42	6.2
gb CN575474.1	rc41b03.xl Meloidogyne hapla egg pAMP1 v1 Meloido...	42	6.2
gb CN574214.1	rc04h06.xl Meloidogyne hapla egg pAMP1 v1 Meloido...	42	6.2
gb CN573213.1	rc15f08.xl Meloidogyne hapla egg pAMP1 v1 Meloido...	42	6.2
gb CK550790.1	swkz0_009396.z1 swk Bombyx mori cDNA, mRNA sequence	42	6.2
dbj AU260586.1	AU260586 Paralichthys olivaceus kidney adult Par...	42	6.2
gb CK427090.1	rl71c02.y1 Meloidogyne javanica J2 SL1 pGEM Meloi...	42	6.2
gb CF980407.1	re04e06.y1 Meloidogyne incognita female SL1 pGEM ...	42	6.2
gb CF803136.1	rd94e05.y1 Meloidogyne incognita female SL1 pGEM ...	42	6.2
dbj BP181391.1	BP181391 ovS3 Bombyx mori cDNA clone ovS327G04f ...	42	6.2
dbj BP180165.1	BP180165 ovS3 Bombyx mori cDNA clone ovS312A08f ...	42	6.2
gb CF522058.1	AGENCOURT_15528907 NICHD_XGC_Kid1 Xenopus laevis ...	42	6.2
gb CB196840.2	AGENCOURT_11244860 NICHD_XGC_Tad2 Xenopus laevis ...	42	6.2
dbj BJ080944.1	BJ080944 NIBB Mochii normalized Xenopus tailbud ...	42	6.2
dbj BJ079923.1	BJ079923 NIBB Mochii normalized Xenopus tailbud ...	42	6.2
gb BI974397.1	saj01b04.y1 Gm-c1065 Glycine max cDNA clone GENOM...	42	6.2
gb BI747251.1	rm37g11.y1 Meloidogyne arenaria egg pAMP1 v1 Chia...	42	6.2
gb AW942998.1	LD29917.3prime LD Drosophila melanogaster embryo ...	42	6.2
gb AW441094.1	ra06b06.y1 Bird-Rao Meloidogyne incognita J2 Melo...	42	6.2

>emb|FM898080.1| FM898080 MS (sb101) Brachionus plicatilis cDNA clone sb101P0003A04
5', mRNA sequence
Length = 496

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
||||||| |||||||||
Sbjct: 459 tatttaaaaaaataaaaaagttaattt 432

>emb|FM898359.1| FM898359 MS (sb101) Brachionus plicatilis cDNA clone sb101P0003M07

5', mRNA sequence
Length = 521

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
||||||| |||||||||||||||||
Sbjct: 460 tatttaaaaaaataaaaaagttaattt 433

>emb|FM927614.1| FM927614 REH (sb103) Brachionus plicatilis cDNA clone sb103P0027M11
5', mRNA sequence
Length = 522

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
||||||| |||||||||||||||||
Sbjct: 460 tatttaaaaaaataaaaaagttaattt 433

>emb|FM924849.1| FM924849 REH (sb103) Brachionus plicatilis cDNA clone sb103P0018F21
5', mRNA sequence
Length = 418

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
||||||| |||||||||||||||||
Sbjct: 368 tatttaaaaaaataaaaaagttaattt 341

>emb|FM913370.1| FM913370 RE (sb102) Brachionus plicatilis cDNA clone sb102P0013J07
5', mRNA sequence
Length = 520

Score = 48.1 bits (24), Expect = 0.10
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaattt 296
 ||||||| |||||||||||||||||
Sbjct: 459 tatttaaaaaataaaaaagttaattt 432

>gb|FD053629.1| CBP02606.b1 CBP0: Normalized channel catfish cDNA library from
 LPS-stimulated peripheral blood leukocytes (JxLPS1)
 Ictalurus punctatus cDNA 5', mRNA sequence
 Length = 729

Score = 46.1 bits (23), Expect = 0.40
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagtt 291
 |||||||||||||||||||||
Sbjct: 419 tatttaaagaaaataaaaaagtt 397

>gb|ES577805.1| FPS016.C7_I22 LSG10-01 Lymnaea stagnalis cDNA clone FPS016_I22 3',
 mRNA sequence
 Length = 870

Score = 46.1 bits (23), Expect = 0.40
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 266 gtttatttaaagaaaataaaaaa 288
 |||||||||||||||||||||
Sbjct: 188 gtttatttaaagaaaataaaaaa 210

>gb|EH469861.1| FDR103-P00035-DEPE-R_A05 FDR103 Danio rerio cDNA clone
 FDR103-P00035-BR_A05 3', mRNA sequence
 Length = 740

Score = 46.1 bits (23), Expect = 0.40
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 1049 agaaaaataataaatcttatatttatgt 1079
 ||||||||||||| ||||| |||||
Sbjct: 362 agaaaaataataaatcttatcttatgt 392

>gb|GW128346.1| CABF3044.b1 CABF Amphimedon queenslandica released competent larvae
Amphimedon queenslandica cDNA clone CABF3044 5', mRNA
sequence
Length = 389

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 931 tattttcaaaaaatattttttat 952
|||||||
Sbjct: 388 tattttcaaaaaatattttttat 367

>gb|GR579840.1| CBZY2359.b1 CBZY Dictyostelium purpureum 18 hr starvation induced
multicellular development (H) Dictyostelium purpureum
cDNA clone CBZY2359 5', mRNA sequence
Length = 700

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttattttaagaaaataaaaaa 288
|||||||
Sbjct: 70 tttattttaagaaaataaaaaa 49

>gb|GR571694.1| CBTG2131.g1 CBTG Dictyostelium purpureum 12 hr vegetative phase for
Dictyostelium discoideum (L) Dictyostelium purpureum
cDNA clone CBTG2131 3', mRNA sequence
Length = 625

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttattttaagaaaataaaaaa 288
|||||||
Sbjct: 66 tttattttaagaaaataaaaaa 45

>gb|GR569517.1| CBTF493.g1 CBTF Dictyostelium purpureum 12 hr vegetative phase for
Dictyostelium discoideum (H) Dictyostelium purpureum
cDNA clone CBTF493 3', mRNA sequence
Length = 739

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 267 tttatttaaagaaaataaaaaa 288
 |||||||
Sbjct: 59 tttatttaaagaaaataaaaaa 38

>emb|FM898411.1| FM898411 MS (sb101) Brachionus plicatilis cDNA clone sb101P0003017
5', mRNA sequence
Length = 517

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 269 tatttaaagaaaataaaaaagttaat 294
 ||||||| |||||||
Sbjct: 459 tatttaaaaaataaaaaagttaat 434

>gb|EG296472.1| MSAM275665_3153_3889 LCM-dissected maize inbred line Mo17 shoot
apical meristem cDNA Zea mays cDNA, mRNA sequence
Length = 114

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 14 attttaattcttaactttatt 35
 |||||||
Sbjct: 55 attttaattcttaactttatt 34

>gb|FC660687.1| CAXW1786.fwd CAXW Lottia gigantea from female gonad Lottia gigantea
cDNA clone CAXW1786 5', mRNA sequence
Length = 151

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 919 aaaaattattcctatttcaaaaaata 944

|||||
Sbjct: 6 aaaaattattcctattttaaaaaata 31

>gb|EY322309.1| CAWX8378.fwd CAWX Helobdella robusta Primary Early Library, Embryo
st. 1-6 Helobdella robusta cDNA clone CAWX8378 5', mRNA
sequence
Length = 822

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttat 952
|||||
Sbjct: 34 tatttcaaaaaatatttttat 55

>gb|EL503163.1| F09_PFLAB1-M-PLATE11B.AB1 Blood stage Plasmodium falciparum cDNA
library PfSuOrig Plasmodium falciparum 3D7 cDNA, mRNA
sequence
Length = 477

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 263 ttagttttatttaaagaaaataaaaaa 288
|||||
Sbjct: 30 ttagttttatttaaagataataaaaaa 55

>gb|EE473560.1| BNYS2DCT_UP_002_G01_27FEB2005_003 Brassica napus seeds BNYS2DCT
Brassica napus cDNA 5', mRNA sequence
Length = 624

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaaa 764
|||||
Sbjct: 577 ttaactttttgttttttaaaaa 598

>gb|DW737772.1| MSAM049071_0042_0724 LCM-dissected maize shoot apical meristem cDNA

Zea mays cDNA, mRNA sequence
Length = 137

Score = 44.1 bits (22), Expect = 1.6
Identities = 22/22 (100%)
Strand = Plus / Minus

Query: 14 attttaattcttaaactttatt 35
|||||||
Sbjct: 123 attttaattcttaaactttatt 102

>gb|DW273902.1| UI-S-GS1-acu-g-13-0-UI.s1 UI-S-GS1 Euprymna scolopes cDNA clone
UI-S-GS1-acu-g-13-0-UI 3', mRNA sequence
Length = 546

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 917 taaaaaattattcctatttcaaaaaa 942
|||||||
Sbjct: 38 taaaaaattattcctatttcaaaaaa 13

>gb|BE682501.1| 180577 MARC 4BOV Bos taurus cDNA 5', mRNA sequence
Length = 307

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaagttaa 293
|||||||
Sbjct: 203 ttatttaaataaaaataaaaaagttaa 228

>gb|GW128347.1| CABF3044.g1 CABF Amphimedon queenslandica released competent larvae
Amphimedon queenslandica cDNA clone CABF3044 3', mRNA
sequence
Length = 389

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 932 atttcaaaaaatattttttat 952
 |||||||
Sbjct: 3 atttcaaaaaatattttttat 23

>gb|GT905149.1| CBWA5555.b1 CBWA Piomyces sp. E2 fungal mat and spores Piomyces
 sp. E2 cDNA clone CBWA5555 5', mRNA sequence
 Length = 645

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
 |||||||
Sbjct: 158 ttatttaaagaaaataaaaaa 178

>gb|GT905946.1| CBWA6101.b1 CBWA Piomyces sp. E2 fungal mat and spores Piomyces
 sp. E2 cDNA clone CBWA6101 5', mRNA sequence
 Length = 566

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
 |||||||
Sbjct: 158 ttatttaaagaaaataaaaaa 178

>gb|GT899067.1| CBWA1102.b1 CBWA Piomyces sp. E2 fungal mat and spores Piomyces
 sp. E2 cDNA clone CBWA1102 5', mRNA sequence
 Length = 648

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
 |||||||
Sbjct: 162 ttatttaaagaaaataaaaaa 182

>gb|G0898162.1| hsxao_0013_A09.ab1 cucumber stamen suppression subtractive

hybridization Cucumis sativus cDNA, mRNA sequence
Length = 538

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1047 agagaaaaataataaattct 1067
 |||||||
Sbjct: 464 agagaaaaataataaattct 484

>gb|G0632170.1| EST_afim_evh_929871 afimevh mixed_tissue Anoplopoma fimbria cDNA
Anoplopoma fimbria cDNA clone afim_evh_511_111 3', mRNA
sequence
Length = 630

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttatTTaaagaaaataaaaa 287
 |||||||
Sbjct: 26 tttatTTaaagaaaataaaaa 46

>gb|G0632169.1| EST_afim_evh_929103 afimevh mixed_tissue Anoplopoma fimbria cDNA
Anoplopoma fimbria cDNA clone afim_evh_511_111 5', mRNA
sequence
Length = 630

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 267 tttatTTaaagaaaataaaaa 287
 |||||||
Sbjct: 605 tttatTTaaagaaaataaaaa 585

>gb|G0619033.1| EST_afim_evh_744874 afimevh mixed_tissue Anoplopoma fimbria cDNA
Anoplopoma fimbria cDNA clone afim_evh_006_106 3', mRNA
sequence
Length = 534

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttattttaagaaaataaaaa 287
 |||||||
Sbjct: 16 tttattttaagaaaataaaaa 36

>gb|G0616757.1| EST_afim_evh_740424 afimevh mixed_tissue Anoplopoma fimbria cDNA
Anoplopoma fimbria cDNA clone afim_evh_002_264 3', mRNA
sequence
Length = 748

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttattttaagaaaataaaaa 287
 |||||||
Sbjct: 16 tttattttaagaaaataaaaa 36

>gb|G0290381.1| CAXN8486.rev CAXN Teleopsis dalmanni Late larval eye-antennal disc
EST library Teleopsis dalmanni cDNA clone CAXN8486 3',
mRNA sequence
Length = 681

Score = 42.1 bits (21), Expect = 6.2
Identities = 33/37 (89%)
Strand = Plus / Minus

Query: 917 taaaaaattatttctattttcaaaaaatattttttatg 953
 ||||||| | |||| | |||||
Sbjct: 104 taaaaaattattttcaatttaacaaaatattttttatg 68

>gb|GE815430.1| EST_scau_evk_976152 scauevk mixed_tissue Sebastes caurinus cDNA
Sebastes caurinus cDNA clone scau_evk_513_312 3', mRNA
sequence
Length = 840

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 267 tttattttaagaaaataaaaa 287
 |||||||
Sbjct: 32 tttattttaagaaaataaaaa 52

>gb|FE945836.1| Sma-USC-EA-2734 *S. maximus* Aeromonas cDNA library Psetta maxima
cDNA 3', mRNA sequence
Length = 169

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 267 tttattttaagaaaataaaaa 287
 |||||||
Sbjct: 138 tttattttaagaaaataaaaa 118

>emb|FM141483.1| FM141483 etnokid *Rattus norvegicus* cDNA clone etnokidP0065H24 5',
mRNA sequence
Length = 693

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 917 taaaaaattattcctatttca 937
 |||||||
Sbjct: 448 taaaaaattattcctatttca 428

>dbj|DC436761.1| DC436761 epM- *Bombyx mori* cDNA clone E_FL_epM-_16P19_F_0 5', mRNA
sequence
Length = 628

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatatatt 994
 |||||||
Sbjct: 516 aatatctatttaagtatatatt 536

>gb|FD375664.1| CBPN7243.g1 CBPN: Subtracted channel catfish cDNA library from
liver, pituitary, ovary and testes (Mixed tissue library)

5, MTL5) Ictalurus punctatus cDNA 3', mRNA sequence
Length = 647

Score = 42.1 bits (21), Expect = 6.2
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 737 gagaaattaactttttgttttttaaaaac 765
||||| ||||||| |||||||
Sbjct: 157 gagaaaataacttttttttttaaaaac 185

>dbj|DC567981.1| DC567981 wd-- Bombyx mori cDNA clone E_FL_wd--_13K20_R_0 3', mRNA
sequence
Length = 560

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994
||||| ||||||| |||||||
Sbjct: 178 aatatctatttaagtatattt 158

>gb|FK484441.1| 454GmaGlobSeed219073 Soybean Seeds Containing Globular-Stage
Embryos Glycine max cDNA, mRNA sequence
Length = 216

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 267 tttatttaaagaaaataaaaa 287
||||| ||||||| |||||||
Sbjct: 48 tttatttaaagaaaataaaaa 28

>gb|FG146004.1| AGN_RPC010xg17f1.ab1 AGN_RPC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 883

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 933 tttcaaaaaatattttttatg 953
 |||||||
Sbjct: 41 tttcaaaaaatattttttatg 61

>dbj|DK032256.1| DK032256 OLBR Oryzias latipes cDNA clone olbr29a11 3', mRNA
 sequence
 Length = 934

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 740 aaattaactttttgtttttta 760
 |||||||
Sbjct: 338 aaattaactttttgtttttta 318

>dbj|DK030432.1| DK030432 OLBR Oryzias latipes cDNA clone olbr23m13 3', mRNA
 sequence
 Length = 921

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 740 aaattaactttttgtttttta 760
 |||||||
Sbjct: 338 aaattaactttttgtttttta 318

>gb|FD480788.1| NADI-aaa35b01.g1 Rhodnius prolixus_EST_NADI_5th_instar_CNS Rhodnius
 prolixus cDNA 5', mRNA sequence
 Length = 540

Score = 42.1 bits (21), Expect = 6.2
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 270 atttaaagaaaaataaaaaagttaatttct 298
 ||||||| |||| |
Sbjct: 388 atttaaaaaaaaaaaaaaagttaatttct 416

>gb|FC800453.1| CBGC3708.fwd CBGC Lottia gigantea 15h 18h embryos Lottia gigantea

cDNA clone CBGC3708 5', mRNA sequence
Length = 842

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||
Sbjct: 618 tcaaagaatatTTTTtatgtctttc 642

>gb|FC796037.1| CBGC23939.fwd CBGC Lottia gigantea 15h 18h embryos Lottia gigantea
cDNA clone CBGC23939 5', mRNA sequence
Length = 693

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||
Sbjct: 511 tcaaagaatatTTTTtatgtctttc 535

>gb|FC796036.1| CBGC23939.rev CBGC Lottia gigantea 15h 18h embryos Lottia gigantea
cDNA clone CBGC23939 3', mRNA sequence
Length = 628

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||
Sbjct: 376 tcaaagaatatTTTTtatgtctttc 352

>gb|FC782133.1| CBGC13519.rev CBGC Lottia gigantea 15h 18h embryos Lottia gigantea
cDNA clone CBGC13519 3', mRNA sequence
Length = 721

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||
Sbjct: 398 tcaaagaatatTTTTtatgtctttc 374

>gb|FC777700.1| CBGC10606.fwd CBGC Lottia gigantea 15h 18h embryos Lottia gigantea
cDNA clone CBGC10606 5', mRNA sequence
Length = 693

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||
Sbjct: 293 tcaaagaatatTTTTtatgtctttc 317

>gb|FC766135.1| CBBN2940.rev CBBN Lottia gigantea 3,4,5,6.5d Larvae (M) Lottia
gigantea cDNA clone CBBN2940 3', mRNA sequence
Length = 725

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||
Sbjct: 400 tcaaagaatatTTTTtatgtctttc 376

>gb|FC753028.1| CBBI6751.rev CBBI Lottia gigantea 26h,37h,61h Larvae (L) Lottia
gigantea cDNA clone CBBI6751 3', mRNA sequence
Length = 720

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||
Sbjct: 399 tcaaagaatatTTTTtatgtctttc 375

>gb|FC756058.1| CBBI9130.rev CBBI Lottia gigantea 26h,37h,61h Larvae (L) Lottia

gigantea cDNA clone CBBI9130 3', mRNA sequence
Length = 774

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||||
Sbjct: 400 tcaaagaatatTTTTtatgtctttc 376

>gb|FC735597.1| CBBG9775.rev CBBG Lottia gigantea 12,15,18h embryos Lottia gigantea
cDNA clone CBBG9775 3', mRNA sequence
Length = 745

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||||
Sbjct: 398 tcaaagaatatTTTTtatgtctttc 374

>gb|FC731985.1| CBBG6977.rev CBBG Lottia gigantea 12,15,18h embryos Lottia gigantea
cDNA clone CBBG6977 3', mRNA sequence
Length = 710

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 935 tcaaaaaaatatTTTTtatgtctttc 959
||||| ||||||||||||||||||
Sbjct: 398 tcaaagaatatTTTTtatgtctttc 374

>gb|EY387612.1| CAXA6853.fwd CAXA Helobdella robusta Subtracted Late Library,
Embryo st. 7-11 Helobdella robusta cDNA clone CAXA6853
5', mRNA sequence
Length = 747

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 274 aaagaaaataaaaaagttaat 294
 |||||||
Sbjct: 25 aaagaaaataaaaaagttaat 45

>gb|EY381443.1| CAXA3466.fwd CAXA Helobdella robusta Subtracted Late Library,
 Embryo st. 7-11 Helobdella robusta cDNA clone CAXA3466
 5', mRNA sequence
 Length = 832

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 274 aaagaaaataaaaaagttaat 294
 |||||||
Sbjct: 48 aaagaaaataaaaaagttaat 68

>gb|EY369837.1| CAXA12577.fwd CAXA Helobdella robusta Subtracted Late Library,
 Embryo st. 7-11 Helobdella robusta cDNA clone CAXA12577
 5', mRNA sequence
 Length = 750

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 274 aaagaaaataaaaaagttaat 294
 |||||||
Sbjct: 23 aaagaaaataaaaaagttaat 43

>gb|EL503377.1| G09_PFLAB1-LARGE-PLATE11B.AB1 Blood stage Plasmodium falciparum
 cDNA library PfSuOrig Plasmodium falciparum 3D7 cDNA,
 mRNA sequence
 Length = 468

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 843 ttctcaccatatttattattatata 867
 |||||||

Sbjct: 76 ttctcacaatatattattattatata 52

>gb|ES451332.1| 26302 Myzus persicae 2001-12 (red), Fenton Myzus persicae cDNA clone
GMAWCDNA60_D10_D10_037 5', mRNA sequence
Length = 506

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1052 aaaataaataaattcttatat 1072
|||||||
Sbjct: 385 aaaataaataaattcttatat 365

>gb|ES389027.1| MUS07-B22.yld-s SHGC-MUS Mytilus californianus cDNA 3', mRNA
sequence
Length = 925

Score = 42.1 bits (21), Expect = 6.2
Identities = 27/29 (93%)
Strand = Plus / Minus

Query: 736 agagaaattaactttttgttttttaaaaa 764
||||||| ||||| |||||||
Sbjct: 557 agagaaattaatttttttttttaaaaa 529

>gb|EB332296.1| CNSN01-F-138072-501 Normalized CNS library (juvenile 1) Aplysia
californica cDNA clone CNSN01-F-138072 5', mRNA sequence
Length = 604

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 267 tttatttaaagaaaataaaaaagtt 291
||||||| |||||
Sbjct: 318 tttatttaaagaaaataagaaagtt 294

>gb|EB304551.1| CNSN01-F-064136-501 Normalized CNS library (juvenile 1) Aplysia
californica cDNA clone CNSN01-F-064136 5', mRNA sequence
Length = 543

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 267 tttatTTaaagaaaataaaaaagtt 291
 |||||
Sbjct: 284 tttatTTaaagaaaataagaaagtt 260

>gb|EB293882.1| CNSN01-F-043505-501 Normalized CNS library (juvenile 1) Aplysia
californica cDNA clone CNSN01-F-043505 5', mRNA sequence
Length = 608

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 267 tttatTTaaagaaaataaaaaagtt 291
 |||||
Sbjct: 336 tttatTTaaagaaaataagaaagtt 312

>gb|EH367395.1| D04_j001_plate_103_j001 Nicotiana benthamiana cDNA 5' similar to
unknown function, mRNA sequence
Length = 113

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 267 tttatTTaaagaaaataaaaa 287
 |||||
Sbjct: 71 tttatTTaaagaaaataaaaa 51

>dbj|DC106228.1| DC106228 Yamamoto/Hyodo-Miura NIBB/NBRP Xenopus DMZ pCS2p+ cDNA
library Xenopus laevis cDNA clone xl241k05 5', mRNA
sequence
Length = 740

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactTTTTgtTTTTtaaaa 763

|||||
Sbjct: 184 ttaactttttgttttttaaaa 204

>dbj|DC006569.1| DC006569 Osada Taira anterior endomesoderm (AEM) pCS105 cDNA
library Xenopus laevis cDNA clone rxlk112c20ex 3', mRNA
sequence
Length = 815

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 743 ttaactttttgttttttaaaa 763
|||||
Sbjct: 139 ttaactttttgttttttaaaa 119

>gb|DW756131.1| MSAM097773_1318_0782 LCM-dissected maize shoot apical meristem cDNA
Zea mays cDNA, mRNA sequence
Length = 109

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 264 tagtttatttaaagaaaataaaaaa 288
|||||
Sbjct: 35 tagtttatttaaagaaaataaaaaa 11

>emb|CU072018.1| CU072018 AGENAE Rainbow trout multi-tissues library (tcce)
Oncorhynchus mykiss cDNA clone tcba0007.e.09 3', mRNA
sequence
Length = 972

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 265 agtttatttaaagaaaataaa 285
|||||
Sbjct: 800 agtttatttaaagaaaataaa 820

>dbj|DB762915.1| DB762915 RIKEN full-length enriched honey bee cDNA library, head Apis

mellifera cDNA clone BH10028M11 3', mRNA sequence
Length = 519

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1057 aaataaattcttatattatat 1077
 |||||||
Sbjct: 498 aaataaattcttatattatat 518

>dbj|DB767567.1| DB767567 RIKEN full-length enriched honey bee cDNA library, head
 Apis mellifera cDNA clone BH10045D23 3', mRNA sequence
 Length = 486

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 265 agtttattttaagaaaataaa 285
 |||||||
Sbjct: 345 agtttattttaagaaaataaa 325

>dbj|BB982965.1| BB982965 ovS3 Bombyx mori cDNA clone ovS3014B06r 3', mRNA sequence
 Length = 435

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994
 |||||||
Sbjct: 184 aatatctatttaagtatattt 164

>dbj|BB982491.1| BB982491 ovS3 Bombyx mori cDNA clone ovS3007D09r 3', mRNA sequence
 Length = 607

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994

|||||
Sbjct: 168 aatatctatttaagtatatatt 148

>gb|EC327493.1| GUTF089549D10 POSSUM_01-POSSUM-GUT-2KB Trichosurus vulpecula cDNA
clone 1061024742945, mRNA sequence
Length = 843

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 278 aaaataaaaaagttaatttctcttt 302
|||||
Sbjct: 510 aaaaaaaaaagttaatttctcttt 486

>gb|EC272309.1| TT1BV58TV Tetrahymena thermophila SB210 cDNA library (starved)
Tetrahymena thermophila cDNA clone TT1BV58, mRNA
sequence
Length = 775

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 931 tatttcaaaaaatatttttta 951
|||||
Sbjct: 57 tatttcaaaaaatatttttta 37

>gb|EC226765.1| 410398 CK01 Drosophila melanogaster cDNA clone 159188, mRNA
sequence
Length = 440

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
|||||
Sbjct: 189 atttaaagaaaataaaaaagt 209

>gb|EC215214.1| 410484 CK01 Drosophila melanogaster cDNA clone 159120, mRNA
sequence

Length = 473

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290

|||||||

Sbjct: 188 atttaaagaaaataaaaaagt 208

>dbj|DB393193.1| DB393193 APE Asterina pectinifera unfertilized egg cDNA library

Patiria pectinifera cDNA clone ape24f18 5', mRNA sequence

Length = 703

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 1045 ttagagaaaataaataaatt 1065

|||||||

Sbjct: 486 ttagagaaaataaataaatt 466

>dbj|BY919518.1| BY919518 fcP8 Bombyx mori cDNA clone E_EL_fcP8_11B06_F_0 5', mRNA
sequence

Length = 814

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 974 aatatctatttaagtatattt 994

|||||||

Sbjct: 175 aatatctatttaagtatattt 155

>gb|DY231459.1| EST02214 BmP Bombyx mori cDNA clone BmpM13_E09 3', mRNA sequence

Length = 402

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 974 aatatctatttaagtatattt 994

|||||
Sbjct: 215 aatatctatttaagtatatatt 235

>gb|DY230884.1| EST01628 BmP Bombyx mori cDNA clone
BmpC_C53R_2005-09-11_WDOTHERS-050911 3', mRNA sequence
Length = 376

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 974 aatatctatttaagtatatatt 994
|||||
Sbjct: 191 aatatctatttaagtatatatt 211

>gb|DY227165.1| ID0AAK10YF21CM1 ApHL3SD Acyrthosiphon pisum cDNA clone ID0AAK10YF21
5', mRNA sequence
Length = 218

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1052 aaaataaataaattcttatat 1072
|||||
Sbjct: 103 aaaataaataaattcttatat 83

>gb|DV791356.1| Hw_liver_61_050822_A05 Bos taurus CF-24-HW liver cDNA library Bos
taurus cDNA, mRNA sequence
Length = 1292

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 740 aaattaactttttgttttttaaaaa 764
|||||
Sbjct: 1081 aaattaactttttgttttttcaaaa 1105

>gb|DV691543.1| CGN-35248 Leaf Coffea canephora cDNA clone cccl15m24 5', mRNA
sequence
Length = 624

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 740 aaattaactttttgttttttaaaaa 764
 ||||| |||||||||||||||
Sbjct: 506 aaattagctttttgttttttaaaaa 482

>gb|DV280402.1| NAAGL61TF Aedes aegypti - Fat Bodies Normalized (NAFFB2) Aedes
aegypti cDNA clone NAAGL61, mRNA sequence
Length = 764

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 1035 ggatctaccattagagaaaaa 1055
 |||||||||||||||||
Sbjct: 174 ggatctaccattagagaaaaa 154

>gb|DT954953.1| CFW136-D04.y1d-s SHGC-CFW Gasterosteus aculeatus cDNA clone
CFW136-D04 5', mRNA sequence
Length = 1282

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatttttta 951
 |||||||||||||||||
Sbjct: 1236 tatttcaaaaaatatttttta 1256

>gb|DT280951.1| JGI_CAAV9522.rev CAAV Pimephales promelas testis 7-8 month adults,
males and females pooled (H) Pimephales promelas cDNA
clone CAAV9522 3', mRNA sequence
Length = 857

Score = 42.1 bits (21), Expect = 6.2
Identities = 24/25 (96%)
Strand = Plus / Minus

Query: 744 taactttttgttttttaaaaactaa 768
|||||||
Sbjct: 210 taactttttgttttttaaaaactaa 186

>gb|DR769667.1| ILLUMIGEN_MCQ_63477 Katze_MMTE Macaca mulatta cDNA clone
IBIUW:35675 5' similar to Bases 28 to 453 highly similar
to human TTF2 (Hs.486818), mRNA sequence
Length = 553

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 209 tactatcttttgtttcattta 229
|||||||
Sbjct: 483 tactatcttttgtttcattta 503

>emb|AJ926041.1| AJ926041 Theileria annulata merozoite Theileria annulata cDNA clone
tam010f09_q1k, mRNA sequence
Length = 1076

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 273 taaagaaaataaaaaagttta 293
|||||||
Sbjct: 1056 taaagaaaataaaaaagttta 1076

>gb|CV503593.1| 70065.1 Mixed Floral Solanum tuberosum cDNA clone 70065 5', mRNA
sequence
Length = 672

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 887 aaaggaagttggatttcttct 907
|||||||
Sbjct: 206 aaaggaagttggatttcttct 226

>gb|C0315764.1| EK262410.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila

melanogaster cDNA clone EK262410 5, mRNA sequence
Length = 473

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
 |||||||
Sbjct: 188 atttaaagaaaataaaaaagt 208

>gb|C0284895.1| EK167420.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila
 melanogaster cDNA clone EK167420 5, mRNA sequence
Length = 440

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 270 atttaaagaaaataaaaaagt 290
 |||||||
Sbjct: 354 atttaaagaaaataaaaaagt 374

>gb|CN575474.1| rc41b03.x1 Meloidogyne hapla egg pAMP1 v1 Meloidogyne hapla cDNA 3'
 similar to SW:YP87_CAEEL Q09444 HYPOTHETICAL 37.7 KD
 PROTEIN C08B11.7 IN CHROMOSOME II. [1] ;, mRNA sequence
Length = 257

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 931 tatttcaaaaaatatatttta 951
 |||||||
Sbjct: 6 tatttcaaaaaatatatttta 26

>gb|CN574214.1| rc04h06.x1 Meloidogyne hapla egg pAMP1 v1 Meloidogyne hapla cDNA 3'
 similar to SW:YP87_CAEEL Q09444 HYPOTHETICAL 37.7 KD
 PROTEIN C08B11.7 IN CHROMOSOME II. [1] ;, mRNA sequence
Length = 435

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)

```
Query: 931 tatttcacaaaaaatatttttta 951
      |||||
Sbjct: 10  tatttcacaaaaaatatttttta 30
```

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

>gb|CK550790.1| swkz0_009396.z1 swk Bombyx mori cDNA, mRNA sequence
Length = 628

```
Query: 974 aatatctatttaagtatatatt 994
          |||||
Sbjct: 135 aatatctatttaagtatatatt 115
```

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 415 gcatgggtggttgacaggtga 435
      |||||
Sbjct: 590 gcatgggtggttgacaggtga 570
```

>gb|CK427090.1| rl71c02.y1 Meloidogyne javanica J2 SL1 pGEM Meloidogyne javanica
cDNA 5' similar to TR:Q21581 Q21581 COSMID M60. [1]
;contains element MER9 repetitive element ;, mRNA
sequence
Length = 548

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286
|||||||
Sbjct: 539 gtttattttaagaaaataaaa 519

>gb|CF980407.1| re04e06.y1 Meloidogyne incognita female SL1 pGEM Meloidogyne
incognita cDNA 5' similar to TR:Q21581 Q21581 COSMID
M60. [1] ;, mRNA sequence
Length = 570

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286
|||||||
Sbjct: 562 gtttattttaagaaaataaaa 542

>gb|CF803136.1| rd94e05.y1 Meloidogyne incognita female SL1 pGEM Meloidogyne
incognita cDNA 5' similar to TR:Q21581 Q21581 COSMID
M60. [1] ;, mRNA sequence
Length = 647

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286
|||||||
Sbjct: 586 gtttattttaagaaaataaaa 566

>dbj|BP181391.1| BP181391 ovS3 Bombyx mori cDNA clone ovS327G04f 5', mRNA sequence
Length = 521

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatatatt 994
 |||||
Sbjct: 175 aatatctatttaagtatatatt 155

>dbj|BP180165.1| BP180165 ovS3 Bombyx mori cDNA clone ovS312A08f 5', mRNA sequence
Length = 521

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 974 aatatctatttaagtatatatt 994
 |||||
Sbjct: 138 aatatctatttaagtatatatt 118

>gb|CF522058.1| AGENCOURT_15528907 NICHG_XGC_Kid1 Xenopus laevis cDNA clone
IMAGE:7009679 5', mRNA sequence
Length = 722

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaa 763
 |||||
Sbjct: 235 ttaactttttgttttttaaaa 255

>gb|CB196840.2| AGENCOURT_11244860 NICHG_XGC_Tad2 Xenopus laevis cDNA clone
IMAGE:6871687 5', mRNA sequence
Length = 834

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 743 ttaactttttgttttttaaaa 763
 |||||

Sbjct: 343 ttaactttttgttttttaaaa 363

>dbj|BJ080944.1| BJ080944 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL069o10 3', mRNA sequence
Length = 596

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 743 ttaactttttgttttttaaaa 763
|||||||
Sbjct: 132 ttaactttttgttttttaaaa 112

>dbj|BJ079923.1| BJ079923 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis cDNA clone XL073p03 3', mRNA sequence
Length = 608

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 743 ttaactttttgttttttaaaa 763
|||||||
Sbjct: 155 ttaactttttgttttttaaaa 135

>gb|BI974397.1| saj01b04.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-8912 5', mRNA sequence
Length = 557

Score = 42.1 bits (21), Expect = 6.2
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 268 ttatttaaagaaaataaaaaa 288
|||||||
Sbjct: 325 ttatttaaagaaaataaaaaa 345

>gb|BI747251.1| rm37g11.y1 Meloidogyne arenaria egg pAMP1 v1 Chiapelli McCarter
Meloidogyne arenaria cDNA 5' similar to TR:Q21581 Q21581
COSMID M60. [1] ;contains element MER9 MER9 repetitive
element ;, mRNA sequence

Length = 421

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286

||||||||||||||||

Sbjct: 412 gtttattttaagaaaataaaa 392

>gb|AW942998.1| LD29917.3prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD29917 3, mRNA sequence

Length = 629

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 270 atttaaagaaaataaaaaagt 290

||||||||||||||||

Sbjct: 31 atttaaagaaaataaaaaagt 11

>gb|AW441094.1| ra06b06.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
cDNA 5' similar to WP:M60.3 CE02832 ;, mRNA sequence

Length = 542

Score = 42.1 bits (21), Expect = 6.2

Identities = 21/21 (100%)

Strand = Plus / Minus

Query: 266 gtttattttaagaaaataaaa 286

||||||||||||||||

Sbjct: 541 gtttattttaagaaaataaaa 521

Database: /usr/local/blast/db/blastlibs/est_others

Posted date: Feb 13, 2010 7:48 AM

Number of letters in database: 29,218,461,503

Number of sequences in database: 51,680,690

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 51680690
Number of Hits to DB: 344,427,558
Number of extensions: 24743020
Number of successful extensions: 7648314
Number of sequences better than 10.0: 108
Number of HSP's gapped: 7648314
Number of HSP's successfully gapped: 108
Length of query: 1082
Length of database: 29,218,461,503
Length adjustment: 23
Effective length of query: 1059
Effective length of database: 28,029,805,633
Effective search space: 29683564165347
Effective search space used: 29683564165347
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 12 (24.3 bits)
S2: 21 (42.1 bits)

BLASTx Output of the 3' Border Sequence Flanking the Insert in Soybean Event DAS-68416-4 against GenBank Non-redundant Protein Sequences (nr)

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 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.

Query= 68416_3_border
(1082 letters)

Database: /usr/local/blast/db/blastlibs/nr
10,432,217 sequences; 3,559,509,877 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
ref NP_001037088.1 hemolin [Bombyx mori] >gi 41350234 gb AAS004...	36	6.6
gb AAS00443.1 hemolin [Bombyx mori]	36	6.6
dbj BAC79387.1 hemolin [Bombyx mori]	36	6.6
gb EFC40574.1 predicted protein [Naegleria gruberi]	36	8.7
ref XP_002011940.1 GI14470 [Drosophila mojavensis] >gi 19390919...	36	8.7

>ref|NP_001037088.1| hemolin [Bombyx mori]
gb|AAS00444.1| hemolin [Bombyx mori]
gb|AAS00445.1| hemolin [Bombyx mori]
Length = 410

Score = 36.2 bits (82), Expect = 6.6
Identities = 25/96 (26%), Positives = 46/96 (47%), Gaps = 4/96 (4%)
Frame = -1

Query: 461 GSNYVFSTHQPVNH-HALPHRRIRSLQQLRRHTYVSRPGSTTASDLSTIEYQWQKEKLT 285
G+ +++T QPVN +P + + L R +R T D S +EY W+K+ + F
Sbjct: 10 GTCVIYTTGQPVNSGDKVPVLKEAPAEVLFREGQATRLECATGDDSGVEYSWRKDGMMHF 69

Query: 284 LFSLNKLNVI---LLLYPSHKVNETKDSRVFCQNFF 186
L+ L I L++ K ++ + + F ++ F
Sbjct: 70 SVGLDTLTTIDAGSLVFSQTKASDEGEYQCFKASDF 105

>gb|AAS00443.1| hemolin [Bombyx mori]

Length = 410

Score = 36.2 bits (82), Expect = 6.6

Identities = 25/96 (26%), Positives = 46/96 (47%), Gaps = 4/96 (4%)

Frame = -1

Query: 461 GSNYVFSTHQPVNHALPHRRIRSLQQLRRHTYVSRPGSTTASDLSTIEYQWQKEKLT 285

G+ +++T QPVN +P + + L R +R T D S +EY W+K+ + F

Sbjct: 10 GTCVIYTTGQPVNSGDKVPVLKEAPAEVLFREGQATRLECATGDDSGVEYSWRKDGMMHF 69

Query: 284 LFSLNKLNVI---LLLYPSHKVNETKDSRVFCQNFF 186

L+ L I L++ K ++ + + F ++ F

Sbjct: 70 SVGLDTLTTIDAGSLVFSQTKASDEGEYQCFAKSDF 105

>dbj|BAC79387.1| hemolin [Bombyx mori]

Length = 410

Score = 36.2 bits (82), Expect = 6.6

Identities = 25/96 (26%), Positives = 46/96 (47%), Gaps = 4/96 (4%)

Frame = -1

Query: 461 GSNYVFSTHQPVNHALPHRRIRSLQQLRRHTYVSRPGSTTASDLSTIEYQWQKEKLT 285

G+ +++T QPVN +P + + L R +R T D S +EY W+K+ + F

Sbjct: 10 GTCVIYTTGQPVNSGDKVPVLKEAPAEVLFREGQATRLECATGDDSGVEYSWRKDGMMHF 69

Query: 284 LFSLNKLNVI---LLLYPSHKVNETKDSRVFCQNFF 186

L+ L I L++ K ++ + + F ++ F

Sbjct: 70 SVGLDTLTTIDAGSLVFSQTKASDEGEYQCFAKSDF 105

>gb|EFC40574.1| predicted protein [Naegleria gruberi]

Length = 716

Score = 35.8 bits (81), Expect = 8.7

Identities = 35/131 (26%), Positives = 58/131 (44%), Gaps = 13/131 (9%)

Frame = -1

Query: 593 TINXXXXXFFALQ--PSRDFFKGNETASQPHNFHIRDIFAPSSVDGG-----SN 453

T+NY ++ S++ +K N + + NF + F S VDGG SN

Sbjct: 163 TVNYRNSRDSFIKLLDSQELYKENMMSDK--NFTLGYSF--DSLVDGGWENKKPLTLVSSN 219

Query: 452 YVFSTHQPVNHHALPHRRIRSLQQLRRHTYVSRPGSTTASDLSTIEYQWQKEKLTFLFSL 273

+ +H+ +IR+L+ LR+HTY S +TT +L+ E + L

Sbjct: 220 MEYKEAVYSIYHS---EKIRTLEALRKHTYRSTTWNTTVEELTICTEDSDMEFMLSCKKL 276

Query: 272 NKLNVILLLYP 240

KLN++ + P

Sbjct: 277 RKLNILTTVMP 287

>ref|XP_002011940.1| GI14470 [Drosophila mojavensis]
gb|EDW08061.1| GI14470 [Drosophila mojavensis]
Length = 2018

Score = 35.8 bits (81), Expect = 8.7
Identities = 22/62 (35%), Positives = 32/62 (51%), Gaps = 1/62 (1%)
Frame = -1

Query: 533 GNETASQPHNFHIRDIFAPSSVDGGSNYVFSTHQPVNHH-ALPHRRIRSLQQLRRHTYVS 357
GNETAS HN I++ + S S+ + H P +H L ++ + QQL +HT
Sbjct: 322 GNETASNSHNPFIKEHYWESPTTYASSLL--HSPTEYHDELQQKQQQEQQLPQHTSAR 378

Query: 356 RP 351
RP
Sbjct: 379 RP 380

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Feb 13, 2010 7:16 AM
Number of letters in database: 3,559,509,877
Number of sequences in database: 10,432,217

Lambda	K	H
0.318	0.134	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 10432217
Number of Hits to DB: 5,113,556,002
Number of extensions: 90438379
Number of successful extensions: 211424
Number of sequences better than 10.0: 5
Number of HSP's gapped: 211246
Number of HSP's successfully gapped: 5
Length of query: 360
Length of database: 3,559,509,877
Length adjustment: 138
Effective length of query: 222
Effective length of database: 2,119,863,931
Effective search space: 470609792682
Effective search space used: 470609792682
Neighboring words threshold: 12

Window for multiple hits: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 33 (17.3 bits)

**BLASTn Output of the Sequence at the Parental Locus of Soybean Event DAS-68416-4
against GenBank Nucleotide Collection (nt/nr)**

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
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.

Query= 68416_parent_locus
(3867 letters)

Database: /usr/local/blast/db/blastlibs/nt
10,930,266 sequences; 30,212,464,392 total letters

Searching.....done

		Score	E
Sequences producing significant alignments:		(bits)	Value
gb BT093225.1	Soybean clone JCVI-FLGm-17C9 unknown mRNA	1039	0.0
gb BT093496.1	Soybean clone JCVI-FLGm-17I24 unknown mRNA	731	0.0
gb EF456703.1	Medicago truncatula peroxidase (PRX1) mRNA, compl...	176	6e-40
gb BT098008.1	Soybean clone JCVI-FLGm-22H8 unknown mRNA	174	3e-39
emb CU137662.1	Medicago truncatula chromosome 5 clone mth2-155l...	172	1e-38
emb CR938710.1	Medicago truncatula chromosome 5 clone mth2-170k...	172	1e-38
gb AF149281.1	AF149281 Phaseolus vulgaris clone pBPERB5 peroxida...	163	1e-35
ref XM_002520789.1	Ricinus communis Peroxidase 52 precursor, pu...	129	1e-25
gb BT052838.1	Medicago truncatula clone MTYFH_FI_FJ_FK1G-0-8 un...	111	3e-20
gb AY311597.1	Gossypium hirsutum class III peroxidase (pod7) mR...	105	2e-18
emb FP100639.1	Phyllostachys edulis cDNA clone: bphyem110n02, f...	103	8e-18
emb FP099994.1	Phyllostachys edulis cDNA clone: bphyem210i11, f...	103	8e-18
dbj AB027752.1	Nicotiana tabacum mRNA for peroxidase, complete ...	96	2e-15
gb AY837788.2	Catharanthus roseus clone Prx4 putative secretory...	90	1e-13
gb FJ644943.1	Sesuvium portulacastrum peroxidase 1 (POD1) mRNA,...	88	5e-13
dbj AK242814.1	Oryza sativa Japonica Group cDNA, clone: J090061...	86	2e-12
ref NM_001072100.1	Oryza sativa (japonica cultivar-group) Os1lg...	86	2e-12
tpe BN000659.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	86	2e-12
dbj AB019228.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	86	2e-12
emb BX000512.1	Oryza sativa chromosome 11, . BAC OSJNBa0025K19 ...	86	2e-12
gb EF661875.2	Catharanthus roseus putative secretory peroxidase...	84	7e-12
ref NM_125225.1	Arabidopsis thaliana peroxidase, putative (AT5G...	80	1e-10
dbj AK117722.1	Arabidopsis thaliana At5g58390 mRNA for putative...	80	1e-10
gb AY085030.1	Arabidopsis thaliana clone 124846 mRNA, complete ...	80	1e-10
gb EZ329073.1	TSA: Artemisia annua strain Madagascar Contig1561...	76	2e-09

ref XM_002450087.1	Sorghum bicolor hypothetical protein, mRNA	76	2e-09
ref XM_002269882.1	PREDICTED: Vitis vinifera hypothetical prote...	76	2e-09
emb AM447728.2	Vitis vinifera contig VV78X018697.9, whole genom...	76	2e-09
ref XM_002278960.1	PREDICTED: Vitis vinifera hypothetical prote...	72	3e-08
gb AY206413.1	Ipomoea batatas anionic peroxidase swpb2 mRNA, co...	72	3e-08
gb EZ399860.1	TSA: Artemisia annua strain Uganda Contig16355, m...	70	1e-07
gb EZ145065.1	TSA: Artemisia annua strain Artemis Contig4471, m...	70	1e-07
gb EZ141680.1	TSA: Artemisia annua strain Artemis Contig1086, m...	70	1e-07
ref XM_002489001.1	Sorghum bicolor hypothetical protein (SORBID...	70	1e-07
ref XM_002441657.1	Sorghum bicolor hypothetical protein, mRNA	70	1e-07
emb AM456467.1	Vitis vinifera, whole genome shotgun sequence, c...	70	1e-07
gb GU230149.1	Ipomoea batatas anionic peroxidase mRNA, complete...	68	4e-07
ref XM_002268223.1	PREDICTED: Vitis vinifera hypothetical prote...	68	4e-07
gb FJ099755.1	Pinus taeda isolate 1286 anonymous locus 2_6350_0...	68	4e-07
emb CU231251.1	Populus EST from mild drought-stressed leaves	68	4e-07
gb AY206412.1	Ipomoea batatas anionic peroxidase swpb1 mRNA, co...	68	4e-07
dbj AK322204.1	Solanum lycopersicum cDNA, clone: LEFL1035AA07, ...	66	2e-06
ref XM_002328955.1	Populus trichocarpa predicted protein, mRNA	66	2e-06
ref XM_002319932.1	Populus trichocarpa predicted protein, mRNA	66	2e-06
gb AC214418.1	Populus trichocarpa clone POP106-D21, complete se...	66	2e-06
gb BT096974.1	Soybean clone JCVI-FLGm-21M8 unknown mRNA	64	7e-06
gb AC235472.1	Glycine max strain Williams 82 clone GM_WBc0099F2...	64	7e-06
gb FJ596178.1	Capsicum annuum peroxidase (POD) mRNA, complete cds	64	7e-06
gb EF433455.1	Ipomoea batatas basic peroxidase swpb4 mRNA, comp...	64	7e-06
gb AC235385.1	Glycine max strain Williams 82 clone GM_WBb0113B1...	62	3e-05
gb GQ258782.1	Brassica rapa peroxidase 52 mRNA, partial cds	60	1e-04
gb FJ099770.1	Pinus taeda isolate 1299 anonymous locus 2_6350_0...	60	1e-04
gb FJ099768.1	Pinus taeda isolate 1282 anonymous locus 2_6350_0...	60	1e-04
gb FJ099767.1	Pinus taeda isolate 1292 anonymous locus 2_6350_0...	60	1e-04
gb FJ099766.1	Pinus taeda isolate 1285 anonymous locus 2_6350_0...	60	1e-04
gb FJ099765.1	Pinus taeda isolate 1288 anonymous locus 2_6350_0...	60	1e-04
gb FJ099762.1	Pinus taeda isolate 1298 anonymous locus 2_6350_0...	60	1e-04
gb FJ099761.1	Pinus taeda isolate 1289 anonymous locus 2_6350_0...	60	1e-04
gb FJ099760.1	Pinus taeda isolate 1297 anonymous locus 2_6350_0...	60	1e-04
gb FJ099759.1	Pinus taeda isolate 1283 anonymous locus 2_6350_0...	60	1e-04
gb FJ099758.1	Pinus taeda isolate 1287 anonymous locus 2_6350_0...	60	1e-04
gb FJ099757.1	Pinus taeda isolate 1291 anonymous locus 2_6350_0...	60	1e-04
gb EF433456.1	Ipomoea batatas basic peroxidase swpb5 mRNA, comp...	60	1e-04
gb AC226196.1	Musa acuminata clone BAC MA4-125A12, complete seq...	60	1e-04
ref XM_001754018.1	Physcomitrella patens subsp. patens predicte...	60	1e-04
emb AM449831.1	Vitis vinifera, whole genome shotgun sequence, c...	60	1e-04
gb AY206414.1	Ipomoea batatas anionic peroxidase swpb3 mRNA, co...	60	1e-04
gb AF485265.1	Gossypium hirsutum class III peroxidase (pod3) mR...	60	1e-04
gb EZ328614.1	TSA: Artemisia annua strain Madagascar Contig1516...	58	4e-04
gb EZ256818.1	TSA: Artemisia annua strain Artemis Contig23488, ...	58	4e-04
gb EZ397212.1	TSA: Artemisia annua strain Uganda Contig13707, m...	58	4e-04
dbj AK328734.1	Solanum lycopersicum cDNA, clone: LEFL3035G12, H...	58	4e-04
gb AC235153.1	Glycine max strain Williams 82 clone GM_WBa0085L0...	58	4e-04
gb AC235140.1	Glycine max strain Williams 82 clone GM_WBa0068I0...	58	4e-04

emb AJ544515.1	Asparagus officinalis partial mRNA for peroxidas...	58	4e-04
ref XM_002521820.1	Ricinus communis Lignin-forming anionic pero...	56	0.002
ref XM_002521805.1	Ricinus communis Lignin-forming anionic pero...	56	0.002
ref XM_002521804.1	Ricinus communis Peroxidase 30 precursor, pu...	56	0.002
gb FJ529216.1	Cucumis sativus 1-aminocyclopropane-1-carboxylate...	56	0.002
ref XM_002450088.1	Sorghum bicolor hypothetical protein, mRNA	56	0.002
gb FJ050772.1	Pinus taeda isolate 4650 anonymous locus 0_13032_...	56	0.002
gb FJ050764.1	Pinus taeda isolate 4651 anonymous locus 0_13032_...	56	0.002
gb FJ050758.1	Pinus taeda isolate 4655 anonymous locus 0_13032_...	56	0.002
gb FJ050757.1	Pinus taeda isolate 4653 anonymous locus 0_13032_...	56	0.002
gb AF149278.1	AF149278 Phaseolus vulgaris peroxidase 3 precursor...	56	0.002
dbj AK320453.1	Solanum lycopersicum cDNA, clone: LEFL1009CA06, ...	54	0.006
dbj AK320190.1	Solanum lycopersicum cDNA, clone: LEFL1006BD07, ...	54	0.006
gb AC235342.1	Glycine max strain Williams 82 clone GM_WBb0088H1...	54	0.006
emb CT832689.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.006
emb CT832688.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.006
emb CT832687.1	Oryza sativa (indica cultivar-group) cDNA clone:...	54	0.006
ref NM_001072503.1	Oryza sativa (japonica cultivar-group) Os12g...	54	0.006
tpe BN000664.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	54	0.006
dbj AK069456.1	Oryza sativa Japonica Group cDNA clone:J023019E0...	54	0.006
emb X91172.1	R. sativus prxK1 gene	54	0.006
emb BX000510.1	Oryza sativa chromosome 12, . BAC OJ1769_D07 of ...	54	0.006
gb EZ315890.1	TSA: Artemisia annua strain Madagascar Contig2436...	52	0.025
gb EZ359220.1	TSA: Artemisia annua strain Uganda Contig6381, mR...	52	0.025
gb EZ166433.1	TSA: Artemisia annua strain Artemis Contig25839, ...	52	0.025
gb BT106781.1	Picea glauca clone GQ03010_F17 mRNA sequence	52	0.025
ref XM_002285606.1	PREDICTED: Vitis vinifera hypothetical prote...	52	0.025
gb AC235417.1	Glycine max strain Williams 82 clone GM_WBb0135A0...	52	0.025
ref XM_002334206.1	Populus trichocarpa predicted protein, mRNA	52	0.025
ref NM_001157951.1	Zea mays peroxidase 2 (LOC100285056), mRNA >...	52	0.025
gb BT044614.1	Arabidopsis thaliana unknown protein (At4g33420) ...	52	0.025
gb FJ099764.1	Pinus taeda isolate 1294 anonymous locus 2_6350_0...	52	0.025
gb FJ099763.1	Pinus taeda isolate 1290 anonymous locus 2_6350_0...	52	0.025
gb BT042071.1	Zea mays full-length cDNA clone ZM_BFb0125B03 mRN...	52	0.025
emb AM450885.2	Vitis vinifera contig VV78X220288.8, whole genom...	52	0.025
ref NM_119496.3	Arabidopsis thaliana peroxidase, putative (AT4G...	52	0.025
emb AM446475.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.025
emb AM436560.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.025
emb AM429435.1	Vitis vinifera, whole genome shotgun sequence, c...	52	0.025
ref NM_101322.1	Arabidopsis thaliana anionic peroxidase, putati...	52	0.025
gb AF453791.1	Ipomoea batatas anionic peroxidase (POD) gene, pr...	52	0.025
dbj AB193816.1	Pisum sativum mRNA for peroxidase, complete cds,...	52	0.025
dbj AK176812.1	Arabidopsis thaliana mRNA for peroxidase ATP17a ...	52	0.025
gb AY089094.1	Arabidopsis thaliana clone 32346 mRNA, complete s...	52	0.025
gb AC108072.3	Homo sapiens BAC clone RP11-704A16 from 2, comple...	52	0.025
gb AF451951.1	Arabidopsis thaliana class III peroxidase ATP32 m...	52	0.025
emb AL161583.2	Arabidopsis thaliana DNA chromosome 4, contig fr...	52	0.025
gb AC010657.3	AC010657 Genomic sequence for Arabidopsis thaliana...	52	0.025
emb AL035678.1	Arabidopsis thaliana DNA chromosome 4, BAC clone...	52	0.025

gb AC012188.2	F14L17 Sequence of BAC F14L17 from Arabidopsis tha...	52	0.025
gb EZ395724.1	TSA: Artemisia annua strain Uganda Contig12219, m...	50	0.099
gb EZ362599.1	TSA: Artemisia annua strain Uganda Contig9760, mR...	50	0.099
gb BT066765.1	Zea mays full-length cDNA clone ZM_BFb0066D03 mRN...	50	0.099
gb BT055307.1	Zea mays full-length cDNA clone ZM_BFc0167H14 mRN...	50	0.099
gb EU962146.1	Zea mays clone 240603 mRNA sequence	50	0.099
gb FJ070719.1	Pinus taeda isolate 7938 anonymous locus 0_3458_0...	50	0.099
gb FJ070718.1	Pinus taeda isolate 7947 anonymous locus 0_3458_0...	50	0.099
gb FJ070717.1	Pinus taeda isolate 7943 anonymous locus 0_3458_0...	50	0.099
gb FJ070716.1	Pinus taeda isolate 7950 anonymous locus 0_3458_0...	50	0.099
gb FJ070715.1	Pinus taeda isolate 7940 anonymous locus 0_3458_0...	50	0.099
gb FJ070714.1	Pinus taeda isolate 7948 anonymous locus 0_3458_0...	50	0.099
gb FJ070713.1	Pinus taeda isolate 7949 anonymous locus 0_3458_0...	50	0.099
gb FJ070712.1	Pinus taeda isolate 7952 anonymous locus 0_3458_0...	50	0.099
gb FJ070711.1	Pinus taeda isolate 7941 anonymous locus 0_3458_0...	50	0.099
gb FJ070710.1	Pinus taeda isolate 7951 anonymous locus 0_3458_0...	50	0.099
gb FJ070709.1	Pinus taeda isolate 7942 anonymous locus 0_3458_0...	50	0.099
gb FJ070708.1	Pinus taeda isolate 7953 anonymous locus 0_3458_0...	50	0.099
gb FJ070707.1	Pinus taeda isolate 7937 anonymous locus 0_3458_0...	50	0.099
gb FJ070706.1	Pinus taeda isolate 7946 anonymous locus 0_3458_0...	50	0.099
gb FJ070705.1	Pinus taeda isolate 7945 anonymous locus 0_3458_0...	50	0.099
gb FJ070703.1	Pinus taeda isolate 7939 anonymous locus 0_3458_0...	50	0.099
ref NM_001137528.1	Zea mays hypothetical protein LOC100192105 (...)	50	0.099
gb DQ244260.1	Zea mays clone 3973 mRNA sequence	50	0.099
tpe BN000615.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	50	0.099
dbj AP004731.3	Oryza sativa Japonica Group genomic DNA, chromos...	50	0.099
dbj AB007645.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	50	0.099
emb Y10465.1	S.oleracea mRNA for peroxidase, clone PC44	50	0.099
gb CP000102.1	Methanosphaera stadtmanae DSM 3091, complete genome	50	0.099
emb FP012230.5	Pig DNA sequence from clone CH242-162F1 on chrom...	48	0.39
gb EZ275595.1	TSA: Artemisia annua strain Madagascar Contig1982...	48	0.39
gb EZ286664.1	TSA: Artemisia annua strain Madagascar Contig1305...	48	0.39
gb EZ342046.1	TSA: Artemisia annua strain Uganda Contig9262, mR...	48	0.39
gb EZ321242.1	TSA: Artemisia annua strain Madagascar Contig7788...	48	0.39
gb EZ318330.1	TSA: Artemisia annua strain Madagascar Contig4876...	48	0.39
gb EZ247069.1	TSA: Artemisia annua strain Artemis Contig13739, ...	48	0.39
gb EZ258457.1	TSA: Artemisia annua strain Madagascar Contig1560...	48	0.39
gb EZ396283.1	TSA: Artemisia annua strain Uganda Contig12778, m...	48	0.39
gb EZ220993.1	TSA: Artemisia annua Contig18004	48	0.39
gb EZ366681.1	TSA: Artemisia annua strain Uganda Contig132, mRN...	48	0.39
gb EZ196247.1	TSA: Artemisia annua strain Artemis Contig9804, m...	48	0.39
gb EZ355157.1	TSA: Artemisia annua strain Uganda Contig2318, mR...	48	0.39
gb EZ173232.1	TSA: Artemisia annua strain Artemis Contig32638, ...	48	0.39
gb BT102799.1	Picea glauca clone GQ02016_E21 mRNA sequence	48	0.39
gb BT101612.1	Picea glauca clone GQ01308_P23 mRNA sequence	48	0.39
gb AC212861.3	Pongo abelii BAC clone CH276-236D6 from chromosom...	48	0.39
ref XM_002451803.1	Sorghum bicolor hypothetical protein, mRNA	48	0.39
gb AC235800.1	Solanum lycopersicum chromosome 3 clone C03HBa013...	48	0.39
ref XM_002285687.1	PREDICTED: Vitis vinifera hypothetical prote...	48	0.39

ref	XM_002269022.1	PREDICTED: Vitis vinifera hypothetical prote...	48	0.39
dbj	AK323976.1	Solanum lycopersicum cDNA, clone: LEFL1068DD08, ...	48	0.39
ref	XM_002320381.1	Populus trichocarpa predicted protein, mRNA	48	0.39
gb	CP001098.1	Halothermothrix orenii H 168, complete genome	48	0.39
gb	EF677600.1	Picea sitchensis clone WS02771_I11 unknown mRNA	48	0.39
gb	FJ050773.1	Pinus taeda isolate 4643 anonymous locus 0_13032_...	48	0.39
gb	FJ050771.1	Pinus taeda isolate 4657 anonymous locus 0_13032_...	48	0.39
gb	FJ050770.1	Pinus taeda isolate 4649 anonymous locus 0_13032_...	48	0.39
gb	FJ050769.1	Pinus taeda isolate 4648 anonymous locus 0_13032_...	48	0.39
gb	FJ050768.1	Pinus taeda isolate 4659 anonymous locus 0_13032_...	48	0.39
gb	FJ050767.1	Pinus taeda isolate 4658 anonymous locus 0_13032_...	48	0.39
gb	FJ050766.1	Pinus taeda isolate 4644 anonymous locus 0_13032_...	48	0.39
gb	FJ050765.1	Pinus taeda isolate 4645 anonymous locus 0_13032_...	48	0.39
gb	FJ050763.1	Pinus taeda isolate 4660 anonymous locus 0_13032_...	48	0.39
gb	FJ050762.1	Pinus taeda isolate 4647 anonymous locus 0_13032_...	48	0.39
gb	FJ050761.1	Pinus taeda isolate 4654 anonymous locus 0_13032_...	48	0.39
gb	FJ050760.1	Pinus taeda isolate 4646 anonymous locus 0_13032_...	48	0.39
gb	FJ050759.1	Pinus taeda isolate 4656 anonymous locus 0_13032_...	48	0.39
gb	FJ050756.1	Pinus taeda isolate 4652 anonymous locus 0_13032_...	48	0.39
gb	EF083074.1	Picea sitchensis clone WS02728_C07 unknown mRNA	48	0.39
gb	EU024896.1	Uncultured bacterium clone tgutfos2_Contig107 gen...	48	0.39
emb	BX548174.1	Prochlorococcus marinus MED4 complete genome	48	0.39
gb	CP000647.1	Klebsiella pneumoniae subsp. pneumoniae MGH 78578...	48	0.39
emb	AM454579.2	Vitis vinifera contig VV78X062755.15, whole geno...	48	0.39
emb	AM428729.2	Vitis vinifera contig VV78X273545.5, whole genom...	48	0.39
emb	AM462968.1	Vitis vinifera, whole genome shotgun sequence, c...	48	0.39
emb	AM473070.1	Vitis vinifera contig VV78X025151.6, whole genom...	48	0.39
emb	AM453059.1	Vitis vinifera, whole genome shotgun sequence, c...	48	0.39
emb	AM481723.1	Vitis vinifera contig VV78X090480.3, whole genom...	48	0.39
dbj	AP006865.1	Lotus japonicus genomic DNA, chromosome 2, clone...	48	0.39
dbj	AB049589.1	Avicennia marina PER mRNA for secretory peroxida...	48	0.39
emb	BX828399.1	Arabidopsis thaliana Full-length cDNA Complete s...	48	0.39
emb	BX832751.1	Arabidopsis thaliana Full-length cDNA Complete s...	48	0.39
dbj	AB010692.1	Arabidopsis thaliana genomic DNA, chromosome 5, ...	48	0.39
emb	Y10467.1	S.oleracea mRNA for peroxidase, clone PC23	48	0.39
ref	XM_670091.1	Plasmodium berghei strain ANKA hypothetical pro...	48	0.39
gb	AF109124.1	AF109124 Ipomoea batatas anionic peroxidase swpa2 ...	48	0.39
gb	EZ295716.1	TSA: Artemisia annua strain Madagascar Contig1601...	46	1.5
gb	EZ256521.1	TSA: Artemisia annua strain Artemis Contig23191, ...	46	1.5
gb	EZ360402.1	TSA: Artemisia annua strain Uganda Contig7563, mR...	46	1.5
gb	EZ150610.1	TSA: Artemisia annua strain Artemis Contig10016, ...	46	1.5
gb	AC233130.7	Solanum lycopersicum strain Heinz 1706 chromosome...	46	1.5
gb	AC239433.3	Solanum lycopersicum strain Heinz 1706 chromosome...	46	1.5
gb	CP001633.1	Francisella tularensis subsp. tularensis NE061598...	46	1.5
ref	NW_003037936.1	Schistosoma mansoni genome sequence supercon...	46	1.5
gb	BT095984.1	Soybean clone JCVI-FLGm-20M19 unknown mRNA	46	1.5
gb	BT093602.1	Soybean clone JCVI-FLGm-17D17 unknown mRNA	46	1.5
gb	AC237089.1	Oryza granulata clone OG_ABa0096023, complete seq...	46	1.5
ref	XM_002448761.1	Sorghum bicolor hypothetical protein, mRNA	46	1.5

ref	XM_002426020.1	Pediculus humanus corporis synaptonemal comp...	46	1.5
emb	AJ749949.2	Francisella tularensis subsp. tularensis SCHU S4...	46	1.5
emb	FN357570.1	Schistosoma mansoni genome sequence supercontig ...	46	1.5
emb	FN357441.1	Schistosoma mansoni genome sequence supercontig ...	46	1.5
gb	BT086529.1	Zea mays full-length cDNA clone ZM_BFc0177005 mRN...	46	1.5
gb	EZ053600.1	TSA: Zea mays contig54722, mRNA sequence	46	1.5
emb	AL844509.2	Plasmodium falciparum 3D7 chromosome 13	46	1.5
gb	AC235371.1	Glycine max strain Williams 82 clone GM_WBb0104B0...	46	1.5
gb	AC235196.1	Glycine max strain Williams 82 clone GM_WBb0014G1...	46	1.5
gb	AC235187.1	Glycine max strain Williams 82 clone GM_WBb0010C0...	46	1.5
gb	AC235182.1	Glycine max strain Williams 82 clone GM_WBb0008C1...	46	1.5
gb	AC235129.1	Glycine max strain Williams 82 clone GM_WBa0052I0...	46	1.5
ref	XM_002319931.1	Populus trichocarpa predicted protein, mRNA	46	1.5
ref	NM_001158468.1	Zea mays peroxidase 52 (LOC100285577), mRNA ...	46	1.5
gb	EU954765.1	Zea mays clone 1482328 mRNA sequence	46	1.5
gb	EU951047.1	Zea mays clone 687198 mRNA sequence	46	1.5
tpg	BK006741.1	TPA: TPA_reasm: Francisella tularensis subsp. ho...	46	1.5
gb	FJ088527.1	Pinus taeda isolate 6658 anonymous locus 2_10243_...	46	1.5
gb	FJ088526.1	Pinus taeda isolate 6661 anonymous locus 2_10243_...	46	1.5
gb	FJ088525.1	Pinus taeda isolate 6650 anonymous locus 2_10243_...	46	1.5
gb	FJ088524.1	Pinus taeda isolate 6653 anonymous locus 2_10243_...	46	1.5
gb	FJ088523.1	Pinus taeda isolate 6663 anonymous locus 2_10243_...	46	1.5
gb	FJ088522.1	Pinus taeda isolate 6662 anonymous locus 2_10243_...	46	1.5
gb	FJ088521.1	Pinus taeda isolate 6654 anonymous locus 2_10243_...	46	1.5
gb	FJ088520.1	Pinus taeda isolate 6655 anonymous locus 2_10243_...	46	1.5
gb	FJ088519.1	Pinus taeda isolate 6657 anonymous locus 2_10243_...	46	1.5
gb	FJ088518.1	Pinus taeda isolate 6664 anonymous locus 2_10243_...	46	1.5
gb	FJ088517.1	Pinus taeda isolate 6651 anonymous locus 2_10243_...	46	1.5
gb	FJ088516.1	Pinus taeda isolate 6649 anonymous locus 2_10243_...	46	1.5
gb	FJ088515.1	Pinus taeda isolate 6666 anonymous locus 2_10243_...	46	1.5
gb	FJ088514.1	Pinus taeda isolate 6660 anonymous locus 2_10243_...	46	1.5
gb	FJ088513.1	Pinus taeda isolate 6665 anonymous locus 2_10243_...	46	1.5
gb	FJ088512.1	Pinus taeda isolate 6656 anonymous locus 2_10243_...	46	1.5
gb	FJ088511.1	Pinus taeda isolate 4039 anonymous locus 2_10243_...	46	1.5
gb	FJ088510.1	Pinus taeda isolate 4033 anonymous locus 2_10243_...	46	1.5
gb	FJ088509.1	Pinus taeda isolate 4024 anonymous locus 2_10243_...	46	1.5
gb	FJ088508.1	Pinus taeda isolate 4026 anonymous locus 2_10243_...	46	1.5
gb	FJ088507.1	Pinus taeda isolate 4025 anonymous locus 2_10243_...	46	1.5
gb	FJ088506.1	Pinus taeda isolate 4031 anonymous locus 2_10243_...	46	1.5
gb	FJ088505.1	Pinus taeda isolate 4032 anonymous locus 2_10243_...	46	1.5
gb	FJ088504.1	Pinus taeda isolate 4037 anonymous locus 2_10243_...	46	1.5
gb	FJ088503.1	Pinus taeda isolate 4022 anonymous locus 2_10243_...	46	1.5
gb	FJ088502.1	Pinus taeda isolate 4028 anonymous locus 2_10243_...	46	1.5
gb	FJ088501.1	Pinus taeda isolate 4034 anonymous locus 2_10243_...	46	1.5
gb	FJ088500.1	Pinus taeda isolate 4038 anonymous locus 2_10243_...	46	1.5
gb	FJ088499.1	Pinus taeda isolate 4030 anonymous locus 2_10243_...	46	1.5
gb	FJ088498.1	Pinus taeda isolate 4035 anonymous locus 2_10243_...	46	1.5
gb	FJ088497.1	Pinus taeda isolate 4036 anonymous locus 2_10243_...	46	1.5
gb	FJ088496.1	Pinus taeda isolate 4029 anonymous locus 2_10243_...	46	1.5

gb FJ088495.1	Pinus taeda isolate 4027 anonymous locus 2_10243_...	46	1.5
gb FJ088494.1	Pinus taeda isolate 4023 anonymous locus 2_10243_...	46	1.5
gb AC189631.2	Brassica rapa subsp. pekinensis clone KBrS003K07,...	46	1.5
dbj AB374543.1	Spirometra erinaceieuropaei mitochondrial DNA, c...	46	1.5
ref XM_001336009.2	PREDICTED: Danio rerio hypothetical LOC10000...	46	1.5
dbj AP010414.1	Lotus japonicus genomic DNA, chromosome 6, clone...	46	1.5
dbj AP009714.1	Lotus japonicus genomic DNA, clone: Ljt08001, TM...	46	1.5
gb CP001056.1	Clostridium botulinum B str. Eklund 17B, complete...	46	1.5
gb CP000915.1	Francisella tularensis subsp. mediasiatica FSC147...	46	1.5
ref XM_001751456.1	Physcomitrella patens subsp. patens predicte...	46	1.5
gb AC206008.3	Pongo abelii BAC clone CH276-282M20 from chromoso...	46	1.5
gb AC216474.1	Populus trichocarpa clone POP081-J22, complete se...	46	1.5
ref XM_001713455.1	Guillardia theta hypothetical protein (orf43...	46	1.5
gb EF087739.1	Picea sitchensis clone WS02740_P19 unknown mRNA	46	1.5
gb AC213540.1	Populus trichocarpa clone POP053-A08, complete se...	46	1.5
gb EU060241.1	Uncultured bacterium clone LMOABA27ZD09RM1 genomi...	46	1.5
gb CP000803.1	Francisella tularensis subsp. holarctica FTNF002-...	46	1.5
gb EF645823.1	Manihot esculenta cultivar MTA18 cationic peroxid...	46	1.5
ref XM_001479242.1	PREDICTED: Mus musculus similar to MK-5 type...	46	1.5
emb AM457942.2	Vitis vinifera contig VV78X124814.1, whole genom...	46	1.5
emb AM446264.2	Vitis vinifera contig VV78X146694.5, whole genom...	46	1.5
emb AM489166.2	Vitis vinifera contig VV78X028632.7, whole genom...	46	1.5
emb AM444565.2	Vitis vinifera contig VV78X153928.11, whole geno...	46	1.5
emb AM436965.2	Vitis vinifera contig VV78X063704.11, whole geno...	46	1.5
ref NM_117724.3	Arabidopsis thaliana peroxidase 40 (PER40) (P40...	46	1.5
gb CP000608.1	Francisella tularensis subsp. tularensis WY96-341...	46	1.5
ref NM_001110031.1	Danio rerio zgc:136903 (zgc:136903), mRNA >g...	46	1.5
emb BX293980.2	Mycoplasma mycoides subsp. mycoides SC str. PG1,...	46	1.5
emb AM485714.1	Vitis vinifera, whole genome shotgun sequence, c...	46	1.5
ref NM_001097269.1	Xenopus (Silurana) tropicalis hypothetical p...	46	1.5
gb CP000439.1	Francisella tularensis subsp. novicida U112, comp...	46	1.5
gb EF055261.1	Sesbania rostrata peroxidase 1 (prx1) mRNA, compl...	46	1.5
emb CT027756.10	Zebrafish DNA sequence from clone DKEY-95F11 in...	46	1.5
gb CP000437.1	Francisella tularensis subsp. holarctica OSU18, c...	46	1.5
ref XM_623898.2	PREDICTED: Apis mellifera similar to Muscle pro...	46	1.5
emb AM286280.1	Francisella tularensis subsp. tularensis strain ...	46	1.5
gb DQ681941.1	Synthetic construct Francisella tularensis clone ...	46	1.5
ref NM_120616.2	Arabidopsis thaliana peroxidase, putative (AT5G...	46	1.5
gb AC151347.2	Xenopus (Silurana) tropicalis clone ISB-394A6, co...	46	1.5
gb BT017949.1	Zea mays clone EL01N0522B07.c mRNA sequence	46	1.5
gb BT013033.1	Lycopersicon esculentum clone 114281R, mRNA sequence	46	1.5
gb BT011747.1	Arabidopsis thaliana At4g16270 gene, complete cds	46	1.5
gb AC125096.3	Mus musculus BAC clone RP24-181K19 from chromosom...	46	1.5
gb AC131109.3	Mus musculus BAC clone RP23-362M7 from chromosome...	46	1.5
gb AY065270.1	Arabidopsis thaliana putative peroxidase (At5g053...	46	1.5
dbj AK137657.1	Mus musculus adult female vagina cDNA, RIKEN ful...	46	1.5
emb AJ809342.1	Picea abies mRNA for peroxidase (px7 gene)	46	1.5
emb AJ809341.1	Picea abies mRNA for peroxidase (px6 gene)	46	1.5
emb CR690313.2	Tetraodon nigroviridis full-length cDNA	46	1.5

gb AC026100.19	Homo sapiens 3 BAC RP11-449F7 (Roswell Park Canc...	46	1.5
gb AC084740.5	Homo sapiens BAC clone RP11-423E20 from 4, comple...	46	1.5
gb AC099520.2	Homo sapiens chromosome 5 clone RP11-6N13, comple...	46	1.5
gb AC012602.4	Homo sapiens chromosome 5 clone CTC-328N13, compl...	46	1.5
gb AF165818.4	Guillardia theta nucleomorph chromosome 1, comple...	46	1.5
emb BX005227.12	Zebrafish DNA sequence from clone CH211-286C23 ...	46	1.5
emb BX548071.7	Zebrafish DNA sequence from clone DKEY-25L23 in ...	46	1.5
dbj AK175982.1	Arabidopsis thaliana mRNA, complete cds, clone: ...	46	1.5
dbj AK175661.1	Arabidopsis thaliana mRNA, complete cds, clone: ...	46	1.5
emb BX537275.8	Zebrafish DNA sequence from clone DKEYP-120E12 i...	46	1.5
emb BX537269.8	Zebrafish DNA sequence from clone DKEY-181H1 in ...	46	1.5
emb BX826801.1	Arabidopsis thaliana Full-length cDNA Complete s...	46	1.5
dbj AP005846.2	Oryza sativa Japonica Group genomic DNA, chromos...	46	1.5
emb BX537286.4	Zebrafish DNA sequence from clone DKEY-28J4 in l...	46	1.5
dbj AP006135.1	Lotus japonicus genomic DNA, chromosome 1, clone...	46	1.5
gb AC008970.4	AC008970 Homo sapiens chromosome 5 clone CTD-2374C...	46	1.5
emb AL161543.2	Arabidopsis thaliana DNA chromosome 4, contig fr...	46	1.5
emb AL132978.1	Arabidopsis thaliana DNA chromosome 3, BAC clone...	46	1.5
emb Z97340.2	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA ...	46	1.5
emb Z82992.1	A. thaliana FCA gene encoding FCA alpha, beta, gamm...	46	1.5
emb AM233362.1	Francisella tularensis subsp. holarctica LVS com...	46	1.5
gb AC151343.2	Xenopus (Silurana) tropicalis clone ISB-373E17, c...	46	1.5
gb AC155316.6	Mus musculus BAC clone RP23-181P9 from chromosome...	46	1.5
gb AC166091.3	Glycine max clone gmw1-1lj16, complete sequence	46	1.5
ref XM_733026.1	Plasmodium chabaudi chabaudi hypothetical prote...	46	1.5
emb AL935040.6	Zebrafish DNA sequence from clone CH211-176L21, ...	46	1.5
gb AY108407.1	Zea mays PC0110242 mRNA sequence	46	1.5
emb AL157764.12	Human DNA sequence from clone RP11-562E17 on ch...	46	1.5
gb AF145349.1	AF145349 Glycine max peroxidase (Prx3) mRNA, parti...	46	1.5
gb AF078691.1	AF078691 Manihot esculenta peroxidase gene, partia...	46	1.5
gb AF067188.1	AF067188 Beta vulgaris cell wall peroxidase mRNA, ...	46	1.5
gb L36231.1	SSNPX12A Stylosanthes humilis peroxidase (px12) mRNA...	46	1.5
gb L36110.1	SSNPEROXIA Stylosanthes humilis peroxidase mRNA	46	1.5
emb FN554766.1	Escherichia coli 042 complete genome	44	6.1
emb FP236458.5	Zebrafish DNA sequence from clone CH73-374P12, c...	44	6.1
gb EZ396827.1	TSA: Artemisia annua strain Uganda Contig13322, m...	44	6.1
gb AC239575.2	Solanum lycopersicum strain Heinz 1706 clone hba-...	44	6.1
ref NG_016144.1	Homo sapiens inositol 1,4,5-triphosphate recept...	44	6.1
gb BT106566.1	Picea glauca clone GQ03005_B15 mRNA sequence	44	6.1
gb FJ415216.1	Gossypium hirsutum clone Ghpox5 class III peroxid...	44	6.1
emb CU633361.7	Pig DNA sequence from clone CH242-1G8 on chromos...	44	6.1
gb AE014187.2	Plasmodium falciparum 3D7 chromosome 14, complete...	44	6.1
gb DQ676955.1	Ipomoea batatas anionic peroxidase (swpa4) gene, ...	44	6.1
emb FP099688.1	Phyllostachys edulis cDNA clone: bphylf045i10, f...	44	6.1
emb FP094559.1	Phyllostachys edulis cDNA clone: bphylf061m22, f...	44	6.1
emb FP093329.1	Phyllostachys edulis cDNA clone: bphyst031i16, f...	44	6.1
emb FP092972.1	Phyllostachys edulis cDNA clone: bphylf025d09, f...	44	6.1
emb FP091819.1	Phyllostachys edulis cDNA clone: bphyem202n22, f...	44	6.1
emb FP101172.1	Phyllostachys edulis cDNA clone: bphyem105e15, f...	44	6.1

ref XM_002442921.1	Sorghum bicolor hypothetical protein, mRNA	44	6.1
ref XM_002455522.1	Sorghum bicolor hypothetical protein, mRNA	44	6.1
ref XM_002455521.1	Sorghum bicolor hypothetical protein, mRNA	44	6.1
ref XM_002432395.1	Pediculus humanus corporis conserved hypothe...	44	6.1
gb EU725468.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725467.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725466.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725465.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725464.1	Triticum aestivum class III peroxidase (Prx109-B)...	44	6.1
gb EU725463.1	Triticum aestivum class III peroxidase (Prx109-A)...	44	6.1
gb AC216032.2	Oryza minuta clone OM_Ba0196N15, complete sequence	44	6.1
gb EZ063624.1	TSA: Zea mays contig64746, mRNA sequence	44	6.1
emb AL844507.2	Plasmodium falciparum 3D7 chromosome 8	44	6.1
dbj AK329676.1	Solanum lycopersicum cDNA, clone: LEFL3153D08, H...	44	6.1
gb AC235246.1	Glycine max strain Williams 82 clone GM_WBb0033G1...	44	6.1
gb AC235231.1	Glycine max strain Williams 82 clone GM_WBb0026L1...	44	6.1
gb AC235115.1	Glycine max strain Williams 82 clone GM_WBa0021N1...	44	6.1
gb AE013600.1	Mus musculus piebald deletion region complete seq...	44	6.1
emb AL844508.1	Plasmodium falciparum 3D7 chromosome 9	44	6.1
ref XM_002338588.1	Populus trichocarpa predicted protein, mRNA	44	6.1
ref XM_002336305.1	Populus trichocarpa predicted protein, mRNA	44	6.1
ref XM_002303984.1	Populus trichocarpa predicted protein, mRNA	44	6.1
gb BT061140.1	Zea mays full-length cDNA clone ZM_BFb0114015 mRN...	44	6.1
emb CU928163.2	Escherichia coli UMN026 chromosome, complete genome	44	6.1
emb CU928164.2	Escherichia coli IAI39 chromosome, complete genome	44	6.1
dbj AK245281.1	Glycine max cDNA, clone: GMFL01-25-021	44	6.1
gb EU960147.1	Zea mays clone 222156 mRNA sequence	44	6.1
gb EU945238.1	Zea mays clone 245264 mRNA sequence	44	6.1
gb AC232892.1	Oryza officinalis clone 00_Ba0082D20, complete s...	44	6.1
dbj AP010895.1	Solanum lycopersicum DNA, chromosome 8, clone: C...	44	6.1
gb FJ078274.1	Pinus taeda isolate 5928 anonymous locus 0_6659_0...	44	6.1
gb FJ078266.1	Pinus taeda isolate 5925 anonymous locus 0_6659_0...	44	6.1
gb FJ078265.1	Pinus taeda isolate 5919 anonymous locus 0_6659_0...	44	6.1
gb FJ078264.1	Pinus taeda isolate 5914 anonymous locus 0_6659_0...	44	6.1
gb FJ078263.1	Pinus taeda isolate 5916 anonymous locus 0_6659_0...	44	6.1
gb FJ078262.1	Pinus taeda isolate 5915 anonymous locus 0_6659_0...	44	6.1
gb FJ078261.1	Pinus taeda isolate 5922 anonymous locus 0_6659_0...	44	6.1
gb BT038706.1	Zea mays full-length cDNA clone ZM_BFb0310H17 mRN...	44	6.1
gb BT037971.1	Zea mays full-length cDNA clone ZM_BFb0205C16 mRN...	44	6.1
ref NM_001143045.1	Zea mays hypothetical protein LOC100216632 (...)	44	6.1
ref NM_001137329.1	Zea mays hypothetical protein LOC100191905 (...)	44	6.1
gb CP001110.1	Pelodictyon phaeoclathratiforme BU-1, complete ge...	44	6.1
gb EU795178.1	Uncultured bacterium HF0010_09016 genomic sequence	44	6.1
gb CP000970.1	Escherichia coli SMS-3-5, complete genome	44	6.1
emb CU570896.5	Zebrafish DNA sequence from clone DKEY-194E13 in...	44	6.1
gb EF444530.1	Oryza sativa Japonica Group putative peroxidase m...	44	6.1
ref XM_001740672.1	Entamoeba dispar SAW760 F-box/leucine rich r...	44	6.1
gb AC216704.1	Solanum lycopersicum chromosome 2 clone C02HBa023...	44	6.1
emb CU570678.3	M.truncatula DNA sequence from clone MTH2-16J21 ...	44	6.1

gb AC215650.1	Populus trichocarpa clone POP108-K22, complete se...	44	6.1
gb AC215390.1	Solanum lycopersicum chromosome 2 clone C02HBa012...	44	6.1
ref XM_001712135.1	Hemiselms andersenii hypothetical protein (...)	44	6.1
gb CP000881.1	Hemiselms andersenii chromosome 1, complete sequ...	44	6.1
gb AC210491.1	Oryza glaberrima clone OG_BBa0088K23, complete se...	44	6.1
ref XM_001553571.1	Botryotinia fuckeliana B05.10 60S ribosomal ...	44	6.1
gb EF533695.1	Glycine max clone BAC GM_WBb098N15, complete sequ...	44	6.1
emb AM483376.2	Vitis vinifera contig VV78X083975.15, whole geno...	44	6.1
emb AM466347.2	Vitis vinifera contig VV78X176098.3, whole genom...	44	6.1
emb AM464800.2	Vitis vinifera contig VV78X220659.11, whole geno...	44	6.1
emb AM445395.2	Vitis vinifera contig VV78X136138.6, whole genom...	44	6.1
emb AM434275.2	Vitis vinifera contig VV78X203901.6, whole genom...	44	6.1
emb CT025903.11	Zebrafish DNA sequence from clone DKEY-66H5 in ...	44	6.1
emb AM432525.2	Vitis vinifera contig VV78X143782.10, whole geno...	44	6.1
emb AM451582.2	Vitis vinifera contig VV78X210575.8, whole genom...	44	6.1
ref XM_001446891.1	Paramecium tetraurelia hypothetical protein ...	44	6.1
ref XM_001428564.1	Paramecium tetraurelia hypothetical protein ...	44	6.1
ref NM_129711.3	Arabidopsis thaliana electron carrier/ heme bin...	44	6.1
ref NM_126037.4	Arabidopsis thaliana peroxidase 72 (PER72) (P72...	44	6.1
dbj AB270792.1	Malus x domestica MdSFBB9-alpha, S9-RNase, MdSFB...	44	6.1
gb EF421197.1	Nelumbo nucifera cationic peroxidase (CP) mRNA, c...	44	6.1
ref XM_001350114.1	Plasmodium falciparum 3D7 hypothetical prote...	44	6.1
ref XM_001349842.1	Plasmodium falciparum 3D7 hypothetical prote...	44	6.1
gb AC187618.3	Pan troglodytes BAC clone CH251-584I16 from chrom...	44	6.1
emb AM463654.1	Vitis vinifera contig VV78X012147.8, whole genom...	44	6.1
emb AM464677.1	Vitis vinifera contig VV78X194278.8, whole genom...	44	6.1
emb AM475805.1	Vitis vinifera contig VV78X097027.7, whole genom...	44	6.1
gb AE014298.4	Drosophila melanogaster chromosome X, complete se...	44	6.1
gb CP000551.1	Prochlorococcus marinus str. AS9601, complete genome	44	6.1
gb AC192762.3	Pan troglodytes BAC clone CH251-676011 from chrom...	44	6.1
emb CT961058.16	M.truncatula DNA sequence from clone MTH2-80N17...	44	6.1
ref XM_001032614.1	Tetrahymena thermophila conserved hypothetic...	44	6.1
gb AC120193.5	Homo sapiens chromosome 8, clone RP11-10H17, comp...	44	6.1
gb AC185364.2	Populus trichocarpa clone Pop1-63B23, complete se...	44	6.1
emb CT830771.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	6.1
emb CT836342.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	6.1
emb CT828052.1	Oryza sativa (indica cultivar-group) cDNA clone:...	44	6.1
dbj AK243473.1	Oryza sativa Japonica Group cDNA, clone: J100072...	44	6.1
ref NM_001071707.1	Oryza sativa (japonica cultivar-group) Os10g...	44	6.1
ref NM_001071706.1	Oryza sativa (japonica cultivar-group) Os10g...	44	6.1
ref NM_001061107.1	Oryza sativa (japonica cultivar-group) Os05g...	44	6.1
ref NM_001055328.1	Oryza sativa (japonica cultivar-group) Os03g...	44	6.1
ref NM_001052935.1	Oryza sativa (japonica cultivar-group) Os02g...	44	6.1
ref NM_001049442.1	Oryza sativa (japonica cultivar-group) Os01g...	44	6.1
emb CT827810.6	Zebrafish DNA sequence from clone DKEY-120E24 in...	44	6.1
emb AM231674.1	Prunus dulcis partial s-RNase gene for ribonucle...	44	6.1
emb AM293547.1	Picea abies mRNA for properoxidase (px17 gene), ...	44	6.1
tpe BN000657.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000656.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1

tpe BN000598.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000562.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000559.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000544.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
tpe BN000535.1	TPA: TPA_inf: Oryza sativa (japonica cultivar-gr...	44	6.1
dbj AK227717.1	Arabidopsis thaliana mRNA for peroxidase, comple...	44	6.1
gb AY206411.1	Ipomoea batatas anionic peroxidase swpa6 mRNA, co...	44	6.1
gb AY206409.1	Ipomoea batatas anionic peroxidase swpa4 mRNA, co...	44	6.1
gb AC154194.2	Mus musculus BAC clone RP24-401L2 from chromosome...	44	6.1
gb AC102440.12	Mus musculus chromosome 1, clone RP24-146C18, co...	44	6.1
gb AC087552.3	Oryza sativa Japonica Group chromosome 5 clone P0...	44	6.1
gb AC091473.2	Mus musculus chromosome X clones RP21-114F21, RP2...	44	6.1
gb AE017263.1	Mesoplasma florum L1 complete genome	44	6.1
gb AC006353.3	Homo sapiens PAC clone RP5-1062J16 from 7, comple...	44	6.1
gb AC132451.3	Mus musculus BAC clone RP23-194C20 from chromosom...	44	6.1
gb AC123834.4	Mus musculus BAC clone RP24-132N9 from chromosome...	44	6.1
gb AC133523.3	Mus musculus BAC clone RP23-34E20 from 19, comple...	44	6.1
gb AC126691.3	Mus musculus BAC clone RP23-221H11 from 14, compl...	44	6.1
gb AC069248.4	Homo sapiens chromosome 3 clone RP11-6I21 map 3p,...	44	6.1
gb AC113010.10	Mus musculus chromosome 18, clone RP23-172F6, co...	44	6.1
gb AC155955.2	Xenopus (Silurana) tropicalis clone CH216-151P9, ...	44	6.1
dbj AP007151.1	Aspergillus oryzae RIB40 DNA, SC005	44	6.1
gb BT008727.1	Arabidopsis thaliana At2g41480 gene, complete cds	44	6.1
gb BT008314.1	Arabidopsis thaliana At5g66390 gene, complete cds	44	6.1
emb BX546477.9	Zebrafish DNA sequence from clone DKEYP-79C5 in ...	44	6.1
emb BX842700.35	Zebrafish DNA sequence from clone DKEY-2P18 in ...	44	6.1
gb AC161005.4	Pan troglodytes BAC clone CH251-668M6 from chromo...	44	6.1
ref XM_651154.1	Entamoeba histolytica HM-1:IMSS hypothetical pr...	44	6.1
gb AC161283.2	Pan troglodytes BAC clone CH251-354N8 from chromo...	44	6.1
dbj AK081398.1	Mus musculus 16 days embryo head cDNA, RIKEN ful...	44	6.1
gb AY139994.1	Arabidopsis thaliana putative peroxidase (At2g414...	44	6.1
gb AC074196.14	Oryza sativa chromosome 10 BAC OSJNBa0040D23 gen...	44	6.1
gb AC105363.2	Oryza sativa Japonica Group chromosome 3 clone OJ...	44	6.1
gb AC113349.2	Homo sapiens chromosome 5 clone CTD-2544H17, comp...	44	6.1

>gb|BT093225.1| Soybean clone JCVI-FLGm-17C9 unknown mRNA

Length = 1274

Score = 1039 bits (524), Expect = 0.0

Identities = 539/544 (99%)

Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

|||||

Sbjct: 639 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 580

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908

|||||
Sbjct: 579 accaacataggaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 520

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||

Sbjct: 519 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 460

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 459 tacttcaagaacctcggttcagaagaagggtttcctccactctgatcagcaactgttcaac 400

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 399 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttcccctct 340

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||

Sbjct: 339 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 280

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtcttgaatattaagggt 2208
|||

Sbjct: 279 gaagtcaggaagaattgtagaaggattaactaatttaattcagtcttgaatattaagggt 220

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 2268
|||||

Sbjct: 219 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 160

Query: 2269 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 2328
|||||

Sbjct: 159 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 100

Query: 2329 tccc 2332
|||

Sbjct: 99 tccc 96

Score = 525 bits (265), Expect = e-145
Identities = 274/277 (98%)
Strand = Plus / Minus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567
|||||
Sbjct: 1272 acaccctttcaatcaaacacaaacactcgaagtactaagttagtgtgttcgagcaaatta 1213

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
|||||
Sbjct: 1212 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 1153

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
|||||
Sbjct: 1152 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 1093

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttct 747
|||||
Sbjct: 1092 tcctctgtgaaatccgcagtgcgaatctgccatatctaaggagaccgcgatgggtgcttct 1033

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 1032 ctcttcgcttggttcttccacgattgctttgtcaatg 996

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 996 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 937

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 936 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 877

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 876 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 817

Query: 1337 tctgttcagatt 1348
|||||

Score = 333 bits (168), Expect = 5e-87
Identities = 168/168 (100%)
Strand = Plus / Minus

Query: 1538 tctgtgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 744 tctgtgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 685

>gb|BT093496.1| Soybean clone JCVI-FLGm-17I24 unknown mRNA
Length = 1217

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 631 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 690

```
Query: 1849  accaacatagaaaccgcatttgcaggactaggcagcaaagctgccctagaacatcaggg 1908
              | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 691    agcaacatagacaccgcatttgcaggggcaaggcaacaaagctgcccagaacatcaggg 750
```

```

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
          ||||| ||||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 751 tcaggggacaataatcttgcaacgcttgatcttcaaactccaaccgaattcgacaactac 810

```

Query: 1969 t a c t t t c a a g a a c c t c g t t c a g a a g a g g t c t c t c c a c t c t g a t c a g c a a c t g t t c a a c 2028

Sbjct: 811 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 870

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 871 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgagctccttctcctct 930

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||

Sbjct: 931 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaacgga 990

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagtcttgaatattaagg 2206
|||||

Sbjct: 991 gaaatcaggaagaattgtagaaggattaactaattactaattgagctctccaatattaagg 1050

Query: 2207 gtc---ctacacatacgcaagcaatttaattgtgtttaataagttgttaaaacatgtttt 2263
|||

Sbjct: 1051 gtcctactacacatacgcaagcaatttaattgtgtttaataagttgttaaaacatgtttt 1110

Query: 2264 ggttgtattttggattcc 2281

|||||

Sbjct: 1111 ggttgtgttttggattcc 1128

Score = 412 bits (208), Expect = e-111

Identities = 260/277 (93%), Gaps = 4/277 (1%)

Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtggtttgagcaaatta 567
|||||

Sbjct: 2 acaccctctcaagcaaacacaaacacttgaagtactaagttagtggtttgagcaaaa--- 58

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
|||||

Sbjct: 59 -ctatggcttcgttttgttctagattgaccatttgtttggctctgtttgtcctcatattg 117

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
|||||

Sbjct: 118 gggagtgccaatgcccaactttctacaaacttctactaccattcgtgtccaaacctcttc 177

Query: 688 tcctctgtgaaatccacagtgaatctgccatatctaaggagacccgcatgggtgcttct 747
||| |||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct: 178 tccactgtgaaatccacagtgaatctgccatatcaaaggagacccgcatgggtgcttct 237

Query: 748 ctctctcgcttgttcttccacgattgctttgtcaatg 784
|||| ||| ||||||||||||||||||||
Sbjct: 238 ctctccgcccgttcttccacgattgctttgtcaatg 274

Score = 331 bits (167), Expect = 2e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 274 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||||||||||||||||||| ||||| ||||||||||||||||||||
Sbjct: 334 aaccccaacaggaactctgctcgtggatacagggtcattgacaacattaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgttctcgtcgcagatatccttgccatcgctgccagagac 1336
||||| |||||||||||| |||||||||||||||||||| |||||||||
Sbjct: 394 gagaaagcatgtccaggagttgtctcgtcgcagatatccttgccatagctgccagagac 453

Query: 1337 tctgttcagat 1347
|||||||
Sbjct: 454 tctgttcagat 464

Score = 293 bits (148), Expect = 4e-75
Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||||||| ||||||||||||||||||||
Sbjct: 466 cttggaggccctagtgtgaatgttaaagttggaagaagagacgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||||||||||||||| ||||||||||||||||||||

Sbjct: 526 tctgctgctaacaatggcatccctccaccacttcaaaccttaaccaactcatctcaaga 585

Sbjct: 586 ttcagegctcttggactttccaccaaggacttggtcgccttgtccggt 633

Score = 176 bits (89), Expect = 6e-40
Identities = 304/376 (80%)
Strand = Plus / Plus

Sbjct: 583 cacacaattggacaagcaaggtgtacaaat ttttagggcacgaatctacaacgagaccaac 642

Sbjct: 643 ataaatgctgcatngctagcacgaggcaatcaaattgcccaaaggcatcaggatcaggt 702

Sbjct: 703 gacaacaatttggcacctcttgatcttcagactcctagttcttttgacaacaactacttc 762

Sbjct: 763 aagaaccttgttcagaacaagggtcttctccattcagaccaacaactttttaacggcggg 822

Sbjct: 823 tccaccaactcaatagtgagtggttatagtactagcccaagctctttttcctctgatttt 882

Sbjct: 883 gccgctgctatgatcaagatgggaaatattaaacctctcaccggatcaaatggagagatt 942

Sbjct: 943 aggaagaactgtagaa 958

Score = 145 bits (73), Expect = 2e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
|||||
Sbjct: 64 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgccccaaactctct 123

Query: 688 tctctgtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttct 747
|||
Sbjct: 124 accacagtgaatccacactgcaaactgccatatcaaaggaggcccgaatgggtgcctct 183

Query: 748 ctcttctgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 184 atctctcgcttgttcttccacgattgctttgtcaatg 220

Score = 123 bits (62), Expect = 8e-24
Identities = 155/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatgggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 220 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 279

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||
Sbjct: 280 aatccaaatagaaactccgctcgtggatttgatgtcatcgacaacataaagacagccgta 339

Query: 1277 gagaaagtgtgtccaggagttgttctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 340 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 399

Query: 1337 tctgtt 1342
|||||
Sbjct: 400 tctgtt 405

Score = 89.7 bits (45), Expect = 1e-13
Identities = 87/101 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 412 cttggaggccaacctggaatgtaaaacttggagaagagatgctaaaacggctagtcaa 471

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacct 1578
|| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 472 tccgctgctaacactgccatcccgccaccaacttcaaacct 512

>gb|BT098008.1| Soybean clone JCVI-FLGm-22H8 unknown mRNA
Length = 1324

Score = 174 bits (88), Expect = 3e-39
Identities = 316/392 (80%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 678 ggtcatacaattggacaagcaaggtgcacaacctttagagcccgaatctacaacgagagc 619

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Sbjct: 618 aacatagatagctcttttgcccgcattgagacaatctaggtgtccccgaacctcaggatca 559

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactac 1971
||||||| || ||||| ||||| || ||||| || ||||| || ||||| || |||||
Sbjct: 558 ggggacaacaaccttgacccattgactttgccactcccacttttctttgacaaccactac 499

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacgggt 2031
||||||| ||||| ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Sbjct: 498 ttcaagaacctcattcagaagaagggttcatccattccgaccaagaactcttcaatgggt 439

Query: 2032 ggggccaccgactccattgtgcgtggtacagcaccaacccgggcaccttctcctctgat 2091
|| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 438 ggttcactgactccttagtgggtacctacagcaccaacccggcctccttttgcggat 379

Query: 2092 ttcgccgcccgcgatgatcaagatgggagacattagtcctctcactggctccaatggagaa 2151
 || |||||
 Sbjct: 378 ttttcgccgcccgcgatgatcaggatgggagacattagtcctctcactggctcccgcgagaa 319

```
Query: 2152 atcaggaagaattgtagaaggattaactaatt 2183
      || ||| |||| | | ||| |||
Sbjct: 318  ataagggagaactgcaggagggtcaactaatt 287
```

Score = 163 bits (82), Expect = 1e-35
Identities = 136/154 (88%)
Strand = Plus / Minus

Query: 1482 gaggcctacatggaatgttaaacttggagaagagacgctagaactgctagccaatctg 1541
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 842 gaggcccaacatgggatgtgaaacttggagaagagactctaggacggcaagccaatctg 783

Query: 1542 ctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaagattta 1601
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 782 ctgccacaatggcatcccaagaccacttcaaaccttaaccaacttatatccagattta 723

```
Query: 1602 gcgctcttggactttccaccaaggacttggtcgc 1635
          | ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 722  acactctcggactttccaccaaggacttggtcgc 689
```

Score = 159 bits (80), Expect = 1e-34
Identities = 161/188 (85%)
Strand = Plus / Minus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
 ||||| || ||||| | |||||||||||||||||||||
 Sbjct: 1035 tgtgatgggtcgattctacttggatgacacatcaagcttcaccggagagaagaacgcggga 976

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
 || ||||| |||| ||||| || || || || || || ||||| |||||
 Sbjct: 975 cctaacaggaattctgcccgaggatttgagtgatcgaccaaatcaaatcagctgtggag 916

Query: 1280 aaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagactct 1339

Sbjct: 915 aaagtgtgtccgggtgtggttttcttgcgctgacattcttgccatcgctgccagagactct 856

Query: 1340 gttcagat 1347

||| |||

Sbjct: 855 gttgagat 848

Score = 121 bits (61), Expect = 3e-23

Identities = 85/93 (91%)

Strand = Plus / Minus

Query: 692 ctgtgaaatccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctcc 751

||||||| ||||||| |||| ||||||||| |||||||||||||||||||||||||

Sbjct: 1130 ctgtgaaacgcacagtgaatcggccatatcaaaggagacccgcatgggtgcttctctcc 1071

Query: 752 ttcgcttgcttctccacgattgctttgtcaatg 784

| || ||||||||||||||||||||| |||

Sbjct: 1070 tacgtttgttcttccacgattgctttgttaatg 1038

>emb|CU137662.1| Medicago truncatula chromosome 5 clone mth2-15518, COMPLETE SEQUENCE
Length = 111929

Score = 172 bits (87), Expect = 1e-38

Identities = 150/171 (87%)

Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535

||||||||||| |||||| | ||| ||||||||||||||||| || ||||| |||||

Sbjct: 97958 agcttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagta 98017

Query: 1536 aatctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaa 1595

|||| ||||| |||||| | ||||| ||||||||||||| || |||||||||||||||

Sbjct: 98018 aatcagctgcaaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaa 98077

Query: 1596 gatttagcgctcttggactttccaccaaggacttggctgccttgctccgta 1646

| |||| | |||||| | ||||||||||||| ||||||| ||||| |||||

Sbjct: 98078 ggtttaatgctcttggctcttccaccaaggatttggctgcattgtctgta 98128

Score = 157 bits (79), Expect = 6e-34

Identities = 172/203 (84%)
Strand = Plus / Plus

Query: 1152 tgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 97540 tgcagggatgtgatggttcaattctctcgtatgacacatcaagcttcaccggagagaaaa 97599

Query: 1212 acgcaaaccacaacaggaactctgctcgtggattcgaggttattgacaacattaaatcag 1271
|||
Sbjct: 97600 ctgccaatcccaacaaaaattcgcccggtggattcgaagtgatcgacaaaatcaaatacag 97659

Query: 1272 ccgtggagaaagtgtgtccaggagttgttctcgcgcagatatccttgccatcgctgcca 1331
|
Sbjct: 97660 cagtggagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgcta 97719

Query: 1332 gagactctgttcagattgtaagt 1354
|||||
Sbjct: 97720 gagactctgttgagatcgtaagt 97742

Score = 119 bits (60), Expect = 1e-22
Identities = 288/364 (79%)
Strand = Plus / Plus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||
Sbjct: 98322 tagggggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacg 98381

Query: 1847 agaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcag 1906
|
Sbjct: 98382 actccaacatagatacttctttgctcgcacaaggcaatcagggtgcccgaagacatcgg 98441

Query: 1907 ggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaact 1966
||
Sbjct: 98442 gttccggggacaataatttgccacccttgatcttgcaacaccaacatcctttgacaacc 98501

Query: 1967 actacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttca 2026
|
Sbjct: 98502 attacttcaagaacctagttagacagtaagggtactccactccgaccaacaactcttta 98561

Query: 2027 acggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcct 2086
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 98562 atggtgatccaccgattccatagtgcacgaatatagcttgatccaagctcttttctcct 98621

```
Query: 2147  gaga 2150
        |||
Sbjct: 98682 gaga 98685
```

```
Query: 709   caatctgccatatctaaggagaccgcgatgggtgcttctctctcttcgcttggttcttccac 768
            |||||
Sbjct: 96891 caatctgccatatcaaaagagactcgcgatgggtgcttctctctcttcgcttggttcttccac 96950
```

>emb|CR938710.1| Medicago truncatula chromosome 5 clone mth2-170k9, COMPLETE SEQUENCE
Length = 123977

```
Query: 1476   agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535
             ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 113949 agcttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagta 113890
```

Query: 1596 gatttagcgtcttggactttccaccaaggacttggtcgccttgtccggta 1646
| |||| ||||||| ||||||||||||| ||||||| |||| ||||
Sbjct: 113829 ggtttaatgctcttggctttccaccaaggatttggtcgcattgtctggta 113779

Score = 157 bits (79), Expect = 6e-34
Identities = 172/203 (84%)
Strand = Plus / Minus

Query: 1152 tgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||||||||||||||||| | |||||||||||||||||||||||||
Sbjct: 114367 tgcagggatgtgatggttcaattctctcgtatgacacatcaagcttcaccggagagaaaa 114308

Query: 1212 acgcaaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcag 1271
|| || ||||||| || || || ||||||||||| || || ||||| || |||||||
Sbjct: 114307 ctgccaatcccaacaaaaattcggcccggtgattcgaaatgatcgacaaaatcaaatcag 114248

Query: 1272 ccgtggagaaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgcc 1331
| ||||||||||| ||||||| | ||||| ||||| || ||||||| ||||| |||||
Sbjct: 114247 cagtggagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgcta 114188

Query: 1332 gagactctgttcagattgtaagt 1354
||||||||||| |||| |||||||
Sbjct: 114187 gagactctgttgagatcgtaagt 114165

Score = 119 bits (60), Expect = 1e-22
Identities = 288/364 (79%)
Strand = Plus / Minus

Query: 1787 taggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacg 1846
|||| ||||||||||||||||||||||||||||| | || ||||||| ||| |||||||
Sbjct: 113586 taggggggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacg 113527

Query: 1847 agaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcag 1906
| ||||||||||| || | ||||| | || ||||| | ||||||| | |||||
Sbjct: 113526 actccaacatagatacttcctttgctcgcacaaggcaatcagggtgcccccaagacatcgg 113467

Query: 1907 ggtcaggggacacaatctggcaccacttgatcttcaaactccaaccagctttgacaact 1966

Score = 163 bits (82), Expect = 1e-35
Identities = 172/202 (85%)
Strand = Plus / Plus

Query: 1152 tgcagggatgtgatgggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||| ||||||| || |||||| | ||||| ||||||||||||||||||||
Sbjct: 359 tgcagggtgtgatgggtcgattctacttgatgatacatcaagcttcaccggagagaaga 418

Query: 1212 acgcaaaccacaacaggaactctgctcgtggattcgaggttattgacaacattaaatcag 1271
||||| || ||||| ||||||||||||||||||| || || || ||||| || || |||||
Sbjct: 419 acgcacgtcctaacaagaactctgctcgtggatttgatgtgatcgacaaaatcaagtcag 478

Query: 1272 ccgtggagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgcca 1331
| ||||||| ||||||| ||||| || || ||||| || || ||||||||||||| |||||||
Sbjct: 479 ctgtggaggaagtgtgccagggtgtggtctcctgtgctgatatccttgccattgctgcca 538

Query: 1332 gagactctgttcagattgtaag 1353
|||| ||||||||| || |||||
Sbjct: 539 gagattctgttcacatcgtaag 560

Score = 133 bits (67), Expect = 9e-27
Identities = 124/143 (86%)
Strand = Plus / Plus

Query: 1493 tggaaatgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||| || ||||||||||||||||| | || || || ||||||||||||| |||||
Sbjct: 679 tggaaacgtgaaacttggagaagagattcgaggacagcaagccaatctgctgccaacaat 738

Query: 1553 ggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612
||||||| ||||||||||||| | ||||||||||||| ||||| | | |||||||
Sbjct: 739 ggcatcccaccacccacttcaaacgtcaaccaactcatctccagattcaactctcttgga 798

Query: 1613 ctttccaccaaggacttggtcgc 1635
||||| |||||||||||||
Sbjct: 799 ctttctcccaaggacttggtcgc 821

>ref|XM_002520789.1| Ricinus communis Peroxidase 52 precursor, putative, mRNA
Length = 957

Score = 129 bits (65), Expect = 1e-25
Identities = 110/125 (88%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
|||||
Sbjct: 421 tggaatgttaaacttgaagaagagatgctagaactgcaagccttctgctgccaataat 480

Query: 1553 ggcattccagctccaacttctaacttgaaccaactcatctcaagatttagcgctcttggc 1612
|||||
Sbjct: 481 ggcattccagctccaacttctaacttgaaccaactcatctcaagatttagtgctcttggc 540

Query: 1613 ctttc 1617
|||||
Sbjct: 541 ctttc 545

Score = 54.0 bits (27), Expect = 0.006
Identities = 33/35 (94%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatc 1191
|||||
Sbjct: 214 ggatgtgatggttcaattctacttgatgacacatc 248

Score = 50.1 bits (25), Expect = 0.099
Identities = 31/33 (93%)
Strand = Plus / Plus

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 182 ttcgcttggttcttccacgactgctttgttaatg 214

Score = 50.1 bits (25), Expect = 0.099
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaa 1823
|||||
Sbjct: 577 cacacaatcgacaagcaaggtgcacaaa 605

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattag 2126
|||||||
Sbjct: 879 catgatcaagatgggagacattag 902

>gb|BT052838.1| Medicago truncatula clone MTYFH_FI_FJ_FK1G-0-8 unknown mRNA
Length = 773

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Minus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| | ||||| ||| ||||| ||||| |||
Sbjct: 464 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccg 405

Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||| || ||||| || ||||| || | || |||||
Sbjct: 404 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 345

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatattccttgccatcgctgccagagactc 1338
|| || || ||||| || || || ||||| ||||| |||||
Sbjct: 344 gtatgccccggagttgtatcatgtgtgatattccttgccattgctgccacagactc 289

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Minus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||||| ||||| ||||| | || || ||||| ||||| |||||
Sbjct: 549 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 490

Query: 765 ccacgattgctttgtcaatg 784
|||||||
Sbjct: 489 ccacgattgctttgtcaatg 470

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| |||||||||||||||| || | ||||||| |||
Sbjct: 278 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 219

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || |||||| | || ||||| ||||||| ||||| |||||
Sbjct: 218 tctgatgcgaacactgccatcccaagaccaacttccaaccttaataactcacctcaatg 159

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgct 1641
|||| | |||| |||||||||||||||| ||||| |||||
Sbjct: 158 tttagaatgttggcttttccaccaaggacttagtcgcattgct 115

Score = 63.9 bits (32), Expect = 7e-06
Identities = 62/72 (86%)
Strand = Plus / Minus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| |||||||||||||||||||| |||||| | || | ||||||| |||
Sbjct: 114 agtgctcacacaattggacaagcaaagtgacacatttaggtacgaatctacaatga 55

Query: 1848 gaccaacataga 1859
|||||||||||
Sbjct: 54 gaccaacataga 43

>gb|AY311597.1| Gossypium hirsutum class III peroxidase (pod7) mRNA, complete cds
Length = 1282

Score = 105 bits (53), Expect = 2e-18
Identities = 238/297 (80%), Gaps = 2/297 (0%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| |||||| |||| |||||||||||||| | |||||| |||||| | |||||||
Sbjct: 732 ctgccaagaacaacaggctcaggggacaacaacttggcacctcttgatatccaaactcc 791

Query: 1950 aaccagctttgacaactactacttcaagaacctcggttcagaagaag-ggtctcctccact 2008
||| ||||| ||||| ||||| ||||| ||| ||| ||| |||||
Sbjct: 792 aacatcttttgacaacaactacttcaagaacct-aatcagtcaaaggacttctccact 850

Query: 2009 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 2068
||||| || ||||| ||||| ||||| || ||||| || ||| ||| ||| |||
Sbjct: 851 ctgatcaacagttgttcaatgggtggatccacggattccatcgttcgcggttacggaaca 910

Query: 2069 acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 2128
||| || ||||| || ||||| | || ||||| ||||| ||||| ||||| |||||
Sbjct: 911 gcccaagctccttcaattcgattttgtggctgccatgatcaagatgggagacattagtc 970

Query: 2129 ctctcactgggtccaatggagaaatcaggaagaattgtagaaggattaactaatttg 2185
| ||||| || ||| || ||||| || ||||| | ||||| |||||
Sbjct: 971 ccctcactggatcacgtggggagatcaggaagaactgcagaagggtgaactaatttg 1027

Score = 85.7 bits (43), Expect = 2e-12
Identities = 109/131 (83%)
Strand = Plus / Plus

Query: 1502 aaacttggaagaagagacgctagaactgtagccaatctgctgctaacaatggcatccct 1561
||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 490 aaacttggaagaagagatgcaagaagtgtagccagtctgcggctaataatggcattcct 549

Query: 1562 gcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||| ||||| ||| | ||||| ||||| || ||| | ||||| ||||| |||||
Sbjct: 550 ccaccaacttcgaacttgaaccgactcacttcagggtcaatgctcttggactctccacc 609

Query: 1622 aaggacttggt 1632
| |||||
Sbjct: 610 aaggacttggt 620

Score = 75.8 bits (38), Expect = 2e-09
Identities = 50/54 (92%)
Strand = Plus / Plus

Query: 731 cccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784

Sbjct: 221 cccgaatgggtgcttctctgcttcgattgttcttccacgactgctttgtcaatg 274

Score = 61.9 bits (31), Expect = 3e-05
Identities = 118/147 (80%)
Strand = Plus / Plus

Query: 1196 ttcaccggagagaagaacgcaaaccccaacaggaactctgtctgtggattcagaggttatt 1255
 ||||||||||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 313 ttcaccggagagaaaaatgctaaccggaatcggaactcgtctcgcggattcgaatgttgtt 372

Query: 1256 gacaacattaaatcagccgtggagaaaagtgtgtccaggagtgtttctgcgcagatatc 1315
|| ||| | | | | | | | | | | | | | | | | |
Sbjct: 373 gataacatcaagtcagctgttgagaatgttgcctggtgtagtttcttgtgtgatatc 432

```

Query: 1316 cttgccatcgctgccagagactctgtt 1342
          | |||| | |||| ||||| |||||
Sbjct: 433  ttggccattgctgctagagactctgtt 459

```

>emb|FP100639.1| Phyllostachys edulis cDNA clone: bphyem110n02, full insert sequence
Length = 1307

Score = 103 bits (52), Expect = 8e-18
Identities = 157/192 (81%)
Strand = Plus / Plus

```
Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||||| || || ||||| | ||||||||| ||||| | ||||| |||||
Sbjct: 710 tcacaccatagccaagcacgctgcacaaacttcagagcccacgtatacaacgacaccaa 769
```

Query: 1854 catagaaaccgcatttgcaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
 ||| || ||| |||| |||| |||| | | ||||| ||||| |||||
 Sbjct: 770 catcgacggcgccctttgcgaggacgaggcagtcaggttgccctaggacatcaggctcagg 829

```
Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
          ||||| ||||| || || || ||||| ||||| ||| || ||| |||||
Sbjct: 830  tgacaacaacctggcgctctggaccttcaaaccceaaccgtcttcgagaacaactacta 889
```

Query: 1974 caagaacctcgt 1985

|||||||
Sbjct: 890 caagaacctcgt 901

Score = 54.0 bits (27), Expect = 0.006
Identities = 78/95 (82%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| |||| |||||||||||||||||||| | | || | || ||||||||||||
Sbjct: 1005 gatttcgtggccggcatgatcaagatgggagacgtcacgccgttgacgggctccaatgga 1064

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt 2183
| ||||||||| || |||||||||
Sbjct: 1065 caggtcaggaagaactgcagaagggttaactaatt 1099

>emb|FP099994.1| Phyllostachys edulis cDNA clone: bphyem210i11, full insert sequence
Length = 1213

Score = 103 bits (52), Expect = 8e-18
Identities = 157/192 (81%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||| || || ||||||| | ||||||||||||||||||| | || ||||||||| |||||
Sbjct: 688 tcacaccataggccaagcacgctgcacaaacttcagagcccacgtatacaacgacaccaa 747

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || ||| ||||| ||||| ||||| | | ||||||| ||||||| |||||
Sbjct: 748 catcgacggcgcctttgcgaggacgaggcagtcaggttgccctaggacatcagggtcagg 807

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||| ||||| || || || ||||||||| ||||| ||| || ||| |||||
Sbjct: 808 tgacaacaacctggcgcctctggaccttcaaaccccaaccgtcttcgagaacaactacta 867

Query: 1974 caagaacctcgt 1985
|||||||
Sbjct: 868 caagaacctcgt 879

Score = 54.0 bits (27), Expect = 0.006
Identities = 78/95 (82%)
Strand = Plus / Plus

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| |||| |
Sbjct: 983 gatttcgtggccggcatgatcaagatgggagacgtcacgccgttgacgggctccaatgga 1042

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt 2183
| |||||
Sbjct: 1043 caggtcaggaagaactgcagaagggttaactaatt 1077

>dbj|AB027752.1| Nicotiana tabacum mRNA for peroxidase, complete cds, clone:tpoxC1
Length = 1356

Score = 95.6 bits (48), Expect = 2e-15
Identities = 111/132 (84%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| |||| |
Sbjct: 719 ctgccaagaagttcaggtcaggggacaacaatttggcaccacttgatcttcaaactcc 778

Query: 1950 aaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactc 2009
| | ||||| | || ||||| | || ||||| |
Sbjct: 779 taacaaatttgacaacaattatttcaagaatctgttgacaaaagggtcttcttccactc 838

Query: 2010 tgatcagcaact 2021
||||| |||||
Sbjct: 839 tgatcaacaact 850

Score = 54.0 bits (27), Expect = 0.006
Identities = 60/71 (84%)
Strand = Plus / Plus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
||||| | |||| |
Sbjct: 333 tctgctagaggatttgaagttattgacaatatcaaactctgctgtggagaaagtgtgcctt 392

Query: 1292 ggagttgtttc 1302
|| |||||
Sbjct: 393 ggtgtgtttc 403

Score = 50.1 bits (25), Expect = 0.099
Identities = 43/49 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctcttcgcttgttcttccacgattgctttgtcaatg 784
||||||| |||| | ||||| ||||| |||||
Sbjct: 210 atgggtgcttctcttcttctgtctattcttccatgattgcttctgtcaatg 258

Score = 46.1 bits (23), Expect = 1.5
Identities = 104/131 (79%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||| | ||||| ||||| || ||| ||||| || |
Sbjct: 465 tggaatgtaaaattgggaagaagagattctagaactgcaagtcaaagtgctgccaatagt 524

Query: 1553 ggcattccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612
||||| || | | ||||| ||||| ||||| || || || |||||
Sbjct: 525 ggcattcctcctgctacttctaaccttaatagactcatctcaagtttcagtgtgttggc 584

Query: 1613 ctttccaccaa 1623
|||||
Sbjct: 585 ctttctaccaa 595

>gb|AY837788.2| Catharanthus roseus clone Prx4 putative secretory peroxidase mRNA,
complete cds
Length = 1055

Score = 89.7 bits (45), Expect = 1e-13
Identities = 126/153 (82%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||||| ||||| || | ||||| ||||| ||||| |||||
Sbjct: 459 tggaatgtgaaacttggaagaagagatgcaacaactgcaagccaagtgtgctgctaacaat 518

>gb|FJ644943.1| Sesuvium portulacastrum peroxidase 1 (POD1) mRNA, complete cds
Length = 1293

Score = 87.7 bits (44), Expect = 5e-13
Identities = 71/80 (88%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| ||||| | ||||| ||||| | ||||| ||||| ||||| |||||
Sbjct: 937 atgatcaagatgggtgacatcaaacctcttactggttcaaatggagaaattaggaagaat 996

Query: 2164 tgtagaaggattaactaatt 2183
|| ||||| ||||| |||||
Sbjct: 997 tgcagaaggattaactaatt 1016

Score = 61.9 bits (31), Expect = 3e-05
Identities = 61/71 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 457 cttggaggaccaacatgggatgtgaaactaggaagaagagatgccagaacagctaaccaa 516

Query: 1538 tctgctgctaa 1548
|||||||
Sbjct: 517 gctgctgctaa 527

Score = 54.0 bits (27), Expect = 0.006
Identities = 51/59 (86%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 622 ggtggccactcaataggacaagcaaggtgcacaaatttcagggtcacatataacaacga 680

>dbj|AK242814.1| Oryza sativa Japonica Group cDNA, clone: J090061H15, full insert
sequence
Length = 1215

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||| | || ||||||| |||||
Sbjct: 662 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 721

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| || ||||| | ||||||| | ||||| |||||
Sbjct: 722 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 781

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||||||| | ||||||| || ||||| || || || || |||||
Sbjct: 782 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 841

Query: 1974 caagaacctcggttcagaagaagggtctcctccactctgatcag 2016
||||||||| ||||||| ||||| |||||||||
Sbjct: 842 caagaacctcgctcgaagaagggtctcctgcactctgatcag 884

>ref|NM_001072100.1| Oryza sativa (japonica cultivar-group) Os11g0112400 (Os11g0112400)
mRNA, complete cds
Length = 975

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||| | || ||||||| |||||
Sbjct: 588 tcacaccattggacaagcagcatgcacaaacttcagagctcacatatacaacgaaaccaa 647

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| || ||||| | ||||||| | ||||| |||||
Sbjct: 648 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 707

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||||||| | ||||||| || ||||| || || || || |||||
Sbjct: 708 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 767

Query: 1974 caagaacctcggttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| ||||| |||||
Sbjct: 768 caagaacctcgctgtaagaagggtcctgcactctgatcag 810

>tpe|BN000659.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx130 gene for
class III peroxidase 130 precursor, exons 1-4
Length = 2195

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||| ||||| ||||||| ||||| ||||| ||||| |||||
Sbjct: 1808 tcacaccattggacaagcagatgcacaaacttcagagctcacatatacaacgaaaccaa 1867

Query: 1854 catagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1868 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcagggtcagg 1927

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||| ||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1928 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 1987

Query: 1974 caagaacctcggttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| ||||| |||||
Sbjct: 1988 caagaacctcgctgtaagaagggtcctgcactctgatcag 2030

>dbj|AB019228.1| Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCK7
Length = 87090

Score = 85.7 bits (43), Expect = 2e-12
Identities = 52/55 (94%)
Strand = Plus / Minus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787
||||||| ||||||| ||||| ||||| ||||| |||||
Sbjct: 74225 cgcatgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatgtaa 74171

>emb|BX000512.1| Oryza sativa chromosome 11, . BAC OSJNBa0025K19 of library OSJNBa from

chromosome 11 of cultivar Nipponbare of ssp. japonica of
Oryza sativa (rice), complete sequence
Length = 181322

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||| | ||||||||| ||| ||||||| |||||
Sbjct: 158955 tcacaccattggacaagcacgatgcacaaacttcagagctcacatatacaacgaaaccaa 158896

Query: 1854 catagaaaccgcatttgcaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| || ||||| | ||||||| | ||||| |||||
Sbjct: 158895 catcgacagtggcttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 158836

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||||||| | ||||||| || ||||| || || ||| |||||
Sbjct: 158835 tgacaacaatctggcaccttggatcttcagacgccaaccgtgttcgagaacaactacta 158776

Query: 1974 caagaacctcggttcagaagaagggtctctccactctgatcag 2016
||||||| ||||| ||||| |||||||||
Sbjct: 158775 caagaacctcgctcgaagaagggtctctccactctgatcag 158733

>gb|EF661875.2| Catharanthus roseus putative secretory peroxidase (Prx3) mRNA,
complete cds
Length = 1233

Score = 83.8 bits (42), Expect = 7e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttgcgccgccatgatcaagatgggagacattagtcctctcactggc 2139
|||| ||||||| || ||||||||||||||||||| ||||||| | |||||
Sbjct: 924 ttctactctgatttgcgccgccatgatcaagatgggagatattagtcctttgactggt 983

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||||| | ||||| ||||||| || |||||
Sbjct: 984 tcaaatggagaggttaggaaaaattgtagagggttaa 1021

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 639 cacacaattggtcaagcaaggtgcaca 665

>ref|NM_125225.1| Arabidopsis thaliana peroxidase, putative (AT5G58390) mRNA,
 complete cds
 Length = 1220

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 229 cgcattgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>dbj|AK117722.1| Arabidopsis thaliana At5g58390 mRNA for putative peroxidase,
 complete cds, clone: RAFL17-40-J20
 Length = 656

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 226 cgcattgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 277

>gb|AY085030.1| Arabidopsis thaliana clone 124846 mRNA, complete sequence
 Length = 1220

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 229 cgcattgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

>gb|EZ329073.1| TSA: Artemisia annua strain Madagascar Contig15619, mRNA sequence
Length = 698

Score = 75.8 bits (38), Expect = 2e-09
Identities = 56/62 (90%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
 ||||| ||||| ||||||||| ||||||||| ||||||||| ||||| |||||||
Sbjct: 169 ctgccaagaacctcagggtcaggagacaacaatttggcaccactagatctccaaactcc 228

Query: 1950 aa 1951
 ||
Sbjct: 229 aa 230

>ref|XM_002450087.1| Sorghum bicolor hypothetical protein, mRNA
Length = 996

Score = 75.8 bits (38), Expect = 2e-09
Identities = 80/94 (85%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948
 ||||||||||| ||||| ||||| ||||||||| ||||| || || || || ||||| |
Sbjct: 704 gctgccctagaacctcagggtcaggtgacaacaatttggcgctctggaccttcaaacc 763

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982
 ||||| |||||| ||| |||||| |||||||
Sbjct: 764 caaccgtctttgagaacaactactacaagaacct 797

Score = 50.1 bits (25), Expect = 0.099
Identities = 40/45 (88%)
Strand = Plus / Plus

Query: 2137 ggctccaatggagaaatcaggaagaattgtagaaggattaactaa 2181
 ||||||||||| | ||||||||| || |||| |||||||
Sbjct: 952 ggctccaatggacagatcaggaagaactgcagaatgattaactaa 996

>ref|XM_002269882.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257005
(LOC100257005), mRNA
Length = 1180

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||||||
Sbjct: 754 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 813

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 814 tactacaagaacct 827

Score = 58.0 bits (29), Expect = 4e-04
Identities = 47/53 (88%)
Strand = Plus / Plus

Query: 732 cgcgatgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
||||||||| ||||||||||| || | ||||||| |||||||||||||
Sbjct: 225 cgcgatgggcgcttctctccttcgcttcttcttccatgattgctttgtcaatg 277

>emb|AM447728.2| Vitis vinifera contig VV78X018697.9, whole genome shotgun sequence
Length = 22220

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||||||
Sbjct: 11004 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 10945

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 10944 tactacaagaacct 10931

Score = 65.9 bits (33), Expect = 2e-06
Identities = 51/57 (89%)
Strand = Plus / Minus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaat 788
||||||| ||||||||| || | ||||||| |||||||||
Sbjct: 12714 ccgcatgggcgcttctctcctccgtctcttcttccatgattgctttgtcaatgtaat 12658

>ref|XM_002278960.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257059
(LOC100257059), mRNA
Length = 966

Score = 71.9 bits (36), Expect = 3e-08
Identities = 101/120 (84%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
||||||| |||| | | ||||||| || ||||| || || |
Sbjct: 694 tcaggggacaacaacttggccctctggatcttcaaactcctac-agcttttgagaacaa 752

Query: 1968 ctacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaa 2027
|||| | ||||||| | |||||| | | ||||||| |||||||
Sbjct: 753 ctactacaagaacctgatcaagaagaagggtctcctccactctgatcagcagctgttcaa 812

Score = 67.9 bits (34), Expect = 4e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||||| ||||| ||||||| |||| | |||| |
Sbjct: 580 cacacaattgggaagcaaggtgcacatccttcagggcccgcatatacaatgagacaaac 639

Query: 1855 at 1856
||
Sbjct: 640 at 641

Score = 65.9 bits (33), Expect = 2e-06
Identities = 129/161 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| |||| | ||||| | ||||| | ||||| | |||||
Sbjct: 409 cttggaggccttagctggaacgtaaaacttgggcgaagagacgcccgaccgcaagccag 468

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| |||| | ||||| | || ||||| ||||| ||||| |||||
Sbjct: 469 gctgctgcaaacaacagcatccctcctccaacttcaaacctgaaccaactaatctctaga 528

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgcctt 1638
|| ||||| || || ||||| ||||| |||||
Sbjct: 529 ttccaagctcttggcctctcaaccaggacttggttgcctt 569

Score = 58.0 bits (29), Expect = 4e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| ||||| || || || ||||| || ||||| || |||||
Sbjct: 889 atgatcaagatgggagatatcagccactcactggatcaaatggagagattaggaagaac 948

Query: 2164 tgtagaagg 2172
|| |||||
Sbjct: 949 tgcagaagg 957

>gb|AY206413.1| Ipomoea batatas anionic peroxidase swpb2 mRNA, complete cds
Length = 1263

Score = 71.9 bits (36), Expect = 3e-08
Identities = 57/64 (89%)
Strand = Plus / Plus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaaga 2161
||||||| |||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 989 ccatgatcaagatggccaacatttcgcctctcactggctccaaggagaaatcaggaaga 1048

Query: 2162 attg 2165
|||
Sbjct: 1049 attg 1052

>gb|EZ399860.1| TSA: Artemisia annua strain Uganda Contig16355, mRNA sequence
Length = 1170

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||||| ||||||| || ||||| |||||||||
Sbjct: 518 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctccaaactcc 459

Query: 1950 aac 1952
|||
Sbjct: 458 aac 456

>gb|EZ145065.1| TSA: Artemisia annua strain Artemis Contig4471, mRNA sequence
Length = 1332

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||||| ||||||| || ||||| |||||||||
Sbjct: 713 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctccaaactcc 772

Query: 1950 aac 1952
|||
Sbjct: 773 aac 775

Score = 58.0 bits (29), Expect = 4e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
||||| ||||||||||||| ||| ||||| |||||||||||||
Sbjct: 207 atgggcgcttctctccttcgcttgcttccatgattgctttgtcaatg 255

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaaga 1513
||||||| ||||||||||||| ||||| |||||
Sbjct: 447 cttggaggacctacatggaatgtgaaactgggaaga 482

>gb|EZ141680.1| TSA: Artemisia annua strain Artemis Contig1086, mRNA sequence
Length = 456

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||||||||| ||||||| ||||||| || ||||| |||||||
Sbjct: 224 ctgccaagaacctcagggtcaggagacaacaatttggcaccgctagatctcaaactcc 283

Query: 1950 aac 1952
|||
Sbjct: 284 aac 286

>ref|XM_002489001.1| Sorghum bicolor hypothetical protein (SORBIDRAFT_0246s002010) mRNA,
complete cds
Length = 1045

Score = 69.9 bits (35), Expect = 1e-07
Identities = 200/255 (78%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaagggtcacaaacttcagagcccgcatctacaacgag 1848
|||| | ||||| || || ||||| | ||||| ||||||||| || |||||||||
Sbjct: 653 ggtgctcacacataggccaagcacgctgcaccaacttcagagaccacatctacaacgac 712

Query: 1849 accaacatagaaacgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
||||| | || || ||||||||| ||||| | || ||||| || |||||
Sbjct: 713 accaacgtcgacggagcctttgcaaggacaaggcaatcaggttgctcctagcacctcagga 772

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 773 acaggtgacaacaacttggcaccattggaccttcaaacaccaaccgtctttgagaacgac 832

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||| ||||| ||||| || || ||||| ||||| ||||| || || |||||

Sbjct: 833 tactacaagaaccttgttagcaacatggggctcctacactctgaccaagagctcttcaac 892

Query: 2029 ggtgggtccaccgac 2043

||||| |||||

Sbjct: 893 ggtggcgccaccgac 907

Score = 46.1 bits (23), Expect = 1.5

Identities = 62/75 (82%)

Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattagtcctctcactgggtccaatggagaaatcaggaagaa 2162

||||| ||||| || || || ||||| ||||| || |||||

Sbjct: 967 catgatcaagatgggtgacattacaccgttgacgggtccgctggggagatcaggaagaa 1026

Query: 2163 ttgtagaaggattaa 2177

|| |||||

Sbjct: 1027 ctgcagaaggattaa 1041

>ref|XM_002441657.1| Sorghum bicolor hypothetical protein, mRNA

Length = 588

Score = 69.9 bits (35), Expect = 1e-07

Identities = 200/255 (78%)

Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacgag 1848

||||| ||||| || || ||||| || ||||| ||||| ||||| |||||

Sbjct: 4 ggtgctcacaccataggccaagcacgctgcaccaacttcagagaccacatctacaacgac 63

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaaagctgccctagaacatcaggg 1908

||||| || || || ||||| ||||| || || || ||||| || |||||

Sbjct: 64 accaacgtcgacggagcctttgcaaggacaaggcaatcaggttgtcctagcacctcaggaa 123

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

Sbjct: 124 acaggtgacaacaacttggcaccattggaccttcaaacaccaaccgctctttgagaacgac 183

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028

Sbjct: 184 ||||| ||||||||| ||| || | ||| ||||| ||||| ||||| ||| ||| |||||
tactacaagaacctgttagcaacatggggtcctacactctgaccaagagctcttcaac 243

Query: 2029 ggtgggtccaccgac 2043

Sbjct: 244 ggtggcgccaccgac 258

Score = 46.1 bits (23), Expect = 1.5

Identities = 62/75 (82%)

Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

Sbjct: 318 catgatcaagatgggtgacattacaccgttgacgggctccgctggggagatcaggaagaa 377

Query: 2163 ttgtagaaggattaa 2177

Sbjct: 378 ctgcagaaggattaa 392

```
>emb|AM456467.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X246626.10,  
      clone ENTAV 115  
      Length = 52838
```

Score = 69.9 bits (35), Expect = 1e-07

Identities = 131/163 (80%)

Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagcc 1535

Sbjct: 14928 agcttgaggaggcctagctggaacgtaaaacttggcggaagagacgcccgaccgcaagcc 14987

Query: 1536 aatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaa 1595

Sbjct: 14988 aggcctgctgcaaacacagcatcctctctccaacttcaaacctgaaccaactaatctcta 15047

Subject: 14988 aggtgctgcaaacaacagcatccctcctccaacttcaaacctgaaccaactaatctcta 15047

Query: 1596 gatttagcgctcttggactttccaccaaggacttggtcgcctt 1638
|||| | ||||| | | | ||| ||||| |||||
Sbjct: 15048 gattccaagctcttggcctctcaaccagggacttggttcctt 15090

Score = 67.9 bits (34), Expect = 4e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 15195 cacacaattgggcaagcaaggtgcacatccttcaggggcccgcatatacaatgagacaaac 15254

Query: 1855 at 1856
||
Sbjct: 15255 at 15256

Score = 67.9 bits (34), Expect = 4e-07
Identities = 100/120 (83%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaactctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
||| ||||| ||| | | ||||| ||||| | ||||| |||||
Sbjct: 15309 tcargggacaacaacttggccctctggatcttcaaactcctac-agcttttgagaacaa 15367

Query: 1968 ctacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaa 2027
|||| ||||| | ||||| || | ||||| ||||| |||||
Sbjct: 15368 ctactacaagaacctgatcaagaagaagggtctcctccactctgatcagcagctgttcaa 15427

Score = 58.0 bits (29), Expect = 4e-04
Identities = 59/69 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| ||||| || | ||||| || ||||| || |||||
Sbjct: 15504 atgatcaagatgggagatatcagccctcactggatcaaatggagagattaggaagaac 15563

Query: 2164 tgtagaagg 2172

|| |||||
Sbjct: 15564 tgcagaagg 15572

>gb|GU230149.1| Ipomoea batatas anionic peroxidase mRNA, complete cds
Length = 1125

Score = 67.9 bits (34), Expect = 4e-07
Identities = 46/50 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctctcttcgcttgttcttccacgattgctttgt 779
|||||||
Sbjct: 289 acccgcatgggtgcttccctcattcgcttgttcttccatgactgctttgt 338

>ref|XM_002268223.1| PREDICTED: Vitis vinifera hypothetical protein LOC100263665
(LOC100263665), mRNA
Length = 1002

Score = 67.9 bits (34), Expect = 4e-07
Identities = 34/34 (100%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttc 1827
|||||||
Sbjct: 516 tcacacaattggacaagcaaggtgcacaaacttc 549

>gb|FJ099755.1| Pinus taeda isolate 1286 anonymous locus 2_6350_01 genomic sequence
Length = 410

Score = 67.9 bits (34), Expect = 4e-07
Identities = 61/70 (87%)
Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||| ||||| ||||| | |||||
Sbjct: 308 taggtgctcatacaattggccaagcacggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>emb|CU231251.1| Populus EST from mild drought-stressed leaves
Length = 584

Score = 67.9 bits (34), Expect = 4e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || |||||||||||||||| ||| |||| ||||| ||||| |||||||||
Sbjct: 138 cacacaatcgggcaagcaaggtgcacaagctttagagctcgcataataaatgagaccaac 197

Query: 1855 at 1856
||
Sbjct: 198 at 199

>gb|AY206412.1| Ipomoea batatas anionic peroxidase swpb1 mRNA, complete cds
Length = 1257

Score = 67.9 bits (34), Expect = 4e-07
Identities = 37/38 (97%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaagaattg 2165
||||||||| |||||||||||||||||||||||||
Sbjct: 1002 cctctcactggtccaatggagaaatcaggaagaattg 1039

Score = 44.1 bits (22), Expect = 6.1
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1217 aaccccaacaggaactctgctcgtgg 1242
||||||||| |||||||||||||
Sbjct: 348 aaccccaacagaaactctgctcgtgg 373

>dbj|AK322204.1| Solanum lycopersicum cDNA, clone: LEFL1035AA07, HTC in leaf
Length = 1170

Score = 65.9 bits (33), Expect = 2e-06
Identities = 48/53 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcacatgggtgcttctctccttcgcttggttcttcacgattgctt 776
||||| ||||| ||||||||| |||||||| | |||||||||
Sbjct: 213 aaggaaaccgaatgggtgcttcctccttcgcctattcttcacgattgctt 265

Score = 58.0 bits (29), Expect = 4e-04
Identities = 47/53 (88%)
Strand = Plus / Plus

Query: 1801 attggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||| ||||||| ||||| | ||||| |||||||||
Sbjct: 642 attggacaagcaaggtgcacaagtttcaggggacgcatatacacgagaccaa 694

Score = 56.0 bits (28), Expect = 0.002
Identities = 70/84 (83%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||||| ||||||| || || ||||| ||||||| || ||||||| |||||||
Sbjct: 945 gccatgattaagatgggtgatatcctccctcactggttctaattggagagatcaggaag 1004

Query: 2161 aattgtagaaggattaactaattt 2184
|| || || || || |||||
Sbjct: 1005 aactgcaggagaatcaactaattt 1028

Score = 50.1 bits (25), Expect = 0.099
Identities = 100/125 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||||| ||||||| ||||||| ||||| | || || || || |||||
Sbjct: 747 tcaggatcaggggataacaatttggcacctcttgatttacagaccctacgcgttcgac 806

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
|| ||||||| ||||| ||| | || ||||| || ||||||| |||||
Sbjct: 807 aatcactacttcataaaccttgtaacaaaaagggactgctccattctgatcagcagctt 866

Query: 2023 ttcaa 2027

|||||

Sbjct: 867 ttcaa 871

>ref|XM_002328955.1| Populus trichocarpa predicted protein, mRNA

Length = 1047

Score = 65.9 bits (33), Expect = 2e-06

Identities = 57/65 (87%)

Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854

|||||||

Sbjct: 633 cacacaattggacaagcaagatgcacaaactttagggcacgcatatataatgagaccacc 692

Query: 1855 ataga 1859

|||||

Sbjct: 693 ataga 697

Score = 54.0 bits (27), Expect = 0.006

Identities = 66/79 (83%)

Strand = Plus / Plus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162

|||||||

Sbjct: 941 catgatcaagatgggagatatcaggcctctcactggatccagaggagagattagaaataa 1000

Query: 2163 ttgtagaaggattaactaa 2181

||| || ||||| |||||

Sbjct: 1001 ttgcaggaggatcaactaa 1019

Score = 44.1 bits (22), Expect = 6.1

Identities = 34/38 (89%)

Strand = Plus / Plus

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactcc 1949

|||||||

Sbjct: 750 ggggacaacaacttggcaccacttgattgcaaactcc 787

>ref|XM_002319932.1| Populus trichocarpa predicted protein, mRNA
Length = 1220

Score = 65.9 bits (33), Expect = 2e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||| |||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 592 cacacaatcgggcaagcaaggtgtacaagctttagagctcgcatatacaatgagaccaac 651

Query: 1855 ataga 1859
|||||
Sbjct: 652 ataga 656

Score = 48.1 bits (24), Expect = 0.39
Identities = 39/44 (88%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctctcttcgcttggttcttccacgattgctttgt 779
||||||||||||| ||||||||||||| || ||||| |||||
Sbjct: 178 atgggtgcttctcttgttcgcttggttcttcatgattgtttgt 221

>gb|AC214418.1| Populus trichocarpa clone POP106-D21, complete sequence
Length = 88637

Score = 65.9 bits (33), Expect = 2e-06
Identities = 57/65 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| || ||||||||||| |||| ||| ||||| ||||| ||||| |||||||||
Sbjct: 88236 cacacaatcgggcaagcaaggtgtacaagctttagagctcgcatatacaatgagaccaac 88295

Query: 1855 ataga 1859
|||||
Sbjct: 88296 ataga 88300

Score = 52.0 bits (26), Expect = 0.025
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtca 781
|||||
Sbjct: 86397 atgggtgcttctcttggttcgcttggttcttcatgattgtttgtca 86442

>gb|BT096974.1| Soybean clone JCVI-FLGm-21M8 unknown mRNA
Length = 1201

Score = 63.9 bits (32), Expect = 7e-06
Identities = 44/48 (91%)
Strand = Plus / Plus

Query: 1810 gcaaggtgcacaaacttcagagcccgcatctacaacgagaccaacata 1857
|||||
Sbjct: 639 gcaaggtgcactaccttcagagaccgcatctacaacgacaccaacata 686

>gb|AC235472.1| Glycine max strain Williams 82 clone GM_WBc0099F23, complete sequence
Length = 134971

Score = 63.9 bits (32), Expect = 7e-06
Identities = 47/52 (90%)
Strand = Plus / Plus

Query: 2997 tatcttttgtttcatcttactttatgtgaggatataatagtaataataacatt 3048
|||||
Sbjct: 77662 tatcttttgtatcatttgctttatgttaggatataatagttataaaacatt 77713

>gb|FJ596178.1| Capsicum annuum peroxidase (POD) mRNA, complete cds
Length = 1353

Score = 63.9 bits (32), Expect = 7e-06
Identities = 59/68 (86%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||||
Sbjct: 646 agtgctcacacaattggacaagcaaggtgcacatcattcagggcacgtatatacaatga 705

Query: 1848 gaccaaca 1855
|||||||
Sbjct: 706 gaccaaca 713

Score = 61.9 bits (31), Expect = 3e-05
Identities = 55/63 (87%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||||| |||| | |||| | ||||| || ||||| ||||| |||||
Sbjct: 965 atgatcaagatgggtgacaatcgccacttactggatctaattggagaaattaggaagaat 1024

Query: 2164 tgt 2166
|||
Sbjct: 1025 tgt 1027

Score = 54.0 bits (27), Expect = 0.006
Identities = 48/55 (87%)
Strand = Plus / Plus

Query: 1157 ggatgtgatgggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| | | | ||||| ||||| ||||| |||||
Sbjct: 290 ggatgtgatggatcactgctccttgatgacacatcaagcttcactggagagaaga 344

Score = 44.1 bits (22), Expect = 6.1
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttggactttc 1617
|||| | ||||| ||||| || |||| | || ||||
Sbjct: 572 acttctaaccttaataactcatctctagtttttagtgctgttggcctttc 621

>gb|EF433455.1| Ipomoea batatas basic peroxidase swpb4 mRNA, complete cds
Length = 1369

Score = 63.9 bits (32), Expect = 7e-06
Identities = 47/52 (90%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| || |||||||||||| | ||||||||||| |||||||||||
Sbjct: 180 cgcatgggcgctctctccttcgcctcttcttccacgactgctttgtcaatg 231

Score = 60.0 bits (30), Expect = 1e-04
Identities = 63/74 (85%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
||||||| |||||||||||||||||||| || || | || ||||||| |||||||
Sbjct: 888 gatttcgcagccgccatgatcaagatgggtgatatcaagcccctcactgggaacaatgga 947

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||
Sbjct: 948 gagatcaggaagaa 961

Score = 44.1 bits (22), Expect = 6.1
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 1160 tgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaa 1209
||||||| ||||||| ||||| || ||||| |||||||||||||
Sbjct: 234 tgtgatggatcaattctcttggacgatacatcttccttcaccggagagaa 283

>gb|AC235385.1| Glycine max strain Williams 82 clone GM_WBb0113B18, complete sequence
Length = 137121

Score = 61.9 bits (31), Expect = 3e-05
Identities = 37/39 (94%)
Strand = Plus / Minus

Query: 277 aaattatTTTTCTTTAATTCTTAATTAATATCCTAA 315
|||| |||||||||||||||| |||||||||||||
Sbjct: 62660 aaataattTTTTCTTTAATTTTAAATTAATATCCTAA 62622

>gb|GQ258782.1| Brassica rapa peroxidase 52 mRNA, partial cds
Length = 1113

Score = 60.0 bits (30), Expect = 1e-04
Identities = 147/186 (79%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| || ||||| ||||| | ||||| ||||| || ||||| | |||||
Sbjct: 172 ggatgcgacggttctattctactagatgacacatcaagctttacgggagaacaaaacgcg 231

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| ||| || || ||||| ||||| || | || || ||||| ||||| ||||| ||
Sbjct: 232 aacccaaaccgcaattctgctcgtgggtttaatgtgatagacaacattaaacagcggtt 291

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|| || ||||| || ||||| || || || ||||| | ||||| || |||||
Sbjct: 292 gaagcagcatgtcccggttgtgtcttgtgctgatatcttagccatcgagctagagac 351

Query: 1337 tctgtt 1342
|||||
Sbjct: 352 tctgtt 357

>gb|FJ099770.1| Pinus taeda isolate 1299 anonymous locus 2_6350_01 genomic sequence
Length = 439

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||| ||||| ||||| | ||||| ||||| ||||| |||||
Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099768.1| Pinus taeda isolate 1282 anonymous locus 2_6350_01 genomic sequence
Length = 448

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)

Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||

Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| ||||||

Sbjct: 248 aatccaacat 239

>gb|FJ099767.1| Pinus taeda isolate 1292 anonymous locus 2_6350_01 genomic sequence
Length = 439

Score = 60.0 bits (30), Expect = 1e-04

Identities = 60/70 (85%)

Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||

Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| ||||||

Sbjct: 248 aatccaacat 239

>gb|FJ099766.1| Pinus taeda isolate 1285 anonymous locus 2_6350_01 genomic sequence
Length = 434

Score = 60.0 bits (30), Expect = 1e-04

Identities = 60/70 (85%)

Strand = Plus / Minus

Query: 1787 taggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||

Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| ||||||

Sbjct: 248 aatccaacat 239

>gb|FJ099765.1| Pinus taeda isolate 1288 anonymous locus 2_6350_01 genomic sequence
Length = 438

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099762.1| Pinus taeda isolate 1298 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 307 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 248

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 247 aatccaacat 238

>gb|FJ099761.1| Pinus taeda isolate 1289 anonymous locus 2_6350_01 genomic sequence
Length = 360

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099760.1| Pinus taeda isolate 1297 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 taggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||| ||||| ||||| | |||||
Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099759.1| Pinus taeda isolate 1283 anonymous locus 2_6350_01 genomic sequence
Length = 357

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 taggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||| ||||| ||||| | |||||
Sbjct: 308 taggtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099758.1| Pinus taeda isolate 1287 anonymous locus 2_6350_01 genomic sequence
Length = 449

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|FJ099757.1| Pinus taeda isolate 1291 anonymous locus 2_6350_01 genomic sequence
Length = 358

Score = 60.0 bits (30), Expect = 1e-04
Identities = 60/70 (85%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | |||||||||||||||||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||||
Sbjct: 248 aatccaacat 239

>gb|EF433456.1| Ipomoea batatas basic peroxidase swpb5 mRNA, complete cds
Length = 1331

Score = 60.0 bits (30), Expect = 1e-04
Identities = 36/38 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaagaattg 2165
|||||||||| ||| |||||||||||||||||||
Sbjct: 1038 cctctcactggttcccatggagaaatcaggaagaattg 1075

>gb|AC226196.1| Musa acuminata clone BAC MA4-125A12, complete sequence
Length = 110853

Score = 60.0 bits (30), Expect = 1e-04
Identities = 51/58 (87%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||| ||||||| || |||| | ||||||| || ||||||| |||||||
Sbjct: 32082 cagggctgtgatggatcagttctgctggatgacacgtccagcttcaccggagagaaga 32139

Score = 46.1 bits (23), Expect = 1.5
Identities = 71/87 (81%)
Strand = Plus / Plus

Query: 1960 gacaactactacttcaagaacctcggtcagaagaagggtctcctccactctgatcagcaa 2019
||||||| ||||||| |||| | || || ||||||| || || ||||| || |||||
Sbjct: 32773 gacaacttctacttcaggaacttggtgaagaagaaggcctgctgcactcggaccagcag 32832

Query: 2020 ctgttcaacgggtgggtccaccgactcc 2046
||||||| || || |||||||
Sbjct: 32833 ctgttcagtggaggatccaccgactcc 32859

>ref|XM_001754018.1| Physcomitrella patens subsp. patens predicted protein
(PHYPADRAFT_115024) mRNA, complete cds
Length = 1095

Score = 60.0 bits (30), Expect = 1e-04
Identities = 36/38 (94%)
Strand = Plus / Plus

Query: 741 tgcttctctccttcgcttggttcttccacgattgctttg 778
|||| | ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 273 tgctgctctgcttcgcttggttcttccacgattgctttg 310

>emb|AM449831.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X191828.16,
clone ENTAV 115
Length = 47040

Score = 60.0 bits (30), Expect = 1e-04
Identities = 33/34 (97%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttc 1827
||||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Sbjct: 34025 tcacacaattggacaagcaaggtgcacaagcttc 33992

>gb|AY206414.1| Ipomoea batatas anionic peroxidase swpb3 mRNA, complete cds
Length = 1290

Score = 60.0 bits (30), Expect = 1e-04
Identities = 63/74 (85%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccgcctatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||||||||||||||| || || | || ||||||| |||||
Sbjct: 918 gatttcgcagccgcccgcctatgatcaagatgggtgatatcaagccactcactgggaacaatgga 977

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||
Sbjct: 978 gagatcaggaagaa 991

Score = 56.0 bits (28), Expect = 0.002
Identities = 46/52 (88%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||||| || ||||||||||||| | ||||||| || |||||||||
Sbjct: 210 cgcatgggcgcctctctccttcgcctcttcttccatgactgctttgtcaatg 261

>gb|AF485265.1| Gossypium hirsutum class III peroxidase (pod3) mRNA, complete cds
Length = 1336

Score = 60.0 bits (30), Expect = 1e-04
Identities = 42/46 (91%)
Strand = Plus / Plus

Query: 737 tgggtgcttctctccttcgcttggttcttccacgattgctttgtcaa 782
||||||||||| ||||||||||||| || || |||||
Sbjct: 257 tgggtgcttctctcctccgcttggttcttccatgactgtttgtcaa 302

Score = 52.0 bits (26), Expect = 0.025
Identities = 53/62 (85%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163

||||| |||||||||||| ||| || ||||| || || ||||| |||||||||||||
Sbjct: 979 atgataaagatgggagatattaagccactcaccgatcaaattggtgaaatcaggaagaat 1038

Query: 2164 tg 2165

||
Sbjct: 1039 tg 1040

>gb|EZ328614.1| TSA: Artemisia annua strain Madagascar Contig15160, mRNA sequence
Length = 324

Score = 58.0 bits (29), Expect = 4e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784

||||| |||||||||||||| ||| ||||| |||||||||||||
Sbjct: 202 atgggcgcttctctccttcgcttggttgcacttccatgattgctttgtcaatg 250

>gb|EZ256818.1| TSA: Artemisia annua strain Artemis Contig23488, mRNA sequence
Length = 426

Score = 58.0 bits (29), Expect = 4e-04
Identities = 44/49 (89%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784

||||| |||||||||||||| ||| ||||| |||||||||||||
Sbjct: 204 atgggcgcttctctccttcgcttggttgcacttccatgattgctttgtcaatg 252

>gb|EZ397212.1| TSA: Artemisia annua strain Uganda Contig13707, mRNA sequence
Length = 491

Score = 58.0 bits (29), Expect = 4e-04
Identities = 44/49 (89%)
Strand = Plus / Minus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784

||||| |||||||||||||| ||| ||||| |||||||||||||
Sbjct: 167 atgggcgcttctctccttcgcttggttgcacttccatgattgctttgtcaatg 119

>dbj|AK328734.1| Solanum lycopersicum cDNA, clone: LEFL3035G12, HTC in root

Length = 1222

Score = 58.0 bits (29), Expect = 4e-04

Identities = 59/69 (85%)

Strand = Plus / Plus

Query: 1215 caaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccg 1274

|||||

Sbjct: 354 caaaccccaacaggaactcggtcgtggatttgatgtcattgatgatattaaatctgcac 413

Query: 1275 tggagaaag 1283

|||||

Sbjct: 414 tggagaaag 422

>gb|AC235153.1| Glycine max strain Williams 82 clone GM_WBa0085L07, complete sequence

Length = 99314

Score = 58.0 bits (29), Expect = 4e-04

Identities = 68/81 (83%)

Strand = Plus / Minus

Query: 2736 ttaaattcattcgaacgtaaataataactaaacattagaaacataatcatccttaacaatc 2795

|||||

Sbjct: 90525 ttaaattcattcaacaaacatcataattaaacattcgaacataaccatttttaatgatc 90466

Query: 2796 aatattttaattcttaaaactt 2816

|||||

Sbjct: 90465 aatatttctaattcttaaaactt 90445

>gb|AC235140.1| Glycine max strain Williams 82 clone GM_WBa0068I04, complete sequence

Length = 138531

Score = 58.0 bits (29), Expect = 4e-04

Identities = 68/81 (83%)

Strand = Plus / Plus

Query: 2736 ttaaattcattcgaacgtaaataataactaaacattagaaacataatcatccttaacaatc 2795

|||||

Sbjct: 102124 ttaaattcattcaacaaacatcataattaaacattcgaacataaccatttttaatgatc 102183

Query: 2796 aatattttaattcttaaaactt 2816

||||| |||||||||
Sbjct: 102184 aatattctaattcttaaactt 102204

>emb|AJ544515.1| Asparagus officinalis partial mRNA for peroxidase (prx2 gene)
Length = 1041

Score = 58.0 bits (29), Expect = 4e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||| ||||||||| ||||| || ||||||| || || ||||| || |||||
Sbjct: 826 gccatgatcaagatgggagatattagccccctcactgggtctaaaggagagattaggaag 885

Query: 2161 a 2161
|
Sbjct: 886 a 886

>ref|XM_002521820.1| Ricinus communis Lignin-forming anionic peroxidase precursor,
putative, mRNA
Length = 978

Score = 56.0 bits (28), Expect = 0.002
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcgatatccttgc 1320
||||| || ||||||| | ||||| ||||||||| |||||||||
Sbjct: 343 aaatctgcagtggagaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>ref|XM_002521805.1| Ricinus communis Lignin-forming anionic peroxidase precursor,
putative, mRNA
Length = 978

Score = 56.0 bits (28), Expect = 0.002
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcgatatccttgc 1320
||||| || ||||||| | ||||| ||||||||| |||||||||
Sbjct: 343 aaatctgcagtggagaagatatgtcctggagttgtttcctgcgctgatatccttgc 398

>ref|XM_002521804.1| Ricinus communis Peroxidase 30 precursor, putative, mRNA
Length = 891

Score = 56.0 bits (28), Expect = 0.002
Identities = 49/56 (87%)
Strand = Plus / Plus

Query: 1265 aaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatataccttgc 1320
||||| || |||||||| | ||||| ||||||||||||||||| |||||||||
Sbjct: 343 aaatctgcagtgagagaagatatgtcctggagttgtttcctgcgctgatataccttgc 398

>gb|FJ529216.1| Cucumis sativus 1-aminocyclopropane-1-carboxylate synthase (ACS2) gene,
ACS2-M allele and putative peroxidase gene, complete cds
Length = 52751

Score = 56.0 bits (28), Expect = 0.002
Identities = 34/36 (94%)
Strand = Plus / Minus

Query: 751 cttegcttgttcttccacgattgctttgtcaatgta 786
||||| ||||||||||||||||||| |||||
Sbjct: 50350 cttegcatgttcttccacgattgctttgtaaatgta 50315

>ref|XM_002450088.1| Sorghum bicolor hypothetical protein, mRNA
Length = 1265

Score = 56.0 bits (28), Expect = 0.002
Identities = 58/68 (85%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||| ||||| ||||| ||||| | ||||| ||||||||||||| || |||||||
Sbjct: 686 ggtgctcacaccattgggcaagcacggtgcaccaacttcagagcccacatatatacaacgac 745

Query: 1849 accaacaat 1856
||| ||||
Sbjct: 746 accgacat 753

>gb|FJ050772.1| Pinus taeda isolate 4650 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.002
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050764.1| Pinus taeda isolate 4651 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.002
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050758.1| Pinus taeda isolate 4655 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.002
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacacgataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|FJ050757.1| Pinus taeda isolate 4653 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 56.0 bits (28), Expect = 0.002
Identities = 61/72 (84%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccatagccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

Query: 1845 cgagaccaacat 1856
||| |||||
Sbjct: 442 cgaatccaacat 431

>gb|AF149278.1|AF149278 Phaseolus vulgaris peroxidase 3 precursor (FBP3) mRNA, complete cds
Length = 1850

Score = 56.0 bits (28), Expect = 0.002
Identities = 46/52 (88%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttcacgattgctttgtcaatg 784
||||||| ||||| ||||| || ||||| || || ||||| |||||
Sbjct: 981 cgcatgggagcttctctccttcgcctcttctttcatgactgctttgtcaatg 1032

>dbj|AK320453.1| Solanum lycopersicum cDNA, clone: LEFL1009CA06, HTC in leaf
Length = 1260

Score = 54.0 bits (27), Expect = 0.006
Identities = 57/67 (85%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||| ||||| ||||| ||||| || || || || || || ||||| |||
Sbjct: 649 ggtgctcacacaattggacaagcaagatgcacaacatttagggcacgtatatacaatgag 708

Query: 1849 accaaca 1855
|||||
Sbjct: 709 accaaca 715

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||||| || ||| ||| || ||||| || ||||| ||||| |||||
Sbjct: 967 atgatcaagatgggcatattcgtccacttactggatcgaatggtgaaattaggaagaa 1025

>dbj|AK320190.1| Solanum lycopersicum cDNA, clone: LEFL1006BD07, HTC in leaf
Length = 1236

Score = 54.0 bits (27), Expect = 0.006
Identities = 48/55 (87%)
Strand = Plus / Plus

Query: 1215 caaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatc 1269
||||||| || ||||| ||||| || ||||| ||||| |||||
Sbjct: 354 caaaccccaacaggaattcagctcgtggattcgaagtccttgacgagattaaatc 408

>gb|AC235342.1| Glycine max strain Williams 82 clone GM_WBb0088H14, complete sequence
Length = 183165

Score = 54.0 bits (27), Expect = 0.006
Identities = 33/35 (94%)
Strand = Plus / Plus

Query: 281 tattttttcttttaatttcttaattaatcctaa 315
||||||| ||||| |||||
Sbjct: 50421 tattttttcttttaatttctcaattaatgtcctaa 50455

>emb|CT832689.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCRN133B17, full
insert sequence
Length = 1270

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaaggaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853

||||| ||||| ||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 717 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 776

Query: 1854 cat 1856

|||
Sbjct: 777 cat 779

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| | |||||||| | |||||||| | ||||| | |||
Sbjct: 826 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 885

Query: 1963 aactactacttcaagaacctcgcttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| ||||||| ||||| | |||||||
Sbjct: 886 aacaactactacaagaacctcgctcgtaagaagggtcctgcattctgatcag 939

>emb|CT832688.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA237B02, full
insert sequence
Length = 2326

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 1773 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 1832

Query: 1854 cat 1856

|||
Sbjct: 1833 cat 1835

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 1882 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 1941

Query: 1963 aactactacttcaagaacctcggtcagaagaagggctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1942 aacaactactacaagaacctcgctcgtaagaagggctcctgcattctgatcag 1995

>emb|CT832687.1| Oryza sativa (indica cultivar-group) cDNA clone:OSIGCFA219E15, full
insert sequence
Length = 1331

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| || ||||| ||||| ||||| || ||||| |||||
Sbjct: 783 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 842

Query: 1854 cat 1856
|||
Sbjct: 843 cat 845

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 892 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 951

Query: 1963 aactactacttcaagaacctcggtcagaagaagggctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 952 aacaactactacaagaacctcgctcgtaagaagggctcctgcattctgatcag 1005

>ref|NM_001072503.1| Oryza sativa (japonica cultivar-group) Os12g0112000 (Os12g0112000)
mRNA, complete cds
Length = 1318

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 719 tcacaccattgggcaagcagcatgcacaaacttcagagctcatatatacaacgaaaccaa 778

Query: 1854 cat 1856
|||
Sbjct: 779 cat 781

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||||||| || ||||||||| || ||||| || ||
Sbjct: 828 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 887

Query: 1963 aactactacttcaagaacctcgcttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| || ||||||| ||||| || |||||||
Sbjct: 888 aacaactactacaagaacctcgctcgtaagaagggtctcctgcattctgatcag 941

>tpe|BN000664.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx135 gene for
class III peroxidase 135 precursor, exons 1-4
Length = 2198

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||||||||||||| | || ||||||| |||||
Sbjct: 1811 tcacaccattgggcaagcagcatgcacaaacttcagagctcatatatacaacgaaaccaa 1870

Query: 1854 cat 1856
|||
Sbjct: 1871 cat 1873

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 1920 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 1979

Query: 1963 aactactacttcaagaacctcgcttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1980 aacaactactacaagaacctcgctcgtaagaagggtctcctgcattctgatcag 2033

>dbj|AK069456.1| Oryza sativa Japonica Group cDNA clone:J023019E08, full insert
sequence
Length = 1319

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| ||||| | ||||| ||||| ||||| || ||||| |||||
Sbjct: 720 tcacaccattgggcaagcacgatgcacaaacttcagagctcatatatacaacgaaaccaa 779

Query: 1854 cat 1856
|||
Sbjct: 780 cat 782

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || ||||| || ||||| || ||||| || ||
Sbjct: 829 tcaggatcaggtgacaataacctggcacctctggatcttcagacccaaccgtgttcgag 888

Query: 1963 aactactacttcaagaacctcgcttcagaagaagggtctcctccactctgatcag 2016

Sbjct: 889 aacaactactacaagaacctcgctcgtaagaaggggctcctgcattctgatcag 942

Score = 52.0 bits (26), Expect = 0.025
Identities = 92/114 (80%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||| ||||| || |||||||| || |||||||| || ||||| || ||
Sbjct: 24220 tcaggatcaggtgacaataacctggcacctctggatcttcagacgccaaccgtgttcgag 24161

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||| ||||| ||||||||| || ||||||| ||||| || |||||||||
Sbjct: 24160 aacaactactacaagaacctcgtcgtcaagaagggtcctgcattctgatcag 24107

>gb|EZ315890.1| TSA: Artemisia annua strain Madagascar Contig2436, mRNA sequence
Length = 309

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Minus

Query: 2089 gatttcgccgccgccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || ||||||||||||||||| || ||||||||| || |||||
Sbjct: 265 gatttcgccgctgccatgatcaagatgggtgatattagtcacttactgg 216

>gb|EZ359220.1| TSA: Artemisia annua strain Uganda Contig6381, mRNA sequence
Length = 492

Score = 52.0 bits (26), Expect = 0.025
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 1907 ggtcaggggacaacaatctggcaccacttgatcttcaaactccaac 1952
||||||| ||||||||| ||||||| || ||||| |||||||||
Sbjct: 11 ggtcaggagacaacaatttggcaccgctagatctcaaactccaac 56

>gb|EZ166433.1| TSA: Artemisia annua strain Artemis Contig25839, mRNA sequence
Length = 448

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 2089 gatttcgccgcccgcgatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || ||||||||||||||||| || ||||||| || |||||
Sbjct: 164 gatttcgcggctgccatgatcaagatgggtgatattagtcacttactgg 213

>gb|BT106781.1| Picea glauca clone GQ03010_F17 mRNA sequence
Length = 722

Score = 52.0 bits (26), Expect = 0.025
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 1957 ttgacaactactacttcaagaacct 1982
|||||||||||||||||||||||
Sbjct: 192 ttgacaactactacttcaagaacct 217

>ref|XM_002285606.1| PREDICTED: Vitis vinifera hypothetical protein LOC100253646
(LOC100253646), mRNA
Length = 1032

Score = 52.0 bits (26), Expect = 0.025
Identities = 50/58 (86%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatataccttgccatcgctgccagagactctgttc 1343
||||||||||||||||||| || || || ||||| || || ||||||| |||||
Sbjct: 382 tgtccaggagttgtttcctgcgctgacatactagccatagccgcccgagactccgttc 439

>gb|AC235417.1| Glycine max strain Williams 82 clone GM_WBb0135A07, complete sequence
Length = 184957

Score = 52.0 bits (26), Expect = 0.025
Identities = 35/38 (92%)
Strand = Plus / Plus

Query: 279 attatTTTTtctTTtaatttcttaattaataatcctaag 316
||||||| ||||||| ||||||||| |||||
Sbjct: 56366 attatTTTTtatttTaatttatttaattaatattcctaag 56403

>ref|XM_002334206.1| Populus trichocarpa predicted protein, mRNA
Length = 954

Score = 52.0 bits (26), Expect = 0.025

Identities = 35/38 (92%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||| ||||| |||||
Sbjct: 874 gccatgatcaaaatgggagacatcagtcactcactgg 911

>ref|NM_001157951.1| Zea mays peroxidase 2 (LOC100285056), mRNA
>gi|195646697|gb|EU970699.1| Zea mays clone 349100
peroxidase 2 precursor, mRNA, complete cds
Length = 1360

Score = 52.0 bits (26), Expect = 0.025
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 2092 ttgccgccgccatgatcaagatggg 2117
||||||| ||||| ||||| |||||
Sbjct: 956 ttgccgccgccatgatcaagatggg 981

>gb|BT044614.1| Arabidopsis thaliana unknown protein (At4g33420) mRNA, complete cds
Length = 978

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
||||||| || ||||| ||||| ||||| |||||
Sbjct: 373 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 422

>gb|FJ099764.1| Pinus taeda isolate 1294 anonymous locus 2_6350_01 genomic sequence
Length = 414

Score = 52.0 bits (26), Expect = 0.025
Identities = 59/70 (84%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||| ||||| ||||| | ||||| ||||| |||||
Sbjct: 308 tagtgctcatacaattggccaagcgcggtgcaccacattcagagtcgcatctacaacg 249

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 248 aatccaacat 239

>gb|FJ099763.1| Pinus taeda isolate 1290 anonymous locus 2_6350_01 genomic sequence
Length = 448

Score = 52.0 bits (26), Expect = 0.025
Identities = 59/70 (84%)
Strand = Plus / Minus

Query: 1787 tagtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacg 1846
||||| ||| ||||||| ||||| ||||||| | ||||||||| |||||
Sbjct: 307 tagtggtcatacaattggccaagcgcggtgcaccacattcagagcccgcatctacaacg 248

Query: 1847 agaccaacat 1856
| |||||
Sbjct: 247 aatccaacat 238

>gb|BT042071.1| Zea mays full-length cDNA clone ZM_BFb0125B03 mRNA, complete cds
Length = 1342

Score = 52.0 bits (26), Expect = 0.025
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 2092 ttgccgccgccatgatcaagatggg 2117
||||||||||||||||||
Sbjct: 1003 ttgccgccgccatgatcaagatggg 1028

>emb|AM450885.2| Vitis vinifera contig VV78X220288.8, whole genome shotgun sequence
Length = 12944

Score = 52.0 bits (26), Expect = 0.025
Identities = 26/26 (100%)
Strand = Plus / Plus

Query: 1797 cacaattggacaagcaaggtgcacaa 1822
||||||||||||||||||
Sbjct: 1055 cacaattggacaagcaaggtgcacaa 1080

>ref|NM_119496.3| Arabidopsis thaliana peroxidase, putative (AT4G33420) mRNA, complete
cds
Length = 1197

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 401 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 450

>emb|AM446475.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X020658.13,
clone ENTAV 115
Length = 18355

Score = 52.0 bits (26), Expect = 0.025
Identities = 50/58 (86%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactctgttc 1343
|||||
Sbjct: 15894 tgtccaggagttgtttcctgcgcgtgacatactagccatagccgcccagactccgttc 15951

>emb|AM436560.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X083975.17,
clone ENTAV 115
Length = 6769

Score = 52.0 bits (26), Expect = 0.025
Identities = 50/58 (86%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
|||||
Sbjct: 5849 cagggatgtgatgcttctatattattggacgacactgcaagctttaccggagagaaga 5792

Score = 44.1 bits (22), Expect = 6.1
Identities = 49/58 (84%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctatttgatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| || ||||| ||| ||| |||||
Sbjct: 1513 cagggatgtgatgcttctatattatttgatgacactgcaaactttactggagagaaga 1456

>emb|AM429435.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X154826.4,
clone ENTAV 115
Length = 7609

Score = 52.0 bits (26), Expect = 0.025
Identities = 50/58 (86%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctatttgatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| || ||||| ||| ||| ||||| |||||
Sbjct: 2278 cagggatgtgatgcttctatattattggacgacactgcaaagctttaccggagagaaga 2221

>ref|NM_101322.1| Arabidopsis thaliana anionic peroxidase, putative (AT1G14550) mRNA,
complete cds
Length = 966

Score = 52.0 bits (26), Expect = 0.025
Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
||||||| ||||| ||||| |||||
Sbjct: 913 cctctcactggctctaattggagaaatcagaaaga 946

>gb|AF453791.1| Ipomoea batatas anionic peroxidase (POD) gene, promoter region and
partial cds
Length = 3741

Score = 52.0 bits (26), Expect = 0.025
Identities = 47/54 (87%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgta 786
||||||| ||||| ||| ||||| | ||||| |||||
Sbjct: 2101 cgcattggggcttcctcattcgtctcttcttccacgattgctttgtcgatgta 2154

>dbj|AB193816.1| Pisum sativum mRNA for peroxidase, complete cds, clone:PsPOX11
Length = 1217

Score = 52.0 bits (26), Expect = 0.025
Identities = 41/46 (89%)
Strand = Plus / Plus

Query: 739 ggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||||| | ||||||||| || ||||||| |||
Sbjct: 197 ggtgcttctatacttcgcttggttcttccatgactgctttgttaatg 242

Score = 44.1 bits (22), Expect = 6.1
Identities = 61/74 (82%)
Strand = Plus / Plus

Query: 1477 gcttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagcca 1536
||||||| || ||||||| || ||||||||| || ||||| || |||||
Sbjct: 433 gcttggaggaccacatggatggttccacttggaagaagagatgcaagaacagcaagcca 492

Query: 1537 atctgctgctaaca 1550
| ||||| |||||
Sbjct: 493 aagtctgccaaca 506

>dbj|AK176812.1| Arabidopsis thaliana mRNA for peroxidase ATP17a like protein, partial
cds, clone: RAFL25-36-D17
Length = 1203

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttctgcgcagatatccttgccatcgctgccagaga 1335
||||||| || ||||||||| ||||| ||||| |||||
Sbjct: 397 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 446

>gb|AY089094.1| Arabidopsis thaliana clone 32346 mRNA, complete sequence
Length = 1179

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
||||||| ||| ||||| ||||| ||||| |||||
Sbjct: 395 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 444

>gb|AC108072.3| Homo sapiens BAC clone RP11-704A16 from 2, complete sequence
Length = 36787

Score = 52.0 bits (26), Expect = 0.025
Identities = 29/30 (96%)
Strand = Plus / Minus

Query: 1045 atatatttaaagataataaatatttctgct 1074
||||||| ||||| ||||| ||||| |||||
Sbjct: 31744 atatatttaaagttaataaatatttctgct 31715

>gb|AF451951.1| Arabidopsis thaliana class III peroxidase ATP32 mRNA, complete cds
Length = 1082

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
||||||| ||| ||||| ||||| ||||| |||||
Sbjct: 373 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 422

>emb|AL161583.2| Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
Length = 199536

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgagatatccttgccatcgctgccagaga 1335
||||||| ||| ||||| ||||| ||||| |||||
Sbjct: 113403 tgtccaggagttgtatcatgcgagatatagttgccatggctgctagaga 113452

>gb|AC010657.3|AC010657 Genomic sequence for Arabidopsis thaliana BAC T5E21 from chromosome I,
complete sequence
Length = 83351

Score = 52.0 bits (26), Expect = 0.025

Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 17743 cctctcactggctctaataatggagaaatcagaaaga 17776

>emb|AL035678.1| Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)
Length = 96475

Score = 52.0 bits (26), Expect = 0.025
Identities = 44/50 (88%)
Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagaga 1335
|||||
Sbjct: 48624 tgtccaggagttgtatcatgcgcagatatagttgccatggctgctagaga 48673

>gb|AC012188.2|F14L17 Sequence of BAC F14L17 from Arabidopsis thaliana chromosome 1, complete
sequence
Length = 111686

Score = 52.0 bits (26), Expect = 0.025
Identities = 32/34 (94%)
Strand = Plus / Plus

Query: 2128 cctctcactggctccaatggagaaatcaggaaga 2161
|||||
Sbjct: 111350 cctctcactggctctaataatggagaaatcagaaaga 111383

>gb|EZ395724.1| TSA: Artemisia annua strain Uganda Contig12219, mRNA sequence
Length = 273

Score = 50.1 bits (25), Expect = 0.099
Identities = 55/65 (84%)
Strand = Plus / Minus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 221 gccatgatcaagatgggtgatattagtcacttactggacgtaatggtgagatcaggaag 162

Query: 2161 aattg 2165
 |||||
Sbjct: 161 aattg 157

>gb|EZ362599.1| TSA: Artemisia annua strain Uganda Contig9760, mRNA sequence
Length = 346

Score = 50.1 bits (25), Expect = 0.099
Identities = 55/65 (84%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
 ||||||| ||||||||||||| ||||| ||||| | || | || ||||| |||||
Sbjct: 216 cttggaggacctacatggaatgtgaaactgggaagacgtgactcaaggactgcgagccaa 275

Query: 1538 tctgc 1542
 |||||
Sbjct: 276 gctgc 280

>gb|BT066765.1| Zea mays full-length cDNA clone ZM_BFb0066D03 mRNA, complete cds
Length = 1217

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
 ||||| ||||||||||||| ||||||||||| || |||||
Sbjct: 665 tgcaccaacttcagagcccacatctacaacgacaccgacat 705

>gb|BT055307.1| Zea mays full-length cDNA clone ZM_BFc0167H14 mRNA, complete cds
Length = 1194

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
 ||||| ||||||||||||| ||||||||||| || |||||
Sbjct: 640 tgcaccaacttcagagcccacatctacaacgacaccgacat 680

>gb|EU962146.1| Zea mays clone 240603 mRNA sequence
Length = 1299

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
||||| ||||||||| ||||||||| ||| ||||
Sbjct: 737 tgcaccaacttcagagcccacatctacaacgacaccgacat 777

>gb|FJ070719.1| Pinus taeda isolate 7938 anonymous locus 0_3458_02 genomic sequence
Length = 364

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 269 ccatgataaagatgggaaacattagccctctcactgg 233

>gb|FJ070718.1| Pinus taeda isolate 7947 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070717.1| Pinus taeda isolate 7943 anonymous locus 0_3458_02 genomic sequence
Length = 359

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||

Sbjct: 263 ccatgataaagatgggaaacattagccctctcactgg 227

>gb|FJ070716.1| Pinus taeda isolate 7950 anonymous locus 0_3458_02 genomic sequence
Length = 350

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070715.1| Pinus taeda isolate 7940 anonymous locus 0_3458_02 genomic sequence
Length = 366

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 270 ccatgataaagatgggaaacattagccctctcactgg 234

>gb|FJ070714.1| Pinus taeda isolate 7948 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070713.1| Pinus taeda isolate 7949 anonymous locus 0_3458_02 genomic sequence
Length = 438

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 293 ccatgataaagatgggaaacattagccctctcactgg 257

>gb|FJ070712.1| Pinus taeda isolate 7952 anonymous locus 0_3458_02 genomic sequence
Length = 349

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 253 ccatgataaagatgggaaacattagccctctcactgg 217

>gb|FJ070711.1| Pinus taeda isolate 7941 anonymous locus 0_3458_02 genomic sequence
Length = 350

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070710.1| Pinus taeda isolate 7951 anonymous locus 0_3458_02 genomic sequence
Length = 360

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 264 ccatgataaagatgggaaacattagccctctcactgg 228

>gb|FJ070709.1| Pinus taeda isolate 7942 anonymous locus 0_3458_02 genomic sequence
Length = 440

Score = 50.1 bits (25), Expect = 0.099

Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 295 ccatgataaagatgggaaacattagccctctcactgg 259

>gb|FJ070708.1| Pinus taeda isolate 7953 anonymous locus 0_3458_02 genomic sequence
Length = 349

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 254 ccatgataaagatgggaaacattagccctctcactgg 218

>gb|FJ070707.1| Pinus taeda isolate 7937 anonymous locus 0_3458_02 genomic sequence
Length = 420

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 275 ccatgataaagatgggaaacattagccctctcactgg 239

>gb|FJ070706.1| Pinus taeda isolate 7946 anonymous locus 0_3458_02 genomic sequence
Length = 297

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 191 ccatgataaagatgggaaacattagccctctcactgg 155

>gb|FJ070705.1| Pinus taeda isolate 7945 anonymous locus 0_3458_02 genomic sequence

Length = 350

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 255 ccatgataaagatgggaaacattagccctctcactgg 219

>gb|FJ070703.1| Pinus taeda isolate 7939 anonymous locus 0_3458_02 genomic sequence
Length = 355

Score = 50.1 bits (25), Expect = 0.099
Identities = 34/37 (91%)
Strand = Plus / Minus

Query: 2102 ccatgatcaagatgggagacattagtcctctcactgg 2138
||||||| ||||||||| ||||||| |||||||||
Sbjct: 259 ccatgataaagatgggaaacattagccctctcactgg 223

>ref|NM_001137528.1| Zea mays hypothetical protein LOC100192105 (LOC100192105), mRNA
>gi|194690673|gb|BT034416.1| Zea mays full-length cDNA
clone ZM_BFc0170D07 mRNA, complete cds
Length = 1217

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856
||||| ||||||||||||| ||||||||||||| ||| |||||
Sbjct: 665 tgcaccaacttcagagcccacatctacaacgacaccgacat 705

>gb|DQ244260.1| Zea mays clone 3973 mRNA sequence
Length = 1224

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 1816 tgcacaaacttcagagcccgcatctacaacgagaccaacat 1856

||||| ||||||||||||| ||||||||||| ||| ||||
Sbjct: 672 tgcaccaacttcagagcccacatctacaacgacaccgacat 712

>tpc|BN000615.1| TPA: TPA_inf: Oryza sativa (japonica cultivar-group) prx86 gene for
class III peroxidase 86 precursor, exons 1-3
Length = 1188

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Plus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
||||||| | ||||||||| ||||||||| |||||||||||||
Sbjct: 197 tccttcgcctcttcttccatgattgcttcgtcaatgtaatt 237

>dbj|AP004731.3| Oryza sativa Japonica Group genomic DNA, chromosome 6, BAC
clone:OSJNBa0016D02
Length = 157822

Score = 50.1 bits (25), Expect = 0.099
Identities = 37/41 (90%)
Strand = Plus / Minus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
||||||| | ||||||||| ||||||||| |||||||||||||
Sbjct: 82216 tccttcgcctcttcttccatgattgcttcgtcaatgtaatt 82176

>dbj|AB007645.1| Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K8K14
Length = 72698

Score = 50.1 bits (25), Expect = 0.099
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 760 ttcttccacgattgctttgtcaatgtaatt 788
||||||||||||||||| |||||||||||||
Sbjct: 46952 ttcttccacgattgcttcgtcaatgtaatt 46980

>emb|Y10465.1| S. oleracea mRNA for peroxidase, clone PC44
Length = 1176

Score = 50.1 bits (25), Expect = 0.099

Identities = 43/49 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
 ||||| | ||||| ||||| |||
Sbjct: 209 atgggtgcttccatacttcgttgttcttccacgactgctttgtaaatg 257

Score = 46.1 bits (23), Expect = 1.5
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 1481 ggaggccctacatggaatgttaaacttgaagaagagacgctagaac 1527
 ||||| ||||| ||| ||| |||
Sbjct: 455 ggaggccccacatggaatgtaaaactaggtagaagagatgcaagaac 501

>gb|CP000102.1| Methanospaera stadtmanae DSM 3091, complete genome
 Length = 1767403

Score = 50.1 bits (25), Expect = 0.099
Identities = 25/25 (100%)
Strand = Plus / Plus

Query: 285 ttttcttttaatttcttaattaata 309
 ||||| |||||
Sbjct: 31679 ttttcttttaatttcttaattaata 31703

>emb|FP012230.5| Pig DNA sequence from clone CH242-162F1 on chromosome X, complete
 sequence
 Length = 116800

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 268 atttctataaaattatTTTTTcttttaa 295
 ||||| |||||
Sbjct: 24562 atttctataaaattatTTTTTcttttaa 24589

>gb|EZ275595.1| TSA: Artemisia annua strain Madagascar Contig1982, mRNA sequence
 Length = 688

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 69 cacacaattggacaagcaagatgcacaa 96

>gb|EZ286664.1| TSA: Artemisia annua strain Madagascar Contig13051, mRNA sequence
 Length = 813

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaaga 1513
 |||||
Sbjct: 789 cttggaggacctacatggaatgtgaaactgggaaga 754

Score = 46.1 bits (23), Expect = 1.5
Identities = 38/43 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
 |||||
Sbjct: 501 tcaggggacaacaatttggcaccactagactccaaactccaa 459

>gb|EZ342046.1| TSA: Artemisia annua strain Uganda Contig9262, mRNA sequence
 Length = 588

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 |||||
Sbjct: 493 cacacaattggacaagcaagatgcacaa 466

>gb|EZ321242.1| TSA: Artemisia annua strain Madagascar Contig7788, mRNA sequence

Length = 1218

Score = 48.1 bits (24), Expect = 0.39

Identities = 27/28 (96%)

Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822

|||||

Sbjct: 599 cacacaattggacaagcaagatgcacaa 626

>gb|EZ318330.1| TSA: Artemisia annua strain Madagascar Contig4876, mRNA sequence

Length = 457

Score = 48.1 bits (24), Expect = 0.39

Identities = 33/36 (91%)

Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaaga 1513

|||||

Sbjct: 236 cttggaggacctacatggaatgtgaaactgggaaga 201

>gb|EZ247069.1| TSA: Artemisia annua strain Artemis Contig13739, mRNA sequence

Length = 438

Score = 48.1 bits (24), Expect = 0.39

Identities = 27/28 (96%)

Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822

|||||

Sbjct: 104 cacacaattggacaagcaagatgcacaa 131

>gb|EZ258457.1| TSA: Artemisia annua strain Madagascar Contig1560, mRNA sequence

Length = 246

Score = 48.1 bits (24), Expect = 0.39

Identities = 27/28 (96%)

Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822

|||||

Sbjct: 68 cacacaattggacaagcaagatgcacaa 95

>gb|EZ396283.1| TSA: Artemisia annua strain Uganda Contig12778, mRNA sequence
Length = 352

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||||
Sbjct: 119 cacacaattggacaagcaagatgcacaa 146

>gb|EZ220993.1| TSA: Artemisia annua Contig18004
Length = 707

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||||
Sbjct: 649 cacacaattggacaagcaagatgcacaa 622

>gb|EZ366681.1| TSA: Artemisia annua strain Uganda Contig132, mRNA sequence
Length = 790

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
|||||||
Sbjct: 723 cacacaattggacaagcaagatgcacaa 696

>gb|EZ196247.1| TSA: Artemisia annua strain Artemis Contig9804, mRNA sequence
Length = 252

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Minus

Query: 1478 cttgaggccctacatggaatgttaaacttggaaga 1513
 ||||||| ||||||||||||| ||||| |||||
Sbjct: 223 cttgaggacctacatggaatgtgaaactgggaaga 188

>gb|EZ355157.1| TSA: Artemisia annua strain Uganda Contig2318, mRNA sequence
 Length = 246

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 ||||||||||||||||| |||||
Sbjct: 67 cacacaattggacaagcaagatgcacaa 94

>gb|EZ173232.1| TSA: Artemisia annua strain Artemis Contig32638, mRNA sequence
 Length = 709

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 1795 cacacaattggacaagcaaggtgcacaa 1822
 ||||||||||||||||| |||||
Sbjct: 622 cacacaattggacaagcaagatgcacaa 595

>gb|BT102799.1| Picea glauca clone GQ02016_E21 mRNA sequence
 Length = 953

Score = 48.1 bits (24), Expect = 0.39
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 2110 aagatgggagacattagtcctctcactggctccaatggagaaatcagg 2157
 ||||||| ||| ||||||| | ||||||| |||||||||
Sbjct: 768 aagatggggaacatcagtcctcttacaggctccaaggagaaatcagg 815

>gb|BT101612.1| Picea glauca clone GQ01308_P23 mRNA sequence
 Length = 919

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)

Strand = Plus / Plus

Query: 1957 tttgacaactactacttcaagaac 1980

|||||

Sbjct: 605 tttgacaactactacttcaagaac 628

>gb|AC212861.3| Pongo abelii BAC clone CH276-236D6 from chromosome 1, complete sequence
Length = 192235

Score = 48.1 bits (24), Expect = 0.39

Identities = 24/24 (100%)

Strand = Plus / Plus

Query: 268 atttctataaaattatTTTTtctt 291

|||||

Sbjct: 126165 atttctataaaattatTTTTtctt 126188

>ref|XM_002451803.1| Sorghum bicolor hypothetical protein, mRNA
Length = 837

Score = 48.1 bits (24), Expect = 0.39

Identities = 53/60 (88%), Gaps = 2/60 (3%)

Strand = Plus / Plus

Query: 2059 tacagcaccaacccgggcac-cttctcctctgatttcgccgccgcatgatcaagatggg 2117

||||| ||||| ||| |||| ||| || ||||| ||||| |||||

Sbjct: 709 tacagctccaacccgg-cactcttcgcctcagacttcgccgccgcatgataaagatggg 767

>gb|AC235800.1| Solanum lycopersicum chromosome 3 clone C03HBa0137K15, complete
sequence
Length = 110892

Score = 48.1 bits (24), Expect = 0.39

Identities = 45/52 (86%)

Strand = Plus / Minus

Query: 736 atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787

||||| || ||||| ||||| | ||||| ||||| |||||

Sbjct: 31655 atgggagcgtctctcattcgccctcttcttccacgactgctttgtcgatgtaa 31604

>ref|XM_002285687.1| PREDICTED: Vitis vinifera hypothetical protein LOC100257440

(LOC100257440), mRNA
Length = 1215

Score = 48.1 bits (24), Expect = 0.39
Identities = 48/56 (85%)
Strand = Plus / Plus

Query: 1156 gggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaaga 1211
||||||| ||| || ||||| |||| | ||||| ||||| |||||
Sbjct: 307 gggatgtgatgcttctatattattggacgacactgcaagctttaccggagagaaga 362

>ref|XM_002269022.1| PREDICTED: Vitis vinifera hypothetical protein LOC100263220
(LOC100263220), mRNA
Length = 960

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcggttcagaagaagggtct 2000
||||||| ||| ||||| ||||| |||||
Sbjct: 748 tacttcaagaatctcattcagaagaagggtct 779

>dbj|AK323976.1| Solanum lycopersicum cDNA, clone: LEFL1068DD08, HTC in leaf
Length = 1123

Score = 48.1 bits (24), Expect = 0.39
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 2087 ctgattttcgccgcccatgatcaagatgggagacattagtcctctcactgg 2138
|||||| || || ||||| || ||||| ||||| ||||| |||||
Sbjct: 924 ctgattttgctgcagccatgattaaatgggagatattagtcctctaactgg 975

>ref|XM_002320381.1| Populus trichocarpa predicted protein, mRNA
Length = 951

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 749 tccttcgcttggttcttccacgattgctttgtcaatg 784

||||| ||||||||| ||||||| |||||
Sbjct: 176 tctccgcttggttcttccacgaactgctttgtgaatg 211

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1298 gtttcctgcgcagatataccttgc 1320
|||||||
Sbjct: 352 gtttcctgcgcagatataccttgc 374

>gb|CP001098.1| Halothermothrix orenii H 168, complete genome
Length = 2578146

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 188 aaactaattaagaaattaataaaaaat 215
||||||| |||||||
Sbjct: 1223172 aaactaattaagagattaataaaaaat 1223199

>gb|EF677600.1| Picea sitchensis clone WS02771_I11 unknown mRNA
Length = 1895

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1999 ctctccactctgatcagcaactgttcaacgg 2030
||||||| ||||| |||||
Sbjct: 1536 ctctccactctgatcaggaactattcaacgg 1567

>gb|FJ050773.1| Pinus taeda isolate 4643 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 503 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 444

>gb|FJ050771.1| Pinus taeda isolate 4657 anonymous locus 0_13032_02 genomic sequence
Length = 597

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 460 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 401

>gb|FJ050770.1| Pinus taeda isolate 4649 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|FJ050769.1| Pinus taeda isolate 4648 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|FJ050768.1| Pinus taeda isolate 4659 anonymous locus 0_13032_02 genomic sequence
Length = 584

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)

Strand = Plus / Minus

```
Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
          ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 485 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 426
```

>gb|FJ050767.1| Pinus taeda isolate 4658 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

```
Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
          ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443
```

>gb|FJ050766.1| Pinus taeda isolate 4644 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

```
Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
          ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 503 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 444
```

>gb|FJ050765.1| Pinus taeda isolate 4645 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

```
Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
          ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcagggcccgcatctacaa 443
```

>gb|FJ050763.1| Pinus taeda isolate 4660 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcaggcccgcatctacaa 443

>gb|FJ050762.1| Pinus taeda isolate 4647 anonymous locus 0_13032_02 genomic sequence
Length = 623

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 486 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcaggcccgcatctacaa 427

>gb|FJ050761.1| Pinus taeda isolate 4654 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcaggcccgcatctacaa 443

>gb|FJ050760.1| Pinus taeda isolate 4646 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||||| |||||||||
Sbjct: 502 attaggtgcgcacaccataggccaagcgcggtgcacaagcttcaggcccgcatctacaa 443

>gb|FJ050759.1| Pinus taeda isolate 4656 anonymous locus 0_13032_02 genomic sequence
Length = 640

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 503 attaggtgcgcacaccatagccaagcgcggtgcacaagcttcagggcccgcatctacaa 444

>gb|FJ050756.1| Pinus taeda isolate 4652 anonymous locus 0_13032_02 genomic sequence
Length = 639

Score = 48.1 bits (24), Expect = 0.39
Identities = 51/60 (85%)
Strand = Plus / Minus

Query: 1785 attaggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaa 1844
||||||| ||||| || || ||||| ||||||||| ||||| |||||||||
Sbjct: 502 attaggtgcgcacaccatagccaagcgcggtgcacaagcttcagggcccgcatctacaa 443

>gb|EF083074.1| Picea sitchensis clone WS02728_C07 unknown mRNA
Length = 690

Score = 48.1 bits (24), Expect = 0.39
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 2110 aagatgggagacattagtcctctcactggctccaatggagaaatcagg 2157
||||||| |||| |||||||| || |||||||| |||||||||
Sbjct: 269 aagatggggaacatcagtcctcttacaggctccaaggagaaatcagg 316

>gb|EU024896.1| Uncultured bacterium clone tgutfos2_Contig107 genomic sequence
Length = 33609

Score = 48.1 bits (24), Expect = 0.39
Identities = 33/36 (91%)
Strand = Plus / Plus

Query: 276 aaaattatTTTTCTTTtaatttcttaattaatatc 311

|||||
Sbjct: 2185 aaaattattttttttataattacttaattaatatc 2220

>emb|BX548174.1| Prochlorococcus marinus MED4 complete genome
Length = 1657990

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 279 attattttttcttttaatttctta 302
|||||
Sbjct: 602985 attattttttcttttaatttctta 602962

>gb|CP000647.1| Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence
Length = 5315120

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 881 gaaacaacacttggttccttttatt 904
|||||
Sbjct: 3390746 gaaacaacacttggttccttttatt 3390723

>emb|AM454579.2| Vitis vinifera contig VV78X062755.15, whole genome shotgun sequence
Length = 6610

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Minus

Query: 192 taattaagaaattaaataaaaaatatttatca 223
|||||
Sbjct: 2152 taattaagaaattaaataaaaaatatttatca 2121

>emb|AM428729.2| Vitis vinifera contig VV78X273545.5, whole genome shotgun sequence
Length = 39883

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 284 tttttcttttaatttcttaattaa 307
|||||||
Sbjct: 39856 tttttcttttaatttcttaattaa 39879

>emb|AM462968.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X116164.8,
clone ENTAV 115
Length = 13500

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcggttcagaagaagggtct 2000
||||||| ||| |||||||
Sbjct: 6764 tacttcaagaatctcattcagaagaagggtct 6795

>emb|AM473070.1| Vitis vinifera contig VV78X025151.6, whole genome shotgun sequence
Length = 4985

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 2789 aacaatcaatattttaattcttaactttatt 2820
||||| ||||||| |||||||
Sbjct: 4576 aacaataaatattttaattgttaactttatt 4607

>emb|AM453059.1| Vitis vinifera, whole genome shotgun sequence, contig VV78X216487.15,
clone ENTAV 115
Length = 18125

Score = 48.1 bits (24), Expect = 0.39
Identities = 30/32 (93%)
Strand = Plus / Plus

Query: 1969 tacttcaagaacctcggttcagaagaagggtct 2000
||||||| ||| |||||||
Sbjct: 4424 tacttcaagaatctcattcagaagaagggtct 4455

>emb|AM481723.1| Vitis vinifera contig VV78X090480.3, whole genome shotgun sequence

Length = 13986

Score = 48.1 bits (24), Expect = 0.39

Identities = 24/24 (100%)

Strand = Plus / Plus

Query: 1747 ttttggttgaggaatattgcatggt 1770

|||||

Sbjct: 3837 ttttggttgaggaatattgcatggt 3860

>dbj|AP006865.1| Lotus japonicus genomic DNA, chromosome 2, clone: LjT37H21, TM1032,
complete sequence

Length = 95067

Score = 48.1 bits (24), Expect = 0.39

Identities = 33/36 (91%)

Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattctattggatgacaca 1189

|||||

Sbjct: 32185 cagggatgtgatgcatcaatactattggatgacaca 32220

>dbj|AB049589.1| Avicennia marina PER mRNA for secretory peroxidase, complete cds

Length = 1345

Score = 48.1 bits (24), Expect = 0.39

Identities = 27/28 (96%)

Strand = Plus / Plus

Query: 1292 ggagttgtttcctgcgcagatattccttg 1319

|||||

Sbjct: 412 ggagttgtttcctgcgcagatattccttg 439

>emb|BX828399.1| Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH84ZE10 of Hormone Treated Callus of strain col-0
of Arabidopsis thaliana (thale cress)

Length = 1002

Score = 48.1 bits (24), Expect = 0.39

Identities = 39/44 (88%)

Strand = Plus / Plus

Query: 1286 tgtccaggagttgtttcctgcgcagatatccttgccatcgctgc 1329
||||||| || ||||| ||||| |||||
Sbjct: 380 tgtccaggagttgtatcatgcgcagatatagttgccatggctgc 423

>emb|BX832751.1| Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTPGH95ZG01 of Hormone Treated Callus of strain col-0
of Arabidopsis thaliana (thale cress)
Length = 1192

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1956 ctttgacaactactacttcaagaacctc 1983
|||| ||||||||| |||||||||
Sbjct: 820 ctttcacaactactacttcaagaacctc 847

>dbj|AB010692.1| Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18I23
Length = 72691

Score = 48.1 bits (24), Expect = 0.39
Identities = 27/28 (96%)
Strand = Plus / Minus

Query: 760 ttcttccacgattgctttgtcaatgtaa 787
||||||| ||||||||| |||||
Sbjct: 31924 ttcttccacgattgctttgtcaacgtaa 31897

>emb|Y10467.1| S.oleracea mRNA for peroxidase, clone PC23
Length = 1091

Score = 48.1 bits (24), Expect = 0.39
Identities = 45/52 (86%)
Strand = Plus / Plus

Query: 733 cgc atgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
||||||| ||||| | ||||||||| || || |||||||||
Sbjct: 127 cgc atgggcgttcaatacttcgcttgttcttcatgactgctttgtcaatg 178

>ref|XM_670091.1| Plasmodium berghei strain ANKA hypothetical protein (PB301568.00.0)
partial mRNA
Length = 2721

Score = 48.1 bits (24), Expect = 0.39
Identities = 24/24 (100%)
Strand = Plus / Minus

Query: 275 taaaattatttttcttttaattt 298
|||||||
Sbjct: 2667 taaaattatttttcttttaattt 2644

>gb|AF109124.1|AF109124 Ipomoea batatas anionic peroxidase swpa2 (swpa2) mRNA, complete cds
Length = 1291

Score = 48.1 bits (24), Expect = 0.39
Identities = 42/48 (87%)
Strand = Plus / Plus

Query: 733 cgcattgggtctctctccttcgcttgttcttccacgattgctttgtc 780
||||||| ||||| ||| |||| | |||||
Sbjct: 322 cgcattggggcttcctcattcgtctcttcttccacgattgctttgtc 369

>gb|EZ295716.1| TSA: Artemisia annua strain Madagascar Contig1601, mRNA sequence
Length = 540

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1796 acacaattggacaagcaaggtgcacaa 1822
||||||| |||||
Sbjct: 72 acacaattggacaagcaagatgcacaa 98

>gb|EZ256521.1| TSA: Artemisia annua strain Artemis Contig23191, mRNA sequence
Length = 253

Score = 46.1 bits (23), Expect = 1.5
Identities = 43/50 (86%)
Strand = Plus / Plus

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgg 2138
||||||| || ||||| || ||||| || |||||
Sbjct: 165 gatttcgcggctgccatgatcaagatggntgatattagtcgcttactgg 214

>gb|EZ360402.1| TSA: Artemisia annua strain Uganda Contig7563, mRNA sequence
Length = 276

Score = 46.1 bits (23), Expect = 1.5
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
|||||||
Sbjct: 208 tcaggggacaacaatttggcaccactagacgtccaaactccaa 250

>gb|EZ150610.1| TSA: Artemisia annua strain Artemis Contig10016, mRNA sequence
Length = 265

Score = 46.1 bits (23), Expect = 1.5
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaa 1951
|||||||
Sbjct: 176 tcaggggacaacaatttggcaccactagacgtccaaactccaa 218

>gb|AC233130.7| Solanum lycopersicum strain Heinz 1706 chromosome 10 clone hba-256116 map
10, complete sequence
Length = 159015

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 3523 agaaattaactttttgttttttaaaaa 3549
|||||||
Sbjct: 155094 agaaattaactttttcttttttaaaaa 155068

>gb|AC239433.3| Solanum lycopersicum strain Heinz 1706 chromosome 1 clone hba-208m24
map 1, complete sequence
Length = 154446

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 274 ataaaattatTTTTCTTTaat 296
|||||||
Sbjct: 83633 ataaaattatTTTTCTTTaat 83655

>gb|CP001633.1| Francisella tularensis subsp. tularensis NE061598, complete genome
Length = 1892681

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 3735 tatgtcttctctaattgatgaa 3757
|||||||
Sbjct: 971539 tatgtcttctctaattgatgaa 971561

>ref|NW_003037936.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000150
Length = 760080

Score = 46.1 bits (23), Expect = 1.5
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 172 aatcagtatctttgaaaactaattaagaaattaa 206
||||||| ||||| ||||| |||||
Sbjct: 116245 aatcagtatctttgaaaactaattatgaaattaa 116279

>gb|BT095984.1| Soybean clone JCVI-FLGm-20M19 unknown mRNA
Length = 1268

Score = 46.1 bits (23), Expect = 1.5
Identities = 38/43 (88%)
Strand = Plus / Plus

Query: 1810 gcaaggtgcacaaacttcagagcccgcatctacaacgagacca 1852
||||||| | ||||| | ||||| |||||
Sbjct: 643 gcaaggtgcactaccttcaggaccgcatctacaacgacacca 685

>gb|BT093602.1| Soybean clone JCVI-FLGm-17D17 unknown mRNA
Length = 1079

Score = 46.1 bits (23), Expect = 1.5

Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattct 1176
 |||||
Sbjct: 850 cagggatgtgatggttcaattct 828

>gb|AC237089.1| Oryza granulata clone OG_ABa0096023, complete sequence
Length = 145921

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Minus

Query: 762 cttccacgattgctttgtcaatgtaat 788
 |||||
Sbjct: 78176 cttccacgattgctttgtaaataatgtaat 78150

>ref|XM_002448761.1| Sorghum bicolor hypothetical protein, mRNA
Length = 2469

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
 |||||
Sbjct: 1616 gttttgcttttgcttctaaatta 1594

>ref|XM_002426020.1| Pediculus humanus corporis synaptonemal complex protein ZIP1,
putative, mRNA
Length = 4083

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 3059 aaagaaaataaaaaagttaattt 3081
 |||||
Sbjct: 1237 aaagaaaataaaaaagttaattt 1259

>emb|AJ749949.2| Francisella tularensis subsp. tularensis SCHU S4 complete genome
Length = 1892775

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 3735 tatgtctttctctaattgatgaa 3757
 |||||
Sbjct: 971474 tatgtctttctctaattgatgaa 971496

>emb|FN357570.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000279
Length = 107846

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 2232 attgtgtttaataagttgttaaa 2254
 |||||
Sbjct: 30598 attgtgtttaataagttgttaaa 30620

>emb|FN357441.1| Schistosoma mansoni genome sequence supercontig Smp_scaff000150
Length = 760080

Score = 46.1 bits (23), Expect = 1.5
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 172 aatcagtatctttgaaaactaattaagaaattaa 206
 ||||| |||| ||||| |||||
Sbjct: 116245 aatcagtatctttgaaaattaattatgaaattaa 116279

>gb|BT086529.1| Zea mays full-length cDNA clone ZM_BFc0177005 mRNA, complete cds
Length = 2218

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
 |||||

Sbjct: 1467 gttttgcttttgcttctaaatta 1445

>gb|EZ053600.1| TSA: Zea mays contig54722, mRNA sequence
Length = 1441

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
|||||
Sbjct: 688 gttttgcttttgcttctaaatta 666

>emb|AL844509.2| Plasmodium falciparum 3D7 chromosome 13
Length = 2895605

Score = 46.1 bits (23), Expect = 1.5
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 193 aattaagaaattaaataaaaaatattt 219
|||||
Sbjct: 2326925 aattaagaaattaaataaaaaatattt 2326951

Score = 44.1 bits (22), Expect = 6.1
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 3054 tatttaaagaaaataaaaaagt 3075
|||||
Sbjct: 611898 tatttaaagaaaataaaaaagt 611919

Score = 44.1 bits (22), Expect = 6.1
Identities = 25/26 (96%)
Strand = Plus / Minus

Query: 3048 ttagtttatttaaagaaaataaaaa 3073
|||||
Sbjct: 1691677 ttagtttatttaaagataataaaaa 1691652

>gb|AC235371.1| Glycine max strain Williams 82 clone GM_WBb0104B04, complete sequence
Length = 191941

Score = 46.1 bits (23), Expect = 1.5
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 269 tttctataaaattatTTTTCTTTtaatttcttaattaatcctaa 315
 ||||| ||||| ||||| ||| ||||| ||||| ||||| |||||
Sbjct: 155381 tttcaataaaaatatTTTTTTTaaattttttaattaatcctaa 155427

>gb|AC235196.1| Glycine max strain Williams 82 clone GM_WBb0014G10, complete sequence
Length = 114082

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1154 cagggatgtgatggttcaattct 1176
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 65728 cagggatgtgatggttcaattct 65750

>gb|AC235187.1| Glycine max strain Williams 82 clone GM_WBb0010C08, complete sequence
Length = 184070

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 281 tattttttcttttaatttcttaa 303
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 7796 tattttttcttttaatttcttaa 7774

>gb|AC235182.1| Glycine max strain Williams 82 clone GM_WBb0008C11, complete sequence
Length = 100806

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 293 taatttcttaattaatatacctaa 315
 |||||
Sbjct: 22206 taatttcttaattaatatacctaa 22184

>gb|AC235129.1| Glycine max strain Williams 82 clone GM_WBa0052I05, complete sequence
 Length = 119088

Score = 46.1 bits (23), Expect = 1.5
Identities = 29/31 (93%)
Strand = Plus / Plus

Query: 3830 ttagagaaaaataaataaattcttatattat 3860
 |||||
Sbjct: 53261 ttagagaaaaataaataaattcatattttat 53291

>ref|XM_002319931.1| Populus trichocarpa predicted protein, mRNA
 Length = 939

Score = 46.1 bits (23), Expect = 1.5
Identities = 41/47 (87%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaa 782
 |||||
Sbjct: 148 atgggtgcttctcttgttcgcttggttcttccatgattgctttgtcaa 194

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1993 aagggtctcctccactctgatca 2015
 |||||
Sbjct: 751 aagggtctcctccactctgatca 773

>ref|NM_001158468.1| Zea mays peroxidase 52 (LOC100285577), mRNA
 >gi|195651250|gb|EU972975.1| Zea mays clone 391021
 peroxidase 52 precursor, mRNA, complete cds
 Length = 1358

Score = 46.1 bits (23), Expect = 1.5
Identities = 53/63 (84%)

Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| || || ||||| | ||||| ||||| ||||| || || ||||| |||||
Sbjct: 670 tcacaccatcggccaagcacgctgcaccaacttcagagcccacgtgtacaacgacaccaa 729

Query: 1854 cat 1856
|||
Sbjct: 730 cat 732

>gb|EU954765.1| Zea mays clone 1482328 mRNA sequence
Length = 1445

Score = 46.1 bits (23), Expect = 1.5
Identities = 47/55 (85%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatgtaa 787
||||||| || || ||||| ||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 241 cgcatggggcgctccctcctccgcctcttcttccacgactgcttcgtcaatgtaa 295

>gb|EU951047.1| Zea mays clone 687198 mRNA sequence
Length = 845

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 2461 gttttgcttttgcttctaaatta 2483
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 231 gttttgcttttgcttctaaatta 209

>tpg|BK006741.1| TPA: TPA_reasm: Francisella tularensis subsp. holarctica OSU18, complete
genome
Length = 1895727

Score = 46.1 bits (23), Expect = 1.5
Identities = 23/23 (100%)
Strand = Plus / Minus

Query: 3735 tatgtctttctctaattgatgaa 3757

|||||
Sbjct: 1193421 tatgtctttctctaattgatgaa 1193399

>gb|FJ088527.1| Pinus taeda isolate 6658 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088526.1| Pinus taeda isolate 6661 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088525.1| Pinus taeda isolate 6650 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||| || | ||||| ||||| || | ||||| |||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088524.1| Pinus taeda isolate 6653 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088523.1| Pinus taeda isolate 6663 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088522.1| Pinus taeda isolate 6662 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088521.1| Pinus taeda isolate 6654 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

>gb|FJ088520.1| Pinus taeda isolate 6655 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactgggtccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088519.1| Pinus taeda isolate 6657 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactgggtccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088518.1| Pinus taeda isolate 6664 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactgggtccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088517.1| Pinus taeda isolate 6651 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactgggtccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccagggagaaattaggaagaa 318

>gb|FJ088516.1| Pinus taeda isolate 6649 anonymous locus 2_10243_02 genomic sequence
Length = 450

Score = 46.1 bits (23), Expect = 1.5
Identities = 50/59 (84%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| || | ||||||||||||| || | ||||||| |||||||
Sbjct: 376 atgataaagatgggcaacctcagtcctctcactgggtcccaggagaaattaggaagaa 318

Database: /usr/local/blast/db/blastlibs/nt
Posted date: Feb 13, 2010 7:27 AM
Number of letters in database: 30,212,464,392
Number of sequences in database: 10,930,266

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 10930266
Number of Hits to DB: 1,401,816,410
Number of extensions: 94213288
Number of successful extensions: 2655515
Number of sequences better than 10.0: 586
Number of HSP's gapped: 2655491
Number of HSP's successfully gapped: 696
Length of query: 3867
Length of database: 30,212,464,392
Length adjustment: 24
Effective length of query: 3843
Effective length of database: 29,950,138,008
Effective search space: 115098380364744
Effective search space used: 115098380364744
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
X3: 50 (99.1 bits)
S1: 14 (28.2 bits)
S2: 22 (44.1 bits)

**BLASTn Output of the Sequence at the Parental Locus of Soybean Event DAS-68416-4
against GenBank No-human and No_mouse ESTs (est_others)**

BLASTN 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
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.

Query= 68416_parent_locus
(3867 letters)

Database: /usr/local/blast/db/blastlibs/est_others
51,680,690 sequences; 29,218,461,503 total letters

Searching.....done

Sequences producing significant alignments:			Score (bits)	E Value
gb CX703225.1	gmrtDrNS01_14-B_M13R_D10_074.s2	Water stressed 5h...	1070	0.0
gb CX709633.1	gmrtDrNS01_10-D_M13R_A04_032.s2	Water stressed 5h...	1063	0.0
gb CF807990.1	psHB031xA07f	USDA-IFAFS:Expression of Phytophthor...	1059	0.0
gb BG509781.1	sad25h05.y1	Gm-c1074 Glycine max cDNA clone GENOM...	924	0.0
gb BM731124.1	sal68a04.y1	Gm-c1061 Glycine max cDNA clone SOYBE...	894	0.0
gb BG882707.1	sae51e08.y2	Gm-c1051 Glycine max cDNA clone GENOM...	880	0.0
gb EV267121.1	GLLBF04TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	731	0.0
gb CF806428.1	psHB011xIO5f	USDA-IFAFS:Expression of Phytophthor...	646	0.0
gb AW349107.1	GM210004A21E9	Gm-r1021 Glycine max cDNA clone Gm-...	626	e-175
gb BG156628.1	sab31a07.y1	Gm-c1026 Glycine max cDNA clone GENOM...	618	e-173
gb FK018609.1	GLND133TF	JCVI-SOY3 Glycine max cDNA 5', mRNA seq...	557	e-154
gb BU577048.1	sar71e12.y1	Gm-c1074 Glycine max cDNA clone SOYBE...	545	e-151
gb BM093025.1	saj04a09.y1	Gm-c1065 Glycine max cDNA clone GENOM...	527	e-145
gb BE210375.1	so42h10.y1	Gm-c1039 Glycine max cDNA clone GENOME...	527	e-145
gb EV263181.1	GLLA357TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	525	e-145
gb CF806168.1	psHB004x020f	USDA-IFAFS:Expression of Phytophthor...	523	e-144
gb BI972311.1	sag89h02.y1	Gm-c1084 Glycine max cDNA clone GENOM...	502	e-138
gb BE209964.1	so37a08.y1	Gm-c1039 Glycine max cDNA clone GENOME...	490	e-134
gb BG725689.1	sae39d12.y1	Gm-c1051 Glycine max cDNA clone GENOM...	464	e-126
gb FG889629.1	UCRVU08_CCNS10828_g1	Cowpea IT97K-461-4 Mixed Tis...	444	e-120
gb BE022389.1	sm85b11.y1	Gm-c1015 Glycine max cDNA clone GENOME...	438	e-118
gb BG359695.1	sac27d09.y1	Gm-c1051 Glycine max cDNA clone GENOM...	436	e-118
gb EV265313.1	GLLAS95TF	JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	412	e-111
gb AW132280.1	se02a03.y1	Gm-c1013 Glycine max cDNA clone GENOME...	381	e-101
gb CF809087.1	psHB042xH14f	USDA-IFAFS:Expression of Phytophthor...	373	5e-99

gb BU577870.1	sar93g05.y1 Gm-c1074 Glycine max cDNA clone SOYBE...	373	5e-99
gb AW432575.1	sh76b11.y1 Gm-c1015 Glycine max cDNA clone GENOME...	361	2e-95
gb FG825601.1	UCRVU04_CCNI8859_g1 Cowpea 524B Mixed Tissue and ...	343	4e-90
gb FF387035.1	MO0BI56TF MOO Vigna unguiculata cDNA 5', mRNA seq...	335	1e-87
gb BE807926.1	ss31h12.y1 Gm-c1061 Glycine max cDNA clone GENOME...	331	2e-86
gb FF386168.1	MO0BI56TRB MOO Vigna unguiculata cDNA, mRNA sequence	321	2e-83
gb AI441922.1	sa51f09.y1 Gm-c1004 Glycine max cDNA clone GENOME...	291	1e-74
gb G0029196.1	LJMAW92T0 JCVI-LJ2 Lotus japonicus cDNA 3', mRNA ...	289	6e-74
dbj BP048143.1	BP048143 Lotus corniculatus var. japonicus pods ...	289	6e-74
dbj BP048038.1	BP048038 Lotus corniculatus var. japonicus pods ...	289	6e-74
dbj AV768169.1	AV768169 Lotus japonicus Young plants (two-weeks...	289	6e-74
dbj BP048158.1	BP048158 Lotus corniculatus var. japonicus pods ...	274	3e-69
gb G0017605.1	LJGBF85T0 JCVI-LJ1 Lotus japonicus cDNA 3', mRNA ...	266	8e-67
gb G0023584.1	LJMCD71TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA ...	262	1e-65
gb FG825600.1	UCRVU04_CCNI8859_b1 Cowpea 524B Mixed Tissue and ...	246	8e-61
gb FF394030.1	MO0DS81TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	8e-61
gb FF387818.1	MO0C268TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	8e-61
gb FF383796.1	MO0B233TF MOO Vigna unguiculata cDNA 5', mRNA seq...	246	8e-61
dbj FS240762.1	FS240762 RPSC Glycyrrhiza uralensis cDNA clone K...	244	3e-60
gb FG889628.1	UCRVU08_CCNS10828_b1 Cowpea IT97K-461-4 Mixed Tis...	238	2e-58
gb FF403045.1	MO0F734TF MOO Vigna unguiculata cDNA 5', mRNA seq...	238	2e-58
gb FF392448.1	MO0CV65TF MOO Vigna unguiculata cDNA 5', mRNA seq...	238	2e-58
gb FF399144.1	MO0EV84TF MOO Vigna unguiculata cDNA 5', mRNA seq...	234	3e-57
gb G0019707.1	LJMAW92TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA ...	208	2e-49
dbj AV412875.1	AV412875 Lotus japonicus young plants (two-week ...	208	2e-49
dbj AV771838.1	AV771838 Lotus japonicus Pods (20-30 mm in lengt...	202	1e-47
dbj BW620524.1	BW620524 Lotus japonicus protoplasts from suspen...	196	6e-46
dbj BW630489.1	BW630489 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj BW629863.1	BW629863 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj BW628107.1	BW628107 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj BW627140.1	BW627140 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj BW624354.1	BW624354 Lotus japonicus salicylic acid and meth...	196	6e-46
dbj BW595840.1	BW595840 Lotus japonicus suspension-cultured cel...	196	6e-46
gb EY976963.1	EST 83 Alfalfa aluminum suppression subtractive l...	190	4e-44
gb EH613355.1	EST 02 Alfalfa aluminum suppression subtractive l...	190	4e-44
dbj BB913062.1	BB913062 Trifolium pratense three week-old plant...	190	4e-44
gb BI969832.1	GM830009A23A12 Gm-r1083 Glycine max cDNA clone Gm...	180	4e-41
gb BI700509.1	sag61f05.y1 Gm-c1082 Glycine max cDNA clone GENOM...	180	4e-41
gb BU578183.1	sar49a02.y1 Gm-c1074 Glycine max cDNA clone SOYBE...	176	6e-40
gb G0258927.1	VBL1_16_M09_E001.g1 Normalized cDNA library from ...	174	2e-39
gb CA852976.1	E14E06_J06_09.ab1 cDNA Peking library 6, 8 day SC...	174	2e-39
gb CA852554.1	E09B05_C17_03.ab1 cDNA Peking library 6, 8 day SC...	174	2e-39
gb AW350788.1	GM210009A20D5 Gm-r1021 Glycine max cDNA clone Gm...	174	2e-39
gb FF401698.1	MO0E192TF MOO Vigna unguiculata cDNA 5', mRNA seq...	168	1e-37
gb EY476317.1	METAQ01TF JCVI-MT3 Medicago truncatula cDNA 5', m...	167	6e-37
gb EX530374.1	MTGland_A066_2007-06-28/MTGlandA066_C04_014_1 Med...	167	6e-37
gb CX528854.1	s13dNF01B01MJ009_243775 Methyl Jasmonate-Elicited...	167	6e-37
gb CF068375.1	EST669096 MTUS Medicago truncatula cDNA clone MTU...	167	6e-37
gb AW268020.1	EST306242 DSIR Medicago truncatula cDNA clone pDS...	167	6e-37

gb	BI969294.1	GM830007B20G07 Gm-r1083 Glycine max cDNA clone Gm...	165	2e-36
gb	FG998035.1	GLPA295TF JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	163	9e-36
gb	EY477044.1	METAY48TF JCVI-MT3 Medicago truncatula cDNA 5', m...	163	9e-36
gb	BG448404.1	NF024B09EC1F1074 Elicited cell culture Medicago t...	155	2e-33
gb	BF644619.1	NF017G06EC1F1051 Elicited cell culture Medicago t...	155	2e-33
gb	CA919059.1	EST636777 MTUS Medicago truncatula cDNA clone MTU...	151	3e-32
gb	AW830120.1	sm23a02.y1 Gm-c1028 Glycine max cDNA clone GENOME...	151	3e-32
gb	C0513054.1	s13dSG89B0900073_122034 Glandular trichomes Medic...	149	1e-31
gb	FG998036.1	GLPA295TR JCVI-SOY1 Glycine max cDNA 5', mRNA seq...	147	5e-31
gb	C0516034.1	s13dSG64B1200101_445396 Glandular trichomes Medic...	147	5e-31
gb	C0514259.1	s13dSG76D0500042_157180 Glandular trichomes Medic...	147	5e-31
gb	AW686470.2	NF041G08NR1F1000 Nodulated root Medicago truncatu...	145	2e-30
gb	BF639633.1	NF015A12IN1F1097 Insect herbivory Medicago trunca...	145	2e-30
gb	CX530413.1	s13dNF99F02MJ016_246858 Methyl Jasmonate-Elicited...	141	3e-29
gb	CX529528.1	s13dNF97C05MJ034_245107 Methyl Jasmonate-Elicited...	141	3e-29
gb	BF647501.1	NF068D03EC1F1029 Elicited cell culture Medicago t...	141	3e-29
gb	BF645317.1	NF030B11EC1F1092 Elicited cell culture Medicago t...	141	3e-29
gb	C0515766.1	s13dSG77F0400043_419681 Glandular trichomes Medic...	139	1e-28
gb	AW830346.1	sm33e02.y1 Gm-c1028 Glycine max cDNA clone GENOME...	139	1e-28
gb	AW703873.1	sk25b09.y1 Gm-c1028 Glycine max cDNA clone GENOME...	139	1e-28
gb	AI495213.1	sb02b01.y1 Gm-c1004 Glycine max cDNA clone GENOME...	139	1e-28
gb	AW830098.1	sm22c01.y1 Gm-c1028 Glycine max cDNA clone GENOME...	137	5e-28
gb	AW704238.1	sk18d12.y1 Gm-c1028 Glycine max cDNA clone GENOME...	135	2e-27
emb	CU524253.1	CU524253 STSSH2Sb_KZOACB Theobroma cacao cDNA ...	133	8e-27
dbj	AV771209.1	AV771209 Lotus japonicus Pods (20-30 mm in lengt...	133	8e-27
gb	C0516246.1	s13dSG69B0900075_445820 Glandular trichomes Medic...	131	3e-26
gb	BF071209.1	st04h08.y1 Gm-c1065 Glycine max cDNA clone GENOME...	131	3e-26
gb	EX660929.1	JS1BF51JG Salt stressed Fragaria vesca (strain Ha...	129	1e-25
gb	DN950706.1	Ost2T_331 Oak tissue culture growing 2 days in hy...	129	1e-25
gb	C0511866.1	s13dSG02H0700064_103632 Glandular trichomes Medic...	129	1e-25
gb	BF650349.1	NF096E02EC1F1017 Elicited cell culture Medicago t...	129	1e-25
gb	BE022178.1	sm68f01.y1 Gm-c1028 Glycine max cDNA clone GENOME...	129	1e-25
gb	AW666186.1	sk33d05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	125	2e-24
gb	AW685593.1	NF029D05NR1F1000 Nodulated root Medicago truncatu...	117	5e-22
dbj	FS263447.1	FS263447 RPSC Glycyrrhiza uralensis cDNA clone S...	113	7e-21
gb	BF650698.1	NF099E07EC1F1053 Elicited cell culture Medicago t...	113	7e-21
gb	EV262518.1	MTYEW71TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	3e-20
gb	EV260463.1	MTYE803TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	3e-20
gb	EV258111.1	MTYDG59TF JCVI-MT1 Medicago truncatula cDNA 5', m...	111	3e-20
gb	DW017370.1	EST1226331 MTY Medicago truncatula cDNA clone MTY...	111	3e-20
gb	DW015340.1	EST1224301 MTY Medicago truncatula cDNA clone MTY...	111	3e-20
gb	C0513179.1	s13dSG23G0900068_129522 Glandular trichomes Medic...	111	3e-20
gb	C0512465.1	s13dSG100C120008_114444 Glandular trichomes Medic...	111	3e-20
gb	BG456493.1	NF082E02PL1F1017 Phosphate starved leaf Medicago ...	111	3e-20
gb	BG456057.1	NF073F02PL1F1025 Phosphate starved leaf Medicago ...	111	3e-20
gb	DW481567.1	GH_RMIRS_031_E08_R Cotton Normalized Library rand...	109	1e-19
gb	DW481566.1	GH_RMIRS_031_E08_056_F Cotton Normalized Library ...	109	1e-19
gb	DV443257.1	CV01009B1D06.f1 CV01-normalized library Manihot e...	107	5e-19
gb	DY633234.1	Medicago--03-I06.g1 Subtracted medicago cDNA libr...	105	2e-18

gb DY633115.1	Medicago--03-I06.b1 Subtracted medicago cDNA libr...	105	2e-18
gb BG359643.1	sac26g07.y1 Gm-c1051 Glycine max cDNA clone GENOM...	105	2e-18
gb GT138697.1	METCC85TF JCVI-MT3 Medicago truncatula cDNA 5', m...	103	7e-18
gb AW235016.1	sf21h05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	103	7e-18
emb CU485516.1	CU485516 CUSHIONC_KZOACAC Theobroma cacao cDNA c...	101	3e-17
gb BG454205.1	NF108A01LF1F1001 Developing leaf Medicago truncat...	101	3e-17
gb BE943474.1	EST423053 MGHG Medicago truncatula cDNA clone pMG...	101	3e-17
gb ES840062.1	UFL_061_05 Cotton fiber 0-10 day post anthesis Go...	100	1e-16
gb BI262826.1	NF091E03EC1F1023 Elicited cell culture Medicago t...	100	1e-16
gb AW666202.1	sk33f05.y1 Gm-c1028 Glycine max cDNA clone GENOME...	100	1e-16
gb G0006531.1	LJGBF85TF JCVI-LJ1 Lotus japonicus cDNA 5', mRNA ...	98	4e-16
gb C0511819.1	s13dSG02D0500046_103538 Glandular trichomes Medic...	98	4e-16
gb BF648119.1	NF027G10EC1F1083 Elicited cell culture Medicago t...	98	4e-16
gb AW309606.1	sf21h05.x1 Gm-c1028 Glycine max cDNA clone GENOME...	98	4e-16
gb C0513848.1	s13dSG73C1100082_156358 Glandular trichomes Medic...	96	2e-15
gb AW691930.2	NF050G04ST1F1000 Developing stem Medicago truncat...	96	2e-15
emb AJ548283.1	AJ548283 MTAPHEU Medicago truncatula cDNA clone ...	88	4e-13
gb BF520761.1	EST458234 DSIL Medicago truncatula cDNA clone pDS...	88	4e-13
emb FN039861.1	FN039861 Petunia axillaris subsp. axillaris pool...	86	2e-12
emb FN039860.1	FN039860 Petunia axillaris subsp. axillaris pool...	86	2e-12
gb EG559283.1	CR03032H04 Root CR03 cDNA library Catharanthus ro...	86	2e-12
gb DW500373.1	GH_TMIRS_045_H05_F Cotton Normalized Library dT p...	86	2e-12
dbj CI189311.1	CI189311 Oryza sativa (japonica cultivar-group) ...	86	2e-12
dbj CI256090.1	CI256090 Oryza sativa (japonica cultivar-group) ...	86	2e-12
gb C0498078.1	G.h.fbr-sw07468 G.h.fbr-sw Gossypium hirsutum cDN...	86	2e-12
gb EY707107.1	CS00-C3-701-064-H11-CT.F Sweet orange fruit, deve...	84	7e-12
gb FD423297.1	RT00024R_T3_024_F11_31MAY2004_085_ab1 CrUniGene r...	84	7e-12
gb FD422675.1	RT00017R_T3_017_E10_31MAY2004_072_ab1 CrUniGene r...	84	7e-12
gb FD422951.1	RT00020R_T3_020_G01_31MAY2004_003_ab1 CrUniGene r...	84	7e-12
gb FD420140.1	1_SM-JB_R10-G12_T3__G12_3100394_14_ab1 CrUniGene ...	84	7e-12
gb DW508346.1	GH_TMIRS_123_D07_F Cotton Normalized Library dT p...	82	3e-11
gb GT143205.1	METCC85TR JCVI-MT3 Medicago truncatula cDNA 3', m...	80	1e-10
gb DR280730.1	157654 CERES-148 Arabidopsis thaliana cDNA clone ...	80	1e-10
gb CN910539.1	030128ABLC005555HT (ABLC) Braeburn cell culture t...	80	1e-10
gb CN908859.1	030122ABLC003031HT (ABLC) Braeburn cell culture t...	80	1e-10
gb CN908310.1	030109ABLC001919HT (ABLC) Braeburn cell culture t...	80	1e-10
dbj AU238571.1	AU238571 RAFL17 Arabidopsis thaliana cDNA clone ...	80	1e-10
emb FN019009.1	FN019009 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN019008.1	FN019008 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN021689.1	FN021689 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN021688.1	FN021688 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN034858.1	FN034858 Petunia axillaris subsp. axillaris pool...	78	4e-10
emb FN019751.1	FN019751 Petunia axillaris subsp. axillaris pool...	78	4e-10
gb FC869557.1	C31102G05EF AbioticR1 Citrus reshni cDNA clone C3...	78	4e-10
gb FC870159.1	C31109C09EF AbioticR1 Citrus reshni cDNA clone C3...	78	4e-10
gb FC924498.1	C31806G11EF StrCleopN Citrus reshni cDNA clone C3...	78	4e-10
gb FC875256.1	C31505H10EF CEVdCidro1 Citrus medica cDNA clone C...	78	4e-10
gb FC921479.1	C32105D10EF RVDevelopN Citrus clementina cDNA clo...	78	4e-10
gb FC875071.1	C31503H10EF CEVdCidro1 Citrus medica cDNA clone C...	78	4e-10

gb EY867689.1	CL06-C4-500-007-B02-CT.F Rangpur lime root, green...	78	4e-10
gb FC325468.1	P00462_C7-H9_M13-F_A09_079.ab1 Onu-Ua-pathc Ulmus...	78	4e-10
gb EG985866.1	GLE049_D04_013 Cyamopsis tetragonoloba (L.) Taub ...	78	4e-10
gb EG356679.1	P00462_C7-H9_M13-F_A09_079 Onu-Ua-pathc Ulmus ame...	78	4e-10
emb FN034857.1	FN034857 Petunia axillaris subsp. axillaris pool...	76	2e-09
emb FN045147.1	FN045147 Petunia axillaris subsp. axillaris pool...	76	2e-09
emb FN019752.1	FN019752 Petunia axillaris subsp. axillaris pool...	76	2e-09
gb G0517646.1	Mdfbg8014P16.g1 Apple_EST_Mdfbg Malus hybrid root...	76	2e-09
gb EV227910.1	VV_PEA016c06.b1 Vitis vinifera cv. perlette LibA ...	76	2e-09
gb EH047301.1	AS2RM4P1E10.ab1 Roots inoculated with Meloidogyne...	76	2e-09
gb EC991497.1	WIN1142.C21_L14 Muscat Hamburg pre-veraison berry...	76	2e-09
gb EC987303.1	WIN1130.C21_E15 Muscat Hamburg pre-veraison berry...	76	2e-09
gb EC985323.1	WIN1124.C21_I01 Muscat Hamburg pre-veraison berry...	76	2e-09
gb CV861937.1	gonad_EST09518 Embryonic gonad cDNA Library Gallu...	76	2e-09
gb CX309187.1	C18022D10Rv Drought2 Citrus reshni cDNA clone C18...	76	2e-09
gb CA105303.1	SCJFHR1C05E10.g HR1 Saccharum officinarum cDNA cl...	76	2e-09
gb CA102350.1	SCBGHR1058E08.g HR1 Saccharum officinarum cDNA cl...	76	2e-09
gb CF205258.1	RR890915I0004_IVa_Ra_B09 Vitis sp. RR890915I Viti...	76	2e-09
dbj FS421608.1	FS421608 normalized full-length tobacco cDNA lib...	74	6e-09
dbj FS420315.1	FS420315 normalized full-length tobacco cDNA lib...	74	6e-09
gb ES441310.1	TSH_EST01528 Theobroma cacao-Moniliophthora perni...	74	6e-09
emb CU488677.1	CU488677 DROUGHTLS_KZOACAF Theobroma cacao cDNA ...	74	6e-09
gb FG154278.1	AGN_RNC104xj04f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	6e-09
gb FG173223.1	AGN_RNC126xi04f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	6e-09
gb FG156951.1	AGN_RNC026xe21f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	6e-09
gb FG157638.1	AGN_RNC025xk16f1.ab1 AGN_RNC Nicotiana tabacum cD...	74	6e-09
dbj DB920515.1	DB920515 full-length enriched cassava cDNA libra...	74	6e-09
gb EB450877.1	KT7C.108P16F.051219T7 KT7 Nicotiana tabacum cDNA ...	74	6e-09
gb DY356036.1	ZO_Ec0009K09.f ZO_Ec Zingiber officinale cDNA c...	74	6e-09
gb CV005110.1	atr02-9ms3-h07 Atr02 Amborella trichopoda cDNA cl...	74	6e-09
gb CN782128.1	EST00224 cqseed Chenopodium quinoa cDNA clone S02...	74	6e-09
gb FC869818.1	C31105F02EF AbioticR1 Citrus reshni cDNA clone C3...	72	3e-08
gb FC874065.1	C31202A05EF BiotPhyR1 Citrus aurantium cDNA clone...	72	3e-08
gb GD471713.1	454PCS0099417 Scarlet Runner Bean globular-stage ...	72	3e-08
gb GD391465.1	454PCS0019156 Scarlet Runner Bean globular-stage ...	72	3e-08
gb FG480776.1	020324KANA001021HT (KANA) Actinidia setosa stem A...	72	3e-08
gb EY845171.1	CA26-C1-002-040-C02-CT.F Sour orange leaf, field ...	72	3e-08
gb EY794850.1	CR05-C3-701-027-F03-CT.F Mandarin fruit, developm...	72	3e-08
gb EY776217.1	CR05-C1-103-015-D05-CT.F Mandarin leaf, infected ...	72	3e-08
gb EY725128.1	CS00-C3-703-086-B09-CT.F Sweet orange fruit, deve...	72	3e-08
gb C0500329.1	KH01008A04 KH01 Ipomoea batatas cDNA, mRNA sequence	72	3e-08
gb DW500299.1	GH_TMIRS_045_B08_F Cotton Normalized Library dT p...	72	3e-08
gb CX670039.1	UCRCP01_048_E06_T7 Swingle citrumelo nematode-cha...	72	3e-08
gb CX050341.1	UCRCS09_31H06_b Ruby Orange Developing Seed cDNA ...	72	3e-08
gb CV717574.1	UCRCS08_0009D08_f Parent Washington Navel Orange ...	72	3e-08
gb CV093292.1	FAMU_USDA_FP_1315 Vitis shuttleworthii L., grape ...	72	3e-08
gb C0866271.1	Mdfrt3046b02.y1 Mdfrt Malus x domestica cDNA clon...	72	3e-08
gb C0417575.1	Mdfrt3031k23.y1 Mdfrt Malus x domestica cDNA clon...	72	3e-08
gb C0070833.1	GR_Ea28B05.r GR_Ea Gossypium raimondii cDNA clo...	72	3e-08

gb	G0566201.1	Mddb5025B21_e2932.g1 Mddb Malus x domestica cDNA ...	70	1e-07
emb	CU537036.1	CU537036 TISCIVS_KZ0AAQ Theobroma cacao cDNA clo...	70	1e-07
emb	CU505430.1	CU505430 PODMEUPA_KZOACAB Theobroma cacao cDNA c...	70	1e-07
emb	CU478688.1	CU478688 COPHAS_KZ0AAL Theobroma cacao cDNA clon...	70	1e-07
emb	CU478933.1	CU478933 COPHAS_KZ0AAL Theobroma cacao cDNA clon...	70	1e-07
emb	CU480774.1	CU480774 CORTEXS_KZ0AAT Theobroma cacao cDNA clo...	70	1e-07
dbj	DC895850.1	DC895850 PCC Citrus unshiu cDNA clone PCC0206 5'...	70	1e-07
gb	EX266960.1	1447232_5_A14_063 PY06 Carica papaya cDNA, mRNA s...	70	1e-07
gb	EX289762.1	1577761_5_L07_022 PY06 Carica papaya cDNA, mRNA s...	70	1e-07
gb	EX272151.1	1452845_5_K11_038 PY06 Carica papaya cDNA, mRNA s...	70	1e-07
gb	EB110403.1	000430AFBC008068HT (AFBC) Royal Gala pre-opened f...	70	1e-07
gb	DW157696.1	CLVX9795.b1_E02.ab1 CLV(XYZ) lettuce virosa Lactu...	70	1e-07
gb	DW145800.1	CLVX10900.b1_H13.ab1 CLV(XYZ) lettuce virosa Lact...	70	1e-07
gb	C0900249.1	Mddb5025b21.y1 Mddb Malus x domestica cDNA clone ...	70	1e-07
gb	C0051719.1	Mdfw2055d05.y1 Mdfw Malus x domestica cDNA clone ...	70	1e-07
gb	CN880015.1	010418AASA009843HT (AASA) Royal Gala 10 DAFB frui...	70	1e-07
gb	GR871114.1	Pq_F_00457 American ginseng Flower cDNA Library P...	68	4e-07
gb	GR875194.1	Pq_R_02677 American ginseng Root cDNA Library Pan...	68	4e-07
gb	GR873483.1	Pq_R_00966 American ginseng Root cDNA Library Pan...	68	4e-07
gb	GR873276.1	Pq_R_00759 American ginseng Root cDNA Library Pan...	68	4e-07
gb	GR871777.1	Pq_F_01120 American ginseng Flower cDNA Library P...	68	4e-07
gb	GR874357.1	Pq_R_01840 American ginseng Root cDNA Library Pan...	68	4e-07
gb	GR874227.1	Pq_R_01710 American ginseng Root cDNA Library Pan...	68	4e-07
emb	CU507988.1	CU507988 PODSSHWB1Sb_KZOACD Theobroma cacao cDNA...	68	4e-07
gb	EY664481.1	CS00-C1-101-067-A09-CT.F Sweet orange leaf, infec...	68	4e-07
gb	EW712042.1	Ginseng-Feq Contig4 Ginseng F. equiseti subtracti...	68	4e-07
gb	EL366609.1	CCES2712.b1_005.ab1 CCE(LMS) endive Cichorium end...	68	4e-07
gb	EH664510.1	11.2E05 Transformed tobacco Lambda Zap II library...	68	4e-07
gb	EC600006.1	PNSSH3G-1469 panax notoginseng subtracted cDNA li...	68	4e-07
dbj	CI205074.1	CI205074 Oryza sativa (japonica cultivar-group) ...	68	4e-07
gb	C0898341.1	Mdfrt3034e04.y3 Mdfrt Malus x domestica cDNA clon...	68	4e-07
gb	CN848323.1	PG07017B01 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN847185.1	PG07026G09 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN846818.1	PG07018H01 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN846698.1	PG07019B09 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN846059.1	PG07005D12 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CN845966.1	PG07006B07 Ginseng cDNA library from MeJA treated...	68	4e-07
gb	CK265901.1	EST711979 potato abiotic stress cDNA library Sola...	68	4e-07
gb	CK259240.1	EST742877 potato callus cDNA library, normalized ...	68	4e-07
gb	CK257963.1	EST741600 potato callus cDNA library, normalized ...	68	4e-07
gb	CK257684.1	EST741321 potato callus cDNA library, normalized ...	68	4e-07
gb	CK256437.1	EST740074 potato callus cDNA library, normalized ...	68	4e-07
gb	CK256141.1	EST739778 potato callus cDNA library, normalized ...	68	4e-07
gb	CK254968.1	EST738605 potato callus cDNA library, normalized ...	68	4e-07
gb	CK254173.1	EST737810 potato callus cDNA library, normalized ...	68	4e-07
gb	CK253943.1	EST737580 potato callus cDNA library, normalized ...	68	4e-07
gb	CK252132.1	EST735769 potato callus cDNA library, normalized ...	68	4e-07
gb	CK250936.1	EST734573 potato callus cDNA library, normalized ...	68	4e-07
gb	CK250929.1	EST734566 potato callus cDNA library, normalized ...	68	4e-07

gb	CK249912.1	EST733549 potato callus cDNA library, normalized ...	68	4e-07
gb	CK249875.1	EST733512 potato callus cDNA library, normalized ...	68	4e-07
gb	CK249724.1	EST733361 potato callus cDNA library, normalized ...	68	4e-07
gb	CK249638.1	EST733275 potato callus cDNA library, normalized ...	68	4e-07
gb	CK248882.1	EST732519 potato callus cDNA library, normalized ...	68	4e-07
gb	CK248392.1	EST732029 potato callus cDNA library, normalized ...	68	4e-07
gb	CK247774.1	EST731411 potato callus cDNA library, normalized ...	68	4e-07
gb	CK247097.1	EST730734 potato callus cDNA library, normalized ...	68	4e-07
gb	CK246328.1	EST729965 potato callus cDNA library, normalized ...	68	4e-07
gb	CK246259.1	EST729896 potato callus cDNA library, normalized ...	68	4e-07
gb	CK246252.1	EST729889 potato callus cDNA library, normalized ...	68	4e-07
gb	CK245537.1	EST729174 potato callus cDNA library, normalized ...	68	4e-07
gb	CK245042.1	EST728679 potato callus cDNA library, normalized ...	68	4e-07
gb	CK243469.1	EST727106 potato callus cDNA library, normalized ...	68	4e-07
gb	CK243468.1	EST727105 potato callus cDNA library, normalized ...	68	4e-07
dbj	AU229763.1	AU229763 RAFL17 Arabidopsis thaliana cDNA clone ...	68	4e-07
gb	BF273768.1	GA_Eb0018024f Gossypium arboreum 7-10 dpa fiber ...	68	4e-07
dbj	FS194878.1	FS194878 Solanum lycopersicum cv Micro-Tom root ...	66	2e-06
dbj	FS205634.1	FS205634 Solanum lycopersicum cv Micro-Tom root ...	66	2e-06
dbj	FS197980.1	FS197980 Solanum lycopersicum cv Micro-Tom root ...	66	2e-06
gb	GE650850.1	EST1177 Tender roots cDNA library of tea plant Ca...	66	2e-06
gb	EY412917.1	pOP-E008268_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	66	2e-06
gb	FG526917.1	030704KAYC002574HT (KAYC) Actinidia chinensis you...	66	2e-06
gb	FG525755.1	030628KAYC001240HT (KAYC) Actinidia chinensis you...	66	2e-06
gb	FE966530.1	PLATE_T3_028_D07_01DEC2004_057 Opium poppy elicit...	66	2e-06
gb	FE968334.1	PLATE_T3_047_H06_03DEC2004_034 Opium poppy elicit...	66	2e-06
gb	FE966485.1	PLATE_T3_027_H10_01DEC2004_066 Opium poppy elicit...	66	2e-06
gb	FE967467.1	PLATE_T3_038_E11_01DEC2004_087 Opium poppy elicit...	66	2e-06
gb	FE966062.1	PLATE_T3_023_D04_02DEC2004_026 Opium poppy elicit...	66	2e-06
gb	EX165442.1	A05_P-14_034 Cotton 1-14 day post anthesis Lambda...	66	2e-06
gb	EH665793.1	26.2D06 Transformed tobacco Lambda Zap II library...	66	2e-06
dbj	DB685271.1	DB685271 Solanum lycopersicum cv. Micro-Tom leaf...	66	2e-06
dbj	DB689063.1	DB689063 Solanum lycopersicum cv. Micro-Tom leaf...	66	2e-06
dbj	DB699350.1	DB699350 Solanum lycopersicum cv. Micro-Tom leaf...	66	2e-06
dbj	DB692736.1	DB692736 Solanum lycopersicum cv. Micro-Tom leaf...	66	2e-06
gb	DW080731.1	CLPX3640.b1_P21.ab1 CLP(XYZ) lettuce perennis Lac...	66	2e-06
gb	DT523193.1	WS02039.B21_A17 PTxN-IB-N-A-11 Populus trichocarp...	66	2e-06
gb	DT517809.1	WS02435.B21_F23 PTxD-ICC-N-A-14 Populus trichocar...	66	2e-06
gb	DT516973.1	WS02432.B21_P02 PTxD-ICC-N-A-14 Populus trichocar...	66	2e-06
gb	DT515726.1	WS02429.B21.1_F18 PTxD-ICC-N-A-14 Populus trichoc...	66	2e-06
gb	DT511026.1	WS02429.BR_F18 PTxD-ICC-N-A-14 Populus trichocarp...	66	2e-06
gb	DT507952.1	WS02419.BR_K15 PTxD-ICC-N-A-14 Populus trichocarp...	66	2e-06
gb	DN586754.1	46565.1 Late Blight-Challenged Tubers Solanum tub...	66	2e-06
gb	DN485372.1	M129C08.3pR Populus female catkins cDNA library P...	66	2e-06
gb	CV475162.1	23658.1 Developing Tubers Solanum tuberosum cDNA ...	66	2e-06
gb	CV269494.1	WS0208.B21_G14 PTxN-IB-N-A-11 Populus trichocarpa...	66	2e-06
gb	CV269008.1	WS0207.B21_B07 PTxN-IB-N-A-11 Populus trichocarpa...	66	2e-06
gb	CV256197.1	WS0243.B21_D05 PTxD-ICC-N-A-14 Populus trichocarp...	66	2e-06
gb	CK298355.1	EST761069 Nicotiana benthamiana mixed tissue cDNA...	66	2e-06

gb	CK296485.1	EST759199 Nicotiana benthamiana mixed tissue cDNA...	66	2e-06
gb	CK295751.1	EST758465 Nicotiana benthamiana mixed tissue cDNA...	66	2e-06
gb	CK293902.1	EST756616 Nicotiana benthamiana mixed tissue cDNA...	66	2e-06
gb	CK283472.1	EST746194 Nicotiana benthamiana mixed tissue cDNA...	66	2e-06
gb	CK277562.1	EST723640 potato abiotic stress cDNA library Sola...	66	2e-06
gb	CK268372.1	EST714450 potato abiotic stress cDNA library Sola...	66	2e-06
gb	CK260187.1	EST706265 potato abiotic stress cDNA library Sola...	66	2e-06
gb	CK245041.1	EST728678 potato callus cDNA library, normalized ...	66	2e-06
gb	CA927256.1	MTU6CR.P6.H02 Aspen root cDNA Library Populus tre...	66	2e-06
gb	BG597610.1	EST496288 cSTS Solanum tuberosum cDNA clone cSTS1...	66	2e-06
gb	BG594826.1	EST493516 cSTS Solanum tuberosum cDNA clone cSTS8...	66	2e-06
gb	AW429264.1	EST306720 tomato flower buds 0-3 mm, Cornell Univ...	66	2e-06
gb	AW035301.1	EST280664 tomato callus, TAMU Solanum lycopersicu...	66	2e-06
gb	G0345282.1	CS01010G03 Hotpepper under oxidative stress Capsi...	64	6e-06
dbj	FS200575.1	FS200575 Solanum lycopersicum cv Micro-Tom root ...	64	6e-06
gb	GD103440.1	KS21047N18 KS21 Capsicum annuum cDNA, mRNA sequence	64	6e-06
gb	FG173286.1	AGN_RNC126xi04r1.ab1 AGN_RNC Nicotiana tabacum cD...	64	6e-06
gb	FG157705.1	AGN_RNC025xk16r1.ab1 AGN_RNC Nicotiana tabacum cD...	64	6e-06
gb	FG157012.1	AGN_RNC026xe21r1.ab1 AGN_RNC Nicotiana tabacum cD...	64	6e-06
gb	EY868947.1	CL06-C4-500-024-E11-CT.F Rangpur lime root, green...	64	6e-06
gb	FE964503.1	PLATE_T3_006_A01_18NOV2004_015 Opium poppy elicit...	64	6e-06
gb	EL689149.1	OPSC00922 Elaeis guineensis Suspension cell cultu...	64	6e-06
gb	EL688532.1	OPSC00287 Elaeis guineensis Suspension cell cultu...	64	6e-06
gb	EL689060.1	OPSC00829 Elaeis guineensis Suspension cell cultu...	64	6e-06
gb	EW741112.1	10 Capsicum annuum with binucleate Rhizoctonia Li...	64	6e-06
emb	AM806126.1	AM806126 seedling library, SL Nicotiana tabacum ...	64	6e-06
gb	EV281455.1	GLNB506TF JCVI-SOY3 Glycine max cDNA 5', mRNA seq...	64	6e-06
gb	EB125073.1	010417AASA002377HT (AASA) Royal Gala 10 DAFB frui...	64	6e-06
gb	DY357012.1	ZO_Ed0001B05.r ZO_Ed Zingiber officinale cDNA c...	64	6e-06
gb	CN910664.1	030221ABLC006597HT (ABLC) Braeburn cell culture t...	64	6e-06
gb	CN909288.1	030123ABLC003427HT (ABLC) Braeburn cell culture t...	64	6e-06
gb	CN908413.1	030121ABLC002155HT (ABLC) Braeburn cell culture t...	64	6e-06
gb	CN908053.1	030109ABLC001478HT (ABLC) Braeburn cell culture t...	64	6e-06
gb	CF446769.1	EST683114 normalized cDNA library of onion Allium...	64	6e-06
gb	CF445486.1	EST681831 normalized cDNA library of onion Allium...	64	6e-06
gb	CF437063.1	EST673408 normalized cDNA library of onion Allium...	64	6e-06
gb	BM878736.1	P12-A07 Sweetpotato Ipomoea batatas cDNA similar ...	64	6e-06
dbj	FS124984.1	FS124984 library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj	FS024422.1	FS024422 library MLF Solanum melongena cDNA clon...	62	2e-05
dbj	FS121328.1	FS121328 library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj	FS117052.1	FS117052 library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj	FS105158.1	FS105158 library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj	FS107745.1	FS107745 library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj	FS109925.1	FS109925 library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj	FS110172.1	FS110172 library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj	FS119211.1	FS119211 library TVR Solanum torvum cDNA clone T...	62	2e-05
dbj	FS049153.1	FS049153 library PST Solanum melongena cDNA clon...	62	2e-05
dbj	FS021644.1	FS021644 library LS5 Solanum melongena cDNA clon...	62	2e-05
dbj	FS020310.1	FS020310 library LS5 Solanum melongena cDNA clon...	62	2e-05

gb	GR347634.1	CCOX3299.g1 CCOX Avena barbata root, pooled from ...	62	2e-05
gb	GE299450.1	P006002D02 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299223.1	P005007B06 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299125.1	P005005G03 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299103.1	P005005D09 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299068.1	P005004H11 Subtractive cDNA library from laminari...	62	2e-05
gb	GE299038.1	P005004D05 Subtractive cDNA library from laminari...	62	2e-05
gb	EY410241.1	pOP-E007772_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	EY410393.1	pOP-E004088_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	EY412233.1	pOP-E002255_EST_C_1_pSK_SK EO (Oil Palm Embryoid)...	62	2e-05
gb	DW248736.1	pOP-EON01090_EST_C_1_pSK_SK EON (Oil Palm Embryoi...	62	2e-05
gb	EY032292.1	CAIT669.fwd CAIT Artemisia annua leaf Artemisia a...	62	2e-05
gb	DY980921.1	CLSS2910.b1_K08.ab1 CLS(LMS) lettuce sativa Lactu...	62	2e-05
gb	DY963072.1	CLSM13334.b1_K22.ab1 CLS(LMS) lettuce sativa Lactu...	62	2e-05
gb	DW141853.1	CLSY9921.b1_B10.ab1 CLS(XYZ) lettuce sativa Lactu...	62	2e-05
gb	DW118586.1	CLRY7219.b1_F06.ab1 CLR(XYZ) lettuce serriola Lac...	62	2e-05
gb	DN494839.1	M129C08.5pR Populus female catkins cDNA library P...	62	2e-05
gb	CX658639.1	P001020D11 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CX658354.1	P001034B06 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	CX656775.1	P002024B08 Poplar SC cDNA library Populus alba x ...	62	2e-05
gb	C0754834.1	Mdfrt3051n10.y1 Mdfrt Malus x domestica cDNA clon...	62	2e-05
gb	GR182521.1	CBPG8855.g1 CBPG Mimulus guttatus IM62 roots, see...	60	1e-04
gb	GR182520.1	CBPG8855.b1 CBPG Mimulus guttatus IM62 roots, see...	60	1e-04
gb	GR101494.1	CCIF25878.b1 CCIF Mimulus guttatus IM62 leaves (H...	60	1e-04
gb	GR030153.1	CCIC14356.g1 CCIC Mimulus guttatus IM62 roots (H)...	60	1e-04
gb	GR010964.1	CCIC3934.g1 CCIC Mimulus guttatus IM62 roots (H) ...	60	1e-04
gb	GR010963.1	CCIC3934.b1 CCIC Mimulus guttatus IM62 roots (H) ...	60	1e-04
gb	GE591881.1	CCPW15817.b1_A19.ab1 CCP(UWX) Globe Artichoke Cyn...	60	1e-04
gb	GE347117.1	MEUB360TF JCVI-MT2 Medicago truncatula cDNA 5', m...	60	1e-04
gb	GE299609.1	P006004H07 Subtractive cDNA library from laminari...	60	1e-04
dbj	BY912248.1	BY912248 Cryptomeria japonica male strobilus Cry...	60	1e-04
gb	FG610783.1	stem_S064_F03.SEQ Opium poppy stem cDNA library P...	60	1e-04
gb	FG230888.1	pvreacc010002_J13_M13rev_phred13_vc root hairs of...	60	1e-04
gb	FD792211.1	08VNAA8_T7_003_G04_17FEB2006_020 08VNAA8 Phaseolu...	60	1e-04
gb	FD793984.1	08VNAA8_T7_031_G10_16MAR2006_068 08VNAA8 Phaseolu...	60	1e-04
gb	EX135466.1	BR119296 root cDNA library KHRT Brassica rapa sub...	60	1e-04
gb	EX114527.1	BR100817 whole plant cDNA library KFYP Brassica r...	60	1e-04
gb	EX032022.1	BR016666 callus cDNA library KBCG Brassica rapa s...	60	1e-04
gb	EL424106.1	CHCM3704.b1_014.ab1 CHC(LMS) Texas blueweed Helia...	60	1e-04
gb	EL362738.1	CCEM7256.b1_P14.ab1 CCE(LMS) endive Cichorium end...	60	1e-04
gb	EL022129.1	EBENXNS02I7QWK 8-day Arabidopsis seedlings, aeria...	60	1e-04
gb	EH665640.1	24E09 Transformed tobacco Lambda Zap II library N...	60	1e-04
gb	EC927161.1	WIN0214.TB24_N12 Cab Sauv flower, leaf and root n...	60	1e-04
gb	DW520518.1	GH_TMIRS_241_D04_F Cotton Normalized Library dT p...	60	1e-04
dbj	BW994485.1	BW994485 Cryptomeria japonica male cone Cryptome...	60	1e-04
dbj	BW990328.1	BW990328 Chamaecyparis obtusa cambium and surrou...	60	1e-04
gb	DV857611.1	col4871 Colonial bentgrass EST Agrostis capillari...	60	1e-04
gb	DV127237.1	CV03047B1C06.f1 CV03-normalized library Euphorbia...	60	1e-04
gb	DV126025.1	CV03044A1B02.f1 CV03-normalized library Euphorbia...	60	1e-04

gb	DT512242.1	WS02418.B21_L24 PTxD-ICC-N-A-14 Populus trichocar...	60	1e-04
gb	DT507614.1	WS02418.BR_L24 PTxD-ICC-N-A-14 Populus trichocarp...	60	1e-04
gb	DT492311.1	WS02550.C21_F01 PT-MB-N-A-15 Populus trichocarpa ...	60	1e-04
gb	DT487692.1	WS02534.B21_G10 PT-MB-N-A-15 Populus trichocarpa ...	60	1e-04
gb	DT487423.1	WS02533.B21_K13 PT-MB-N-A-15 Populus trichocarpa ...	60	1e-04
gb	DT483262.1	WS02522.B21_B19 PT-MB-N-A-15 Populus trichocarpa ...	60	1e-04
gb	DT482024.1	WS02533.BR_K13 PT-MB-N-A-15 Populus trichocarpa c...	60	1e-04
gb	DT478196.1	WS02522.BR_B19 PT-MB-N-A-15 Populus trichocarpa c...	60	1e-04
gb	CX169952.1	B06_69-16_04.ab1 leaf inoculated with Marssonina p...	60	1e-04
gb	CV278268.1	WS0145.B21_O21 PTxD-IL-A-5 Populus trichocarpa x ...	60	1e-04
gb	CV277650.1	WS0144.B21_C22 PTxD-IL-A-5 Populus trichocarpa x ...	60	1e-04
gb	CV131018.1	L1P03d05 Populus stem seasonal library Populus de...	60	1e-04
gb	CN848150.1	PG07006D08 Ginseng cDNA library from MeJA treated...	60	1e-04
gb	CK288635.1	EST751357 Nicotiana benthamiana mixed tissue cDNA...	60	1e-04
gb	CK258594.1	EST742231 potato callus cDNA library, normalized ...	60	1e-04
gb	CK255769.1	EST739406 potato callus cDNA library, normalized ...	60	1e-04
gb	CK255201.1	EST738838 potato callus cDNA library, normalized ...	60	1e-04
gb	CK244542.1	EST728179 potato callus cDNA library, normalized ...	60	1e-04
gb	CK244541.1	EST728178 potato callus cDNA library, normalized ...	60	1e-04
gb	CA992234.1	HC0822 GIBCOBRL CAT. NO. 19643-014 Brassica rapa ...	60	1e-04
gb	CA296237.1	SCAGLV1043F09.g LV1 Saccharum officinarum cDNA cl...	60	1e-04
dbj	BP175580.1	BP175580 Cryptomeria japonica inner bark Cryptom...	60	1e-04
gb	AI054926.1	coau0002I16 Cotton Boll Abscission Zone cDNA Libr...	60	1e-04
dbj	FS184353.1	FS184353 Solanum lycopersicum cv Micro-Tom root ...	58	4e-04
dbj	FS185438.1	FS185438 Solanum lycopersicum cv Micro-Tom root ...	58	4e-04
gb	GD111776.1	KS23009A10 KS23 Capsicum annuum cDNA, mRNA sequence	58	4e-04
gb	GE508830.1	CCFT6761.b1_A12.ab1 CCF(STU) sunflower Helianthus...	58	4e-04
gb	GE507030.1	CCFT5541.g1_J17.ab1 CCF(STU) sunflower Helianthus...	58	4e-04
gb	GE507029.1	CCFT5541.b1_J17.ab1 CCF(STU) sunflower Helianthus...	58	4e-04
gb	ES294238.1	_08Y_C12 Bermudagrass Normalized cDNA Library Cyn...	58	4e-04
gb	GD594567.1	454PCS0222258 Scarlet Runner Bean globular-stage ...	58	4e-04
gb	FG509216.1	030312KAPC001477HT (KAPC) Actinidia eriantha peta...	58	4e-04
gb	FG486094.1	021104KAUB001004HT (KAUB) Actinidia chinensis CK5...	58	4e-04
gb	FG486083.1	021015KAUB999084HT (KAUB) Actinidia chinensis CK5...	58	4e-04
gb	ES595125.1	000001603252_M19.ab1 Eucalyptus globulus under lo...	58	4e-04
gb	EY948213.1	RS3DN57TF RS3(RT) Raphanus sativus cDNA 5', mRNA ...	58	4e-04
gb	EY063068.1	CATF7534.fwd CATF Artemisia annua, Tanzanian, fro...	58	4e-04
gb	EY063067.1	CATF7534.rev CATF Artemisia annua, Tanzanian, fro...	58	4e-04
gb	EY091175.1	CAZI19752.rev CAZI Artemisia annua normalized lea...	58	4e-04
gb	EX515663.1	Hops-Column-29R_2007-06-04/Hops-Column-29R_F02_00...	58	4e-04
gb	DN965021.1	218e04 longbai no.2 one month old leaves Brassica...	58	4e-04
gb	EL434417.1	CHTL1481.b2_B12.ab1 CHT (LMS) Jerusalem artichoke ...	58	4e-04
gb	EL425067.1	CHCM4607.b1_N24.ab1 CHC (LMS) Texas blueweed Helia...	58	4e-04
gb	EL424239.1	CHCM3838.b1_L24.ab1 CHC (LMS) Texas blueweed Helia...	58	4e-04
gb	DY012178.1	40JKME7D_UP_003_D09_25MAR2004_073 40JKME7D Brassi...	58	4e-04
gb	DT212598.1	E002_B10 Embryogenic SSH library Cichorium intybu...	58	4e-04
gb	DT014039.1	VVH007H01_739521 CabSau Flower Nectary Stage 25 (...)	58	4e-04
gb	DT010226.1	VVH055D09_748099 CabSau Flower Nectary Stage 25 (...)	58	4e-04
gb	DR929061.1	EST1120600 Aquilegia cDNA library Aquilegia formo...	58	4e-04

gb DR742871.1	RTCU1_7_C01.g2_A029	Roots plus added copper Pinus...	58	4e-04
gb DR742794.1	RTCU1_7_C01.b2_A029	Roots plus added copper Pinus...	58	4e-04
gb DR094964.1	STRR1_17_H08.g1_A033	Stem Response Resistant Pinu...	58	4e-04
gb DR094953.1	STRR1_17_G08.g1_A033	Stem Response Resistant Pinu...	58	4e-04
gb DR094872.1	STRR1_17_G08.b1_A033	Stem Response Resistant Pinu...	58	4e-04
gb DR090538.1	RTAL1_15_F06.g1_A029	Roots plus added aluminum Pi...	58	4e-04
gb DR090469.1	RTAL1_15_F06.b1_A029	Roots plus added aluminum Pi...	58	4e-04
gb DR089595.1	RTAL1_9_E05.g1_A029	Roots plus added aluminum Pin...	58	4e-04
gb DR088958.1	RTAL1_5_E09.g1_A029	Roots plus added aluminum Pin...	58	4e-04
gb DR023270.1	STRS1_56_B11.g1_A034	Shoot tip pitch canker susce...	58	4e-04
gb DR021354.1	STRS1_44_C09.b1_A034	Shoot tip pitch canker susce...	58	4e-04
gb CX658976.1	P001024H07	Poplar SC cDNA library Populus alba x ...	58	4e-04
gb C0499512.1	G.h.fbr-sw08902	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0498821.1	G.h.fbr-sw08211	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0498720.1	G.h.fbr-sw08110	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0496527.1	G.h.fbr-sw05917	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0494300.1	G.h.fbr-sw03690	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb C0491848.1	G.h.fbr-sw01238	G.h.fbr-sw Gossypium hirsutum cDN...	58	4e-04
gb CV094175.1	FAMU_USDA_FP_2198	Vitis shuttleworthii L., grape ...	58	4e-04
emb AJ805072.1	AJ805072	Antirrhinum majus whole plant Antirrhin...	58	4e-04
emb AJ795563.1	AJ795563	Antirrhinum majus whole plant Antirrhin...	58	4e-04
emb AJ795101.1	AJ795101	Antirrhinum majus whole plant Antirrhin...	58	4e-04
emb AJ793569.1	AJ793569	Antirrhinum majus whole plant Antirrhin...	58	4e-04
gb C0200887.1	RTCNT2_2_F01.b1_A029	Root control 2 (late) Pinus ...	58	4e-04
gb CN604982.1	USDA_FP_132082	Vitis shuttleworthii L., grape Vit...	58	4e-04
gb CN604205.1	USDA_FP_131305	Vitis shuttleworthii L., grape Vit...	58	4e-04
gb CF476953.1	RTWW3_4_G10.g1_A022	Well-watered loblolly pine ro...	58	4e-04
gb CF401192.1	RTWW1_10_H07.g1_A015	Well-watered loblolly pine r...	58	4e-04
gb CF401118.1	RTWW1_10_H07.b1_A015	Well-watered loblolly pine r...	58	4e-04
gb CF400173.1	RTWW1_3_F07.g1_A015	Well-watered loblolly pine ro...	58	4e-04
gb CF400086.1	RTWW1_3_F07.b1_A015	Well-watered loblolly pine ro...	58	4e-04
gb CF387460.1	RTDR1_20_H12.b1_A015	Loblolly pine roots recoveri...	58	4e-04
gb CF387171.1	RTDR1_11_H09.b1_A015	Loblolly pine roots recoveri...	58	4e-04
gb CF387078.1	RTDR1_10_H09.g1_A015	Loblolly pine roots recoveri...	58	4e-04

>gb|CX703225.1| gmrtDrNS01_14-B_M13R_D10_074.s2 Water stressed 5h segment 2
gmrtDrNS01 Glycine max cDNA 3', mRNA sequence
Length = 743

Score = 1070 bits (540), Expect = 0.0
Identities = 543/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 640 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 581

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagAACATcaggg 1908
|||||
Sbjct: 580 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagAACATcaggg 521

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 520 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 461

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 460 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 401

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 2088
|||||
Sbjct: 400 ggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctct 341

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||
Sbjct: 340 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 281

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtcttgaatattaagggt 2208
|||||
Sbjct: 280 gaaatcaggaagaattgtagaaggattaactaatttaattcagtcttgaatattaagggt 221

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 2268
|||||
Sbjct: 220 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 161

Query: 2269 tatttttgattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 2328
|||||
Sbjct: 160 tatttttgattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 101

Query: 2329 tccc 2332
||||
Sbjct: 100 tccc 97

Score = 210 bits (106), Expect = 4e-50
Identities = 106/106 (100%)
Strand = Plus / Minus

Query: 1540 tgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatt 1599
|||||
Sbjct: 743 tgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatt 684

Query: 1600 tagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645
|||||
Sbjct: 683 tagcgctcttggactttccaccaaggacttggtcgccttgtccggt 638

Score = 79.8 bits (40), Expect = 1e-10
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 40 tcctttatcaagcatttatcaagaacggagtttgcttttt 1

>gb|CX709633.1| gmrtDrNS01_10-D_M13R_A04_032.s2 Water stressed 5h segment 2
gmrtDrNS01 Glycine max cDNA 3', mRNA sequence
Length = 791

Score = 1063 bits (536), Expect = 0.0
Identities = 542/544 (99%)
Strand = Plus / Minus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 640 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 581

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 580 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 521

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 520 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 461

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjet: 460 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 401

Query: 2029 ggtgggtccaccgactccattgtgctgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjet: 400 ggtgggtccaccgactccattgtgctgggtacagcaccaacccgggcaccttttcctct 341

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||

Sbjet: 340 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 281

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||

Sbjet: 280 gaaatcaggaagaattgtagaaggattaactaatttaattcagtccttgaatattaagggt 221

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 2268
|||||

Sbjet: 220 cctacacatacgcaagcaatttaattgtgtttaataagttgttaaacatgttttggttg 161

Query: 2269 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 2328
|||||

Sbjet: 160 tattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtgtgttctact 101

Query: 2329 tccc 2332
||||

Sbjet: 100 tccc 97

Score = 297 bits (150), Expect = 2e-76
Identities = 153/154 (99%)
Strand = Plus / Minus

Query: 1492 atggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaaca 1551
|||||

Sbjet: 791 atggaatgttaaacttggaagaagagacgctagaattgctagccaatctgctgctaaca 732

Query: 1552 tggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgg 1611
|||||

Sbjet: 731 tggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgg 672

Query: 1612 actttccaccaaggacttggtcgccttggtccggt 1645
|||||
Sbjct: 671 actttccaccaaggacttggtcgccttggtccggt 638

Score = 79.8 bits (40), Expect = 1e-10
Identities = 40/40 (100%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
|||||
Sbjct: 40 tcctttatcaagcatttatcaagaacggagtttgcttttt 1

>gb|CF807990.1| psHB031xA07f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB031A07 5, mRNA sequence
Length = 708

Score = 1059 bits (534), Expect = 0.0
Identities = 543/545 (99%), Gaps = 1/545 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 149 ggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacgag 208

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 209 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 268

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 269 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 328

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 329 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 388

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 389 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 448

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 449 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 508

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 509 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 568

Query: 2209 cctacacatacgaagcaatttaattgtgtttaataagttgttaaaacat-gttttggtt 2267
|||||
Sbjct: 569 cctacacatacgaagcaatttaattgtgtttaataagttgttaaaacatggttttggtt 628

Query: 2268 gtattttggattcctagtgtagtttcggtgatcaatgccgtctactttagtggttctac 2327
|||||
Sbjct: 629 gtattttggattcctagtgtagnttcggtgatcaatgccgtctactttagtggttctac 688

Query: 2328 ttccc 2332
|||||
Sbjct: 689 ttccc 693

Score = 299 bits (151), Expect = 6e-77
Identities = 151/151 (100%)
Strand = Plus / Plus

Query: 1495 gaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatgg 1554
|||||
Sbjct: 1 gaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatgg 60

Query: 1555 catccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgact 1614
|||||
Sbjct: 61 catccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgact 120

Query: 1615 ttccaccaaggacttggctgccttgtccggt 1645
|||||
Sbjct: 121 ttccaccaaggacttggctgccttgtccggt 151

>gb|BG509781.1| sad25h05.y1 Gm-c1074 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1074-1498 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 493

Score = 924 bits (466), Expect = 0.0
Identities = 472/474 (99%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 20 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 79

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 80 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagatcatcaggg 139

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 140 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 199

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 200 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 259

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 2088
|||||
Sbjct: 260 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 319

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||
Sbjct: 320 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 379

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 380 gaaatcaggaagaattgtagaaggattaactaatttaattcagtccttgaatattaagggt 439

Query: 2209 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgttt 2262
|||||
Sbjct: 440 cctacacatacgaagcaatttaattgtgtttaataagttgttaaacatgttt 493

Score = 44.1 bits (22), Expect = 5.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1624 ggacttggtcgccttgtccggt 1645
 |||||
Sbjct: 1 ggacttggtcgccttgtccggt 22

>gb|BM731124.1| sal68a04.y1 Gm-cl061 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-cl061-4231 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
 ;, mRNA sequence
 Length = 506

Score = 894 bits (451), Expect = 0.0
Identities = 454/455 (99%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
 |||||
Sbjct: 52 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 111

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
 |||||
Sbjct: 112 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 171

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
 |||||
Sbjct: 172 tcagaggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 231

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
 |||||
Sbjct: 232 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 291

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 2088
 |||||
Sbjct: 292 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 351

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
 |||||
Sbjct: 352 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 411

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 2208
|||||
Sbjct: 412 gaaatcaggaagaattgtagaaggattaactaatttgattcagtccttgaatattaagggt 471

Query: 2209 cctacacatacgcaagcaatttaattgtgtttaat 2243
|||||
Sbjct: 472 cctacacatacgcaagcaatttaattgtgtttaat 506

Score = 107 bits (54), Expect = 5e-19
Identities = 54/54 (100%)
Strand = Plus / Plus

Query: 1592 tcaagatttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 1 tcaagatttagcgctcttggactttccaccaaggacttggcgccttgtccggt 54

>gb|BG882707.1| sae51e08.y2 Gm-cl051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl051-8679 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 483

Score = 880 bits (444), Expect = 0.0
Identities = 444/444 (100%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948
|||||
Sbjct: 1 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 60

Query: 1949 caaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctcctccact 2008
|||||
Sbjct: 61 caaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctcctccact 120

Query: 2009 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 2068
|||||
Sbjct: 121 ctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcacca 180

Query: 2069 acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 2128

|||||
Sbjct: 181 acccgggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtc 240

Query: 2129 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatttgatt 2188
|||||

Sbjct: 241 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatttgatt 300

Query: 2189 cagtcttgaatattaagggtcctacacatacgcaagcaatttaattgtgtttaataagtt 2248
|||||

Sbjct: 301 cagtcttgaatattaagggtcctacacatacgcaagcaatttaattgtgtttaataagtt 360

Query: 2249 gttaaaacatgttttggttgattttggattcctagtgtagtttcggtgatcaatgccgt 2308
|||||

Sbjct: 361 gttaaaacatgttttggttgattttggattcctagtgtagtttcggtgatcaatgccgt 420

Query: 2309 ctacttttagtgtgttctacttccc 2332
|||||

Sbjct: 421 ctacttttagtgtgttctacttccc 444

>gb|EV267121.1| GLLBF04TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 719

Score = 731 bits (369), Expect = 0.0
Identities = 467/498 (93%), Gaps = 5/498 (1%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||

Sbjct: 113 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 172

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
| |||||

Sbjct: 173 agcaacatagacaccgcatttgcaaggacaaggcaaaaagctgccaagaacatcaggg 232

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||

Sbjct: 233 tcaggggacaataatcttgacgacttgatcttcaaactccaaccgaattcgacaactac 292

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 293 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 352

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||||

Sbjct: 353 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgagctccttctcctct 412

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|| |||||

Sbjct: 413 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaacgga 472

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagtccttgaatattaagg 2206
|||||||

Sbjct: 473 gaaatcaggaagaattgtagaaggattaactaattactaattgagtcctcaatattaagg 532

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaacaatgtttt 2263
||| |||||

Sbjct: 533 gtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaacaatgtttt 592

Query: 2264 ggttgtattttgattcc 2281

|||||

Sbjct: 593 ggttgtgttttgattcc 610

Score = 210 bits (106), Expect = 4e-50

Identities = 112/114 (98%)

Strand = Plus / Plus

Query: 1532 agccaatctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatc 1591
|||||||

Sbjct: 2 agccaatctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatc 61

Query: 1592 tcaagatttagcgctcttggactttccaccaaggacttggtcgccttgtccgggt 1645
|||||||

Sbjct: 62 tcaagattcagcgctcttggactttccaccaaggacttggtcgccttgtccgggt 115

>gb|CF806428.1| psHB011xI05f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB011I05 5, mRNA sequence
Length = 606

Score = 646 bits (326), Expect = 0.0
Identities = 415/443 (93%), Gaps = 5/443 (1%)
Strand = Plus / Minus

Query: 1844 acgagaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacat 1903
||||| ||||||| ||||||||||||||| |||| ||||||||||| |||||||
Sbjct: 606 acgagagcaacatagacaccgcatttgcaaggacaaggcaacaaagctgccaagaacat 547

Query: 1904 cagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgaca 1963
||||||||||||||| ||||| ||||| ||||||||||||||||||| || |||||
Sbjct: 546 cagggtcaggggacaataatcttgaccgcttgatcttcaaactccaaccgaattcgaca 487

Query: 1964 actactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgt 2023
||||||||||||||| || |||||||||||||||||||||||||||||||
Sbjct: 486 actactacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgt 427

Query: 2024 tcaacgggtgggtccaccgactccattgtgcgtgggtacagcaccaaccgggcaccttct 2083
|||| ||||||||||||||||||||||||||||||||||| || |||||||
Sbjct: 426 tcaatgggtgggtccaccgactccattgtgcgtgggtacagcaccaaccgagctccttct 367

Query: 2084 cctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtcca 2143
||||||| |||||||||||||||||||||||||||||||||||
Sbjct: 366 cctctgacttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtcca 307

Query: 2144 atggagaaatcaggaagaattgtagaaggattaactaatt--tgattcagtccttgaatat 2201
| ||||||||||||||||||||||||||||||| | ||| ||||| |||||||
Sbjct: 306 acggagaaatcaggaagaattgtagaaggattaactaattactaattgagtcctcgaatat 247

Query: 2202 taagggtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaaacat 2258
||||||| |||||||||||||||||||||||||||||||
Sbjct: 246 taagggtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaaacat 187

Query: 2259 gttttggttgatttttgattcc 2281
||||||| |||||||
Sbjct: 186 gttttggttgatttttgattcc 164

Score = 63.9 bits (32), Expect = 6e-06
Identities = 38/40 (95%)
Strand = Plus / Minus

Query: 2388 tcctttatcaagcatttatcaagaacggagtttgcttttt 2427
||||||| ||||||| |||||||
Sbjct: 41 tcctttatcaagaatttatcaagaacagagtttgcttttt 2

>gb|AW349107.1| GM210004A21E9 Gm-r1021 Glycine max cDNA clone Gm-r1021-1362 3', mRNA
sequence
Length = 609

Score = 626 bits (316), Expect = e-175
Identities = 449/498 (90%), Gaps = 5/498 (1%)
Strand = Plus / Minus

Query: 1789 ggtgggtcacacaattggacaaggaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||||||| ||||||| |||||||
Sbjct: 604 ggtgggtcacacaannnnacaaggaaggtgcacnannnnnngagcccgcanctacaacgag 545

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcaggg 1908
| ||||||| ||||||| ||||||| |||||||
Sbjct: 544 agcaacatagannncgcatttgcaaggacaaggcaacaaagctgcccagaacatcaggg 485

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||| ||||| || | ||||||| ||||||| || ||| ||||
Sbjct: 484 tcaggggacaataatcttgcaacgcttgatcttcaaactccaaccgaattcgacnnctac 425

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||| || ||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 424 tacttcaagaatcttggttcaaaagaagggtctcctccactctgatcagcnctgttcaat 365

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
||||||| ||||||| ||||||| ||||||| || |||||||
Sbjct: 364 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgagctccttctcctct 305

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|| ||||||| ||||||| ||||||| ||||||| ||||
Sbjct: 304 gacttcgccgccgcatgatcaagatgggagacattagtcctctcactgggtccaacgga 245

Query: 2149 gaaatcaggaagaattgtagaaggattaactaatt--tgattcagtcttgaatattaagg 2206
||||||| ||||||| ||||||| || ||| ||||| |||||||
Sbjct: 244 gaaatcaggaagaattgtagaaggattaactaattactaattgagtcctccaatattaagg 185

Query: 2207 gtc---ctacacatacgaagcaatttaattgtgtttaataagttgttaaaacatgtttt 2263
||| ||||||||||||||||||||||||||||||||||||||||
Sbjct: 184 gtcctactacacatacgaagcaatttaattgtgtttaataagttgttaaaacatgtttt 125

Query: 2264 ggttgtattttggattcc 2281
||||| |||||||||
Sbjct: 124 ggttgtgttttggattcc 107

>gb|BG156628.1| sab31a07.y1 Gm-c1026 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1026-3086 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 425

Score = 618 bits (312), Expect = e-173
Identities = 325/328 (99%), Gaps = 1/328 (0%)
Strand = Plus / Plus

Query: 2005 cactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagc 2064
||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3 cactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagc 62

Query: 2065 accaaccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacatt 2124
|||||||||||||||||||||||||||||||||||||||
Sbjct: 63 accaaccgggcaccttctcctctgatttcgccgccgc-atgatcaagatgggagacatt 121

Query: 2125 agtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaattt 2184
|||||||||||||||||||||||||||||||||||||||
Sbjct: 122 agtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaattt 181

Query: 2185 gattcagtccttgaatattaagggtcctacacatacgaagcaatttaattgtgtttaata 2244
||||||||||||||||||||||||||||||| |||||||||||||
Sbjct: 182 aattcagtccttgaatattaagggtcctacacatacggcagcaatttaattgtgtttaata 241

Query: 2245 agttgttaaaacatgttttggttgtattttggattcctagtgtagtttcggtgatcaatg 2304
||||||||||||||||||||||||||||||| |||||||||
Sbjct: 242 agttgttaaaacatgttttggttgtattttggattcctagtgtagtttcggtgatcaatg 301

Query: 2305 ccgtctacttttagtgtgttctacttccc 2332
|||||||||||||||||||

Sbjct: 302 ccgtctacttttagtgtgttctacttccc 329

>gb|FK018609.1| GLND133TF JCVI-SOY3 Glycine max cDNA 5', mRNA sequence
Length = 464

Score = 557 bits (281), Expect = e-154
Identities = 291/293 (99%), Gaps = 1/293 (0%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgag 1848
|||||
Sbjct: 172 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgag 231

Query: 1849 accaacaatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908
|||||
Sbjct: 232 accaacaatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 291

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 292 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 351

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 352 tacttcaaggacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 411

Query: 2029 ggtgggtccaccgactcca-ttgtgcgtggctacagcaccaaccgggcacct 2080
|||||
Sbjct: 412 ggtgggtccaccgactccatttgcgtggctacagcaccaaccgggcacct 464

Score = 333 bits (168), Expect = 4e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 7 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 66

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 67 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 126

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 1645

|||||

Sbjct: 127 tttagcgctcttggactttccaccaaggacttggtcgccttgtccggt 174

>gb|BU577048.1| sar71e12.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-7896 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 432

Score = 545 bits (275), Expect = e-151
Identities = 376/408 (92%), Gaps = 5/408 (1%)
Strand = Plus / Plus

Query: 1879 aggcagcaaagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgat 1938

|||||

Sbjct: 1 aggcaacaaagctgcccaagaacatcagggtcaggggacaataatcttgcaacgcttgat 60

Query: 1939 cttcaaactccaaccagctttgacaactactacttcaagaacctcggtcagaagaagggt 1998

|||||

Sbjct: 61 cttcaaactccaaccgaattcgacaactactacttcaagaatcttgttcagaagaagggt 120

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggc 2058

|||||

Sbjct: 121 ctctccactctgatcagcaactgttcaatgggtgggtccaccgactccattgtgcgtggc 180

Query: 2059 tacagcaccaacccgggcaccttctcctctgatttcgccgccgcatgatcaagatggga 2118

|||||

Sbjct: 181 tacagcaccaacttttttcttctcctctgacttcgccgccgcatgatcaagatggga 240

Query: 2119 gacattagtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaac 2178

|||||

Sbjct: 241 gacattagtcctctcactggctccaacggagaaatcaggaagaattgtagaaggattaac 300

Query: 2179 taatt--tgattcagtccttgaatattaagggtc---ctacacatacgcaagcaatttaac 2233

|||||

Sbjct: 301 taattactaattgagtcctcaatattaagggtcctactacacatacgcaagcaatttaac 360

Query: 2234 tgtgtttaataagttgttaaaacatgttttggttgatttttgattcc 2281

```
|||||
Sbjct: 361 tgtgtttaataagttgttaaacaatgttttggttggttttgattcc 408
```

```
>gb|BM093025.1| saj04a09.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl065-9257 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE ;, mRNA sequence
Length = 568
```

```
Score = 527 bits (266), Expect = e-145
Identities = 266/266 (100%)
Strand = Plus / Plus
```

```
Query: 519 atcaaacacaaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 578
|||||
Sbjct: 1 atcaaacacaaacacttgaagtactaagttagtggtttgagcaaattaactatggcttc 60
```

```
Query: 579 gttttgttctagattgacaatttgttggctctgtttgtcctcatatgggggagtgccaa 638
|||||
Sbjct: 61 gttttgttctagattgacaatttgttggctctgtttgtcctcatatgggggagtgccaa 120
```

```
Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698
|||||
Sbjct: 121 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 180
```

```
Query: 699 atccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctccttcgctt 758
|||||
Sbjct: 181 atccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctccttcgctt 240
```

```
Query: 759 gttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 241 gttcttccacgattgctttgtcaatg 266
```

```
Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus
```

```
Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 266 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 325
```

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 326 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 385

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 386 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 445

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 446 tctgttcagatt 457

Score = 218 bits (110), Expect = 2e-52
Identities = 110/110 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 458 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 517

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaact 1587
|||||
Sbjct: 518 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaact 567

>gb|BE210375.1| so42h10.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-668 5' similar to TR:024336 024336
KOREAN-RADISH ISOPEROXIDASE ;, mRNA sequence
Length = 520

Score = 527 bits (266), Expect = e-145
Identities = 266/266 (100%)
Strand = Plus / Plus

Query: 519 atcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaattaactatggcttc 578
|||||
Sbjct: 7 atcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaattaactatggcttc 66

Query: 579 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 638
|||||

Sbjct: 67 gttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaa 126

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698
|||||

Sbjct: 127 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 186

Query: 699 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 758
|||||

Sbjct: 187 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 246

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||

Sbjct: 247 gttcttccacgattgctttgtcaatg 272

Score = 373 bits (188), Expect = 5e-99
Identities = 191/192 (99%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||

Sbjct: 272 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 331

Query: 1217 aaccccaacaggaactctgctcgatcgaggttattgacaacattaaatcagccgtg 1276
|||||

Sbjct: 332 aaccccaacaggaactctgctcgatcgaggttattgacaacattaaatcagccgtg 391

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 392 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 451

Query: 1337 tctgttcagatt 1348
|||||

Sbjct: 452 tctgttcagatt 463

Score = 97.6 bits (49), Expect = 4e-16
Identities = 55/57 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagc 1534
||||| ||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct: 464 cttggaagccctacatggaatgttaaacttgaaagaagagacgctagaactgctagc 520

>gb|EV263181.1| GLLA357TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 813

Score = 525 bits (265), Expect = e-145
Identities = 274/277 (98%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 3 acaccctttcaatcaaacacaaacactcgaagtactaagttagtgtgttcgagcaaatta 62

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 63 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 122

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 123 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 182

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttct 747
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 183 tcctctgtgaaatccgacagtgcgaatctgccatatctaaggagacccgcatgggtgcttct 242

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784
||||| ||||||||||||||||||||||| |||||||
Sbjct: 243 ctcttcgcttggttcttccacgattgctttgtcaatg 279

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||||||||||||||||||||| ||||||||||||||||||||||| |||||||
Sbjct: 279 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 338

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||||
Sbjct: 339 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 398

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 399 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 458

Query: 1337 tctgttcagatt 1348
|||||||
Sbjct: 459 tctgttcagatt 470

Score = 333 bits (168), Expect = 4e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 471 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 530

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||||
Sbjct: 531 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 590

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||||
Sbjct: 591 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 638

Score = 270 bits (136), Expect = 5e-68
Identities = 178/184 (96%), Gaps = 6/184 (3%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcacatctacaacgag 1848
|||||||
Sbjct: 636 ggtggtcacacaattggacaagcaag-tgcacaaacttcagagcccgcacatctacaacgag 694

Query: 1849 accaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcaggg 1908

|||||
Sbjct: 695 accaacatag-aaccgcatttgcaaggacta-gcagcaaagctgccctagaacatca-gg 751

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||

Sbjct: 752 tcaggggacaacaatctggcaccacttgatcttc-aactccaaccagctttgac-actac 809

Query: 1969 tact 1972

||||
Sbjct: 810 tact 813

>gb|CF806168.1| psHB004x020f USDA-IFAFS:Expression of Phytophthora sojae genes
during infection and propagation Glycine max cDNA clone
sHB004020 5, mRNA sequence
Length = 397

Score = 523 bits (264), Expect = e-144

Identities = 264/264 (100%)

Strand = Plus / Plus

Query: 521 caaacacaaacacttgaagtactaagttagtgtgtttgagcaaattaactatggcttcgt 580
|||||

Sbjct: 9 caaacacaaacacttgaagtactaagttagtgtgtttgagcaaattaactatggcttcgt 68

Query: 581 tttgttctagattgacaattttgtttggctctgtttgtcctcatatgggggagtgccaatg 640
|||||

Sbjct: 69 tttgttctagattgacaattttgtttggctctgtttgtcctcatatgggggagtgccaatg 128

Query: 641 cacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaat 700
|||||

Sbjct: 129 cacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaat 188

Query: 701 ccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgt 760
|||||

Sbjct: 189 ccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgt 248

Query: 761 tttccacgattgctttgtcaatg 784

|||||
Sbjct: 249 tttccacgattgctttgtcaatg 272

Score = 250 bits (126), Expect = 5e-62
Identities = 126/126 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 272 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 331

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 332 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 391

Query: 1277 gagaaa 1282
|||||
Sbjct: 392 gagaaa 397

>gb|BI972311.1| sag89h02.y1 Gm-c1084 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1084-1515 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE ;, mRNA sequence
Length = 573

Score = 502 bits (253), Expect = e-138
Identities = 253/253 (100%)
Strand = Plus / Plus

Query: 532 acttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctaga 591
|||||
Sbjct: 1 acttgaagtactaagttagtggtttgagcaaattaactatggcttcgttttgttctaga 60

Query: 592 ttgacaatttgtttggtctgtttgtcctcatatgggggagtgccaatgcacaactttct 651
|||||
Sbjct: 61 ttgacaatttgtttggtctgtttgtcctcatatgggggagtgccaatgcacaactttct 120

Query: 652 acaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaa 711
|||||
Sbjct: 121 acaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaa 180

Query: 712 tctgccatatctaaggagacccgatgggtgcttctctccttcgcttgttcttccacgat 771
|||||
Sbjct: 181 tctgccatatctaaggagacccgatgggtgcttctctccttcgcttgttcttccacgat 240

Query: 772 tgctttgtcaatg 784
 |||||||
Sbjct: 241 tgctttgtcaatg 253

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||||
Sbjct: 253 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 312

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||||
Sbjct: 313 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 372

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
 |||||||
Sbjct: 373 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 432

Query: 1337 tctgttcagatt 1348
 |||||||
Sbjct: 433 tctgttcagatt 444

Score = 240 bits (121), Expect = 5e-59
Identities = 127/129 (98%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
 |||||||
Sbjct: 445 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 504

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
 |||||||
Sbjct: 505 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 564

Query: 1598 ttttagcgct 1606
|||||||
Sbjct: 565 ttttagcgct 573

>gb|BE209964.1| so37a08.y1 Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-111 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 391

Score = 490 bits (247), Expect = e-134
Identities = 247/247 (100%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 114 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 173

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 174 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 233

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 234 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 293

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 294 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 353

Query: 2029 ggtgggt 2035
|||||||
Sbjct: 354 ggtgggt 360

Score = 230 bits (116), Expect = 5e-56
Identities = 116/116 (100%)
Strand = Plus / Plus

Query: 1530 ctagccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactca 1589
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1 ctagccaatctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactca 60

Query: 1590 tctcaagatttagcgctcttggactttccaccaaggacttggtcgcccttggtccggt 1645
|||||
Sbjct: 61 tctcaagatttagcgctcttggactttccaccaaggacttggtcgcccttggtccggt 116

>gb|BG725689.1| sae39d12.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-7487 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 499

Score = 464 bits (234), Expect = e-126
Identities = 285/302 (94%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 197 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 256

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
| |||||
Sbjct: 257 agcaacatagacaccgcatttgcaaggacaaggcaacaaagctgccaagaacatcaggg 316

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 317 tcaggggacaataatcttgaccgcttgatcttcaaactccaaccgaattcgacaactac 376

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 377 tacttcaagaatcttgttcagaagaagggtctcctccactctgatcagcaactgttcaat 436

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcacettctcctct 2088
|||||
Sbjct: 437 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgagctccttctcctct 496

Query: 2089 ga 2090
||
Sbjct: 497 ga 498

Score = 293 bits (148), Expect = 4e-75

Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 32 cttggaggccctagttggaatgttaaagtiggaagaagagacgctagaactgctagccaa 91

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 92 tctgctgctaacaatggcatccctccaccacttcaaaccttaaccaactcatctcaaga 151

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgcttgtccggt 1645
||
Sbjct: 152 ttcagcgctcttggactttccaccaaggacttggtcgcttgtccggt 199

Score = 50.1 bits (25), Expect = 0.092
Identities = 28/29 (96%)
Strand = Plus / Plus

Query: 1319 gccatcgctgccagagactctgttcagat 1347
|||||
Sbjct: 2 gccatagctgccagagactctgttcagat 30

>gb|FG889629.1| UCRVU08_CCNS10828_g1 Cowpea IT97K-461-4 Mixed Tissue and Conditions
cDNA Library UCRVU08-1-2 Vigna unguiculata cDNA clone
CCNS10828.g1, mRNA sequence
Length = 670

Score = 444 bits (224), Expect = e-120
Identities = 341/380 (89%)
Strand = Plus / Minus

Query: 1800 aattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaacataga 1859
|||||
Sbjct: 670 aattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgagagcaacattga 611

Query: 1860 aaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcaggggacaa 1919
|||
Sbjct: 610 tacctcatttgccaggacaagacaatcaagctgccccagaacatcagggtcaggggacaa 551

Query: 1920 caatctggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaagaa 1979
||||||| ||||||| ||||| ||| || ||||||||| |||
Sbjct: 550 caatctggcaccgcttgatcttcagactccgaccacattcgacaactactacttcaggaa 491

Query: 1980 cctcgttcagaagaaggtctctccactctgatcagcaactgttcaacgggtgggtccac 2039
||| ||||||||| ||||||| ||||||| ||||| ||||| |||||
Sbjct: 490 cctggttcagaagaaggtctctccactctgaccagcaactcttcaatgggtgggtccac 431

Query: 2040 cgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctctgatttcgccgc 2099
||||||| ||||||||| ||||||||| || ||| ||||||||| |||
Sbjct: 430 tgactccatagtgcgtgggtacagcaccaacccgagctccttttcctctgattttgtctc 371

Query: 2100 cgccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaa 2159
||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||
Sbjct: 370 cgccattatcaagatgggagacattagtcctcctcactggctccaaaggagaaatcagaaa 311

Query: 2160 gaattgtagaaggattaact 2179
||| || |||||||||
Sbjct: 310 gaactgcagaaggattaact 291

>gb|BE022389.1| sm85b11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-6838 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 571

Score = 438 bits (221), Expect = e-118
Identities = 278/297 (93%)
Strand = Plus / Plus

Query: 1834 cgcactctacaacgagaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgc 1893
||||||| ||||||| ||||||||| ||||| |||||||||
Sbjct: 6 cgcactctacaacgagagcaacatagacaccgcatttgcaaggacaaggcaacaaagctgc 65

Query: 1894 cctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaacc 1953
|| ||||||||| ||||| ||| ||||||||| |||||
Sbjct: 66 ccaagaacatcagggtcaggggacaataatcttgcaacgcttgatcttcaaactccaacc 125

Query: 1954 agctttgacaactactacttcaagaacctcgttcagaagaaggtctcctccactctgat 2013
|| ||||||||| || ||||||||| ||||||||| |||||
Sbjct: 126 gaattcgacaactactacttcaagaatcttgttcagaagaaggtctcctccactctgat 185

Query: 2014 cagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccg 2073
|||||||
Sbjct: 186 cagcaactgttcaatgggtgggtccaccgactccattgtgcgtggctacagcaccaaccg 245

Query: 2074 ggcaccttctcctctgatttcgccgcccatgatcaagatgggagacattagtcct 2130
||
Sbjct: 246 agtccttctcctctgacttcgccgcccatgatcaagatgggagacattagtcct 302

>gb|BG359695.1| sac27d09.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1051-3617 5' similar to TR:Q9XIV9 Q9XIV9
PEROXIDASE :, mRNA sequence
Length = 233

Score = 436 bits (220), Expect = e-118
Identities = 230/232 (99%), Gaps = 1/232 (0%)
Strand = Plus / Plus

Query: 533 cttgaagtactaagttagtgtgtttgagcaaattaactatggcttcgttttgttctagat 592
|||||||
Sbjct: 2 cttgaagtactaagttagtgtgtttgagcaaattaactatggcttc-ttttgttctagat 60

Query: 593 tgacaattttgtttggctctgtttgtcctcatatgggggagtgccaatgcacaactttcta 652
|||||||
Sbjct: 61 tgacaatttttttggctctgtttgtcctcatatgggggagtgccaatgcacaactttcta 120

Query: 653 caaaccttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgaat 712
|||||||
Sbjct: 121 caaaccttttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgaat 180

Query: 713 ctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctt 764
|||||||
Sbjct: 181 ctgccatatctaaggagaccgcatgggtgcttctctccttcgcttgttctt 232

>gb|EV265313.1| GLLAS95TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 652

Score = 412 bits (208), Expect = e-111
Identities = 260/277 (93%), Gaps = 4/277 (1%)
Strand = Plus / Plus

Query: 508 acaccctttcaatcaaacacaaacacttgaagtactaagttagtgtgtttgagcaaatta 567
||||||| |||| |
Sbjct: 2 acaccctctcaagcaaacacaaacacttgaagtactaagttagtgtttttgagcaa--- 58

Query: 568 actatggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatgg 627
|||||||
Sbjct: 59 -ctatggcttcgttttgttctagattgaccatttgtttggctctgtttgtcctcatattg 117

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
|||||||
Sbjct: 118 gggagtgccaatgccaaactttctacaaacttctactaccattcgtgtccaaacctcttc 177

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttct 747
||| |||||
Sbjct: 178 tccactgtgaaatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttct 237

Query: 748 ctctctcgcttggttcttccacgattgctttgtcaatg 784
||||| |||
Sbjct: 238 ctctctcgcccggttcttccacgattgctttgtcaatg 274

Score = 331 bits (167), Expect = 2e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 274 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||||
Sbjct: 334 aaccccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 394 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 453

Query: 1337 tctgttcagat 1347
|||||||

Sbjct: 454 tctgttcagat 464

Score = 293 bits (148), Expect = 4e-75
Identities = 163/168 (97%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 466 cttggaggccctagtgtgaatgttaaagtggagaagagacgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||||
Sbjct: 526 tctgctgctaacaatggcatccctccacccacttcaaaccttaaccaactcatctcaaga 585

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
||
Sbjct: 586 ttcagcgctcttggactttccaccaaggacttggcgccttgtccggt 633

Score = 44.1 bits (22), Expect = 5.7
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaag 1810
|||||||
Sbjct: 631 ggtggtcacacaattggacaag 652

>gb|AW132280.1| se02a03.y1 Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1013-2309 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 552

Score = 381 bits (192), Expect = e-101
Identities = 192/192 (100%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 151 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 210

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||
Sbjct: 211 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 270

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 271 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 330

Query: 1337 tctgttcagatt 1348
|||||
Sbjct: 331 tctgttcagatt 342

Score = 325 bits (164), Expect = 1e-84
Identities = 167/168 (99%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 343 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 402

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 403 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 462

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
| |||||
Sbjct: 463 ttagcgctcttggactttccaccaaggacttggcgccttgtccggt 510

Score = 299 bits (151), Expect = 6e-77
Identities = 151/151 (100%)
Strand = Plus / Plus

Query: 634 gccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctct 693
|||||
Sbjct: 1 gccaatgcacaactttctacaaacttttactaccattcatgtccaaaccttctctctct 60

Query: 694 gtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctcctt 753

|||||
Sbjct: 61 gtgaaatccacagtgcgaatctgccatatctaaggagaccgcatgggtgcttctctcctt 120

Query: 754 cgcttggttcttccacgattgctttgtcaatg 784

|||||
Sbjct: 121 cgcttggttcttccacgattgctttgtcaatg 151

Score = 83.8 bits (42), Expect = 7e-12
Identities = 44/45 (97%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcc 1833

|||||
Sbjct: 508 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcc 552

>gb|CF809087.1| psHB042xH14f USDA-IFAFS:Expression of Phytophthora sojae genes during
infection and propagation Glycine max cDNA clone
sHB042H14 5, mRNA sequence
Length = 364

Score = 373 bits (188), Expect = 5e-99
Identities = 188/188 (100%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

|||||
Sbjct: 177 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 236

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908

|||||
Sbjct: 237 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 296

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

|||||
Sbjct: 297 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 356

Query: 1969 tacttcaa 1976

|||||
Sbjct: 357 tacttcaa 364

Score = 333 bits (168), Expect = 4e-87
Identities = 168/168 (100%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 12 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 71

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 72 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 131

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 1645
|||||
Sbjct: 132 tttagcgctcttggactttccaccaaggacttggcgccttgtccggt 179

>gb|BU577870.1| sar93g05.y1 Gm-cl074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl074-9922 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 426

Score = 373 bits (188), Expect = 5e-99
Identities = 231/245 (94%), Gaps = 4/245 (1%)
Strand = Plus / Plus

Query: 540 tactaagttagtgtgtttgagcaaattaactatggcttcgttttgttctagattgacaat 599
|||||
Sbjct: 1 tactaagttagtgtttttagcaaa----ctatggcttcgttttgttctagattgaccat 56

Query: 600 ttgtttggctctgtttgtcctcatatgggggagtccaatgcacaactttctacaaactt 659
|||||
Sbjct: 57 ttgtttggctctgtttgtcctcatattgggggagtccaatgcccaactttctacaaactt 116

Query: 660 ttactaccattcatgtccaaacctcttctcctctgtgaaatccacagtgaatctgccat 719
|||||
Sbjct: 117 ctactaccattcgtgtccaaacctcttctccactgtgaaatccacagtgaatctgccat 176

Query: 720 atctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgt 779
||| |||||

Sbjct: 177 atcaaaggagaccgcgatgggtgcttctctctccgcctgttcttccacgattgctttgt 236

Query: 780 caatg 784

|||||

Sbjct: 237 caatg 241

Score = 321 bits (162), Expect = 2e-83

Identities = 180/186 (96%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct: 241 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 300

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

||||||||||||||||||||||||||| ||||| |||||||||||||||||||||||

Sbjct: 301 aaccccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 360

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

||||||| ||||||||||||||| ||||||||||||||||||||||| |||||||||||

Sbjct: 361 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 420

Query: 1337 tctgtt 1342

|||||

Sbjct: 421 tctgtt 426

>gb|AW432575.1| sh76b11.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1015-5686 5' similar to SW:PERX_BRARA P00434

PEROXIDASE P7 ;, mRNA sequence

Length = 313

Score = 361 bits (182), Expect = 2e-95

Identities = 263/290 (90%)

Strand = Plus / Plus

Query: 1791 tggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagac 1850

||||| ||||||||||||||||| ||||||||||||||||||||||| |||||||||||

Sbjct: 1 tggtcgcacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagac 60

Query: 1851 caacatagaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtc 1910
||||| ||||| ||||||| ||| ||||||| ||||| ||||||| ||||||| |||||||
Sbjct: 61 caacgtagagaccgcattggcatggactaggcggcaaaactgccctagaacatcagggtc 120

Query: 1911 aggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactacta 1970
||||||| ||||||| ||||||| ||| ||||||| || ||| ||||||| ||
Sbjct: 121 aggggacagcaatctggcaccacttgataacttaaaactccgacatagtatgacaactagta 180

Query: 1971 cttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacgg 2030
||| ||||||| ||||||| ||||||| ||||| ||||||| ||||||| |||||||
Sbjct: 181 cttgtagaacctcggttcataagaagggtctcctccactctgatcagcaactgttcaacgg 240

Query: 2031 tgggtccaccgactccattgtgcgtggctacagcaccaaccgggcacct 2080
||||| ||||||| ||||||| ||||||| || ||| ||||||| ||
Sbjct: 241 tgggtccaccgactccgttgtgcgtggctacagcagcagcccgggcacct 290

>gb|FG825601.1| UCRVU04_CCNI8859_g1 Cowpea 524B Mixed Tissue and Conditions cDNA
Library UCRVU04-1-2 Vigna unguiculata cDNA clone
CCNI8859.g1, mRNA sequence
Length = 604

Score = 343 bits (173), Expect = 4e-90
Identities = 263/293 (89%)
Strand = Plus / Minus

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946
||||||| ||||||| ||||||| ||||||| ||||||| || ||| ||||||| ||
Sbjct: 589 aagctgccccagaacatcagggtcaggggacaacaatctggccccgcttgatcttcagac 530

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctcca 2006
||| |||| || ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 529 tccgaccacattcgacaactactacttcaggaacctgggttcagaagaagggtcttctcca 470

Query: 2007 ctctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcac 2066
||||| ||||||| ||||| ||||| ||||| ||||| ||||||| |||||||
Sbjct: 469 ctctgaccagcaactcttcaatggtggtccactgactccatagtgcgtggctacagcac 410

Query: 2067 caaccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacattag 2126
||||| || |||| ||||||| || ||| ||||||| ||||||| |||||||
Sbjct: 409 caaccgaagctcctttcctctgattttgtctccgcatatcaagatgggagacattag 350

```
Query: 2127 tcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaact 2179
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 349 tccctcactggctccaaaggagaaatcagaaagaactgcagaaggattaact 297
```

>gb|FF387035.1| M00BI56TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 502

Score = 335 bits (169), Expect = 1e-87
Identities = 262/293 (89%)
Strand = Plus / Plus

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Sbjct: 31 aagctccccagaacaccagggtcaggggacaacaatctggcacccgttgatcttcagac 90

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctctcca 2006
||| ||| | | | | | | | | | | | | | | | | | | | |
Sbjct: 91 tccgaccacattcgacaactactacttcaggaacctgggtcagaagaagggtcttctcca 150

```
Query: 2007 ctctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcac 2066
          ||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 151 ctctgaccagcaactcttcaatgggtggctccactgactccatagtgcgtggctacagcac 210
```

```
Query: 2067 caaccgggcaccttctctctgatttcgccgcccatgatcaagatgggagacattag 2126
          |||||  || |||| ||||| ||| | ||||| ||||| ||||| |||||
Sbjct: 211  caaccgaagctccttttctctgatttgcctccgcattatcaagatgggagacattag 270
```

Query: 2127 tcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaact 2179
 ||| |||| |||||| ||||||||| |||| | |||||||||
 Sbjct: 271 tcccctcaccggctccaaaggagaaatcagaaagaactgcagaaggattaact 323

```
>gb|BE807926.1| ss3lh2.y1 Gm-c1061 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
      Gm-c1061-384 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;,
      mRNA sequence
      Length = 634
```

Score = 331 bits (167), Expect = 2e-86
Identities = 185/191 (96%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||

Sbjct: 122 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 181

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||

Sbjct: 182 aaccccaacaggaactctgctcgtggatacgaggtcattgacaacattaaatcagccgtg 241

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 242 gagaaagcatgtccaggagttgtctcctgcgcagatatccttgccatagctgccagagac 301

Query: 1337 tctgttcagat 1347
|||||

Sbjct: 302 tctgttcagat 312

Score = 281 bits (142), Expect = 1e-71
Identities = 159/165 (96%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||

Sbjct: 314 cttggaggccctagttggaatgttaaagttggaagaagagacgctagaactgctagccaa 373

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 374 tctgctgctaacaatggcatccctccacccacttcaaaccttaaccaactcatctcaaga 433

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtcc 1642
||

Sbjct: 434 ttcagcgctcttggactntccaccaaggacttggcgccttgtcc 478

Score = 202 bits (102), Expect = 1e-47
Identities = 117/122 (95%)
Strand = Plus / Plus

Query: 663 ctaccattcatgtccaaacctcttctcctctgtgaaatccacagtgaatctgccatctc 722
|||||

Sbjct: 1 ctaccattcgtgtccaaacctcttctccactgtgaaatccacagtgcaatctgccatatc 60

Sbjct: 61 aaaggagaccgcgcatgggtgcttctctcctccgcctgttcttccacgattgctttgtcaa 120

Sbjct: 121 tg 122

Query: 1790 gtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgaga 1849

Query: 1850 ccaacatagaaaccgcatttgcaggactaggcagcaaagctg-ccctagaacatcaggg 1908

Query: 1909 tcaggggacaa 1919

>gb|FF386168.1| M00BI56TRB M00 Vigna unguiculata cDNA, mRNA sequence
Length = 598

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctcca 2006

Sbjct: 91 tccgaccacattcgacaactactacttcaggaacctggttcagaagaagggtcttctcca 150

Query: 2007 ctctgatcagcaactgttcaa-cggtgggtccaccgactccattgtgcgtggctacagca 2065
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 151 ctctgaccagcaactcttcaataggtggctccactgactccatagtgcgtggctacagca 210

Query: 2066 ccaacccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacatta 2125
||||| || |||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 211 ccaaccaagctccttttctctgattttgtctccgcattatcaagatgggagacatta 270

Query: 2126 gtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaact 2179
|||| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| |||||

Sbjct: 271 gtccctcaccggctccaaggagaaatcagaagaactgcagaaggattaact 324

>gb|AI441922.1| sa51f09.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1004-2850 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 480

Score = 291 bits (147), Expect = 1e-74
Identities = 165/171 (96%)
Strand = Plus / Plus

Query: 1177 attggatgacacatcaagcttcaccggagagaagaacgcaaaccccaacaggaactctgc 1236
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 6 attggatgacacatcaagcttcaccggagagaagaacgcaaaccccaacaggaactctgc 65

Query: 1237 tcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtccaggagt 1296
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 66 tcgtggatacagaggtcattgacaacattaaatcagccgtggagaaagcatgtccaggagt 125

Query: 1297 tgtttcctgcgcagatatccttgccatcgctgccagagactctgttcagat 1347
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 126 tgtctcctgcgcagatatccttgccatagctgccagagactctgttcagat 176

Score = 287 bits (145), Expect = 2e-73
Identities = 160/165 (96%)
Strand = Plus / Plus

```
Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
          ||||||||||||| ||||||||||| ||||| ||||||||| ||||||||| ||
Sbjct: 388 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 329
```

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 328 tacttcaagaacctggttcagaacaaggcctcctacactccgaccagcaactcttcaac 269

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 268 ggtgggtccaccgactccaccgtgcgtggctacagcaccaacccgagctcatcttctcctct 209

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
|||||
Sbjct: 208 gatttcgcccagcgccatggtcaagatgggagatatcagtcctctcactggatccaacggt 149

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||
Sbjct: 148 gaaatcaggaagaattgcagaa 127

Score = 180 bits (91), Expect = 4e-41
Identities = 160/183 (87%)
Strand = Plus / Minus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 865 tgtgatggttcagttctacttgatgacacatcaagcttcaccgggagaagaatgcaaac 806

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 805 cccaacagaaactctgctcgcggatttgatgttattgacaacatcaagtcagcagtagag 746

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|| ||
Sbjct: 745 gcagcatgcccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 686

Query: 1340 gtt 1342
|||
Sbjct: 685 gtt 683

Score = 123 bits (62), Expect = 8e-24
Identities = 134/158 (84%)

Strand = Plus / Minus

Query: 1484 ggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgct 1543
||||| ||||||| ||| | ||||||| ||||||| ||||||| ||| ||

Sbjct: 670 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 611

Query: 1544 gctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| |||| | ||||||| ||||||| ||| | ||||||| ||||||| || ||

Sbjct: 610 gccaacacagggcatccctgcacccacttctagcttgagccaactcacctcaaggttcagt 551

Query: 1604 gctcttggactttccaccaaggacttggcgccttgtc 1641
||||| ||||||| ||| ||||||| || |||||

Sbjct: 550 gctcttggactttccagcaaagacttggttgcattgtc 513

>dbj|BP048143.1| BP048143 Lotus corniculatus var. japonicus pods (less than 20 mm in
length) Lotus japonicus cDNA clone SPD052d03_f 3', mRNA
sequence
Length = 472

Score = 289 bits (146), Expect = 6e-74

Identities = 233/262 (88%)

Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| ||||| ||||||| ||||||| ||| ||

Sbjct: 418 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 359

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||| ||||||| ||||||| ||||| ||||| ||||| || ||||||| |||||||

Sbjct: 358 tacttcaagaacctgggttcagaacaaggcctcctacactccgaccagcaactcttcaac 299

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
||||| ||||||| ||||||| ||||||| ||||||| ||||| || |||||||

Sbjct: 298 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcatcttctcctct 239

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
||||||| ||||||| ||||||| ||||| ||||||| ||||||| ||||| ||

Sbjct: 238 gatttcgccagcgccatgggtcaagatgggagatatcagtcctctcactgggtccaacggt 179

Query: 2149 gaaatcaggaagaattgtagaa 2170

|||||
Sbjct: 178 gaaatcaggaagaattgcagaa 157

>dbj|BP048038.1| BP048038 Lotus corniculatus var. japonicus pods (less than 20 mm in
length) Lotus japonicus cDNA clone SPD051a08_f 3', mRNA
sequence
Length = 513

Score = 289 bits (146), Expect = 6e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 453 tcaggggacaacaatttggcaccacttgaccttcagactccaacctccttgacaacaac 394

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 393 tacttcaagaacctgggttcagaacaaggcctcctacactccgaccagcaactcttcaac 334

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 333 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcatcttctctct 274

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||
Sbjct: 273 gatttcgccagcgccatgggtcaagatgggagatatcagtcctctcactggatccaacggt 214

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||
Sbjct: 213 gaaatcaggaagaattgcagaa 192

>dbj|AV768169.1| AV768169 Lotus japonicus Young plants (two-weeks old) Lotus japonicus
cDNA clone MWM225a08_f 3', mRNA sequence
Length = 587

Score = 289 bits (146), Expect = 6e-74
Identities = 233/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

|||||
Sbjct: 452 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 393

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 392 tacttcaagaacctgggttcagaacaaggcctcctacactccgaccagcaactcttcaac 333

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 332 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcattttcctct 273

Query: 2089 gatttcgccgcgcatgatcaagatgggagacattagtcctctcactgggtccaatgga 2148
|||||

Sbjct: 272 gatttcgccagcgcatggtcaagatgggagatatcagtcctctcactggatccaacggt 213

Query: 2149 gaaatcaggaagaattgtagaa 2170
|||||

Sbjct: 212 gaaatcaggaagaattgcagaa 191

>dbj|BP048158.1| BP048158 Lotus corniculatus var. japonicus pods (less than 20 mm in
length) Lotus japonicus cDNA clone SPD052e08_f 3', mRNA
sequence
Length = 495

Score = 274 bits (138), Expect = 3e-69
Identities = 231/262 (88%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
|||||

Sbjct: 442 tcaggggacaacaatttggcaccactggaccttcagactcccacctcctttgacaacaac 383

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 382 tacttcaagaacctgggttcagaacaaggcctcctacactccgaccagcaactcttcaac 323

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 322 ggtgggtccaccgactccaccgtgcgtgggtacagcaccaacccgagctcattttcctct 263

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||| || ||||||||| ||||| ||
Sbjct: 262 gatttcgccagcgccatggtcaagatgggagatatcagtcctctcactggatccaacggt 203

Query: 2149 gaaatcaggaagaattgtagaa 2170
||||||| |||||
Sbjct: 202 gaaatcaggaagaattgcagaa 181

>gb|G0017605.1| LJGBF85T0 JCVI-LJ1 Lotus japonicus cDNA 3', mRNA sequence
Length = 420

Score = 266 bits (134), Expect = 8e-67
Identities = 230/262 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||||| ||||| ||||| || ||||| || ||||| ||
Sbjct: 265 tcaggggacaacaatttggcaccacttgaccttcagacaccaacctccttcgacaacaac 206

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
||||| ||||| ||||| || ||||| ||||| ||||||||| |||||
Sbjct: 205 tactttaagaacctggttcaaaacaaggcctcctacactctgatcagcaacttttcaac 146

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
||||| || ||||| ||||||||| ||||| || || |||||
Sbjct: 145 ggtggtccgccgactccaccgtgcgtggctacagcaccaacccgagctcattttctct 86

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||| ||||||||| || ||||||||| ||||| ||
Sbjct: 85 gatttcgccagcgccatggtcaagatgggagatatcagtcctctcactggatccaacggt 26

Query: 2149 gaaatcaggaagaattgtagaa 2170
||||||| |||||
Sbjct: 25 gaaatcaggaagaattgcagaa 4

>gb|G0023584.1| LJMCD71TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA sequence
Length = 630

Score = 262 bits (132), Expect = 1e-65
Identities = 210/236 (88%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||
Sbjct: 387 tcaggggacaacaatttggcaccacttgaccttcagactccaacctcctttgacaacaac 446

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||
Sbjct: 447 tacttcaagaacctgggttcagaacaaggcctcctacactccgaccagcaactcttcaac 506

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
|||||
Sbjct: 507 ggtgggtccaccgactccaccgtgcgtggctacagcaccaacccgagctcattttcctct 566

Query: 2089 gatttcgccgcgccatgatcaagatgggagacattagtcctctcactgggtccaa 2144
|||||
Sbjct: 567 gatttcgccagcgccatgggtcaagatgggagatatcagtcctctcactgggtccaa 622

Score = 123 bits (62), Expect = 8e-24
Identities = 134/158 (84%)
Strand = Plus / Plus

Query: 1484 ggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaatctgct 1543
|||||
Sbjct: 105 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 164

Query: 1544 gctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| ||||
Sbjct: 165 gccaacacaggcatccctgcacccacttctagcttgagccaactcacctcaaggttcagt 224

Query: 1604 gctcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 225 gctcttggactttccagcaaagacttgggttcattgtc 262

Score = 69.9 bits (35), Expect = 1e-07
Identities = 77/91 (84%)
Strand = Plus / Plus

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||||||| ||||||| ||||||||||||||||||||| |||
Sbjct: 510 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 569

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgct 1641
|| || ||||| |||||||||||||||||||||||||||||
Sbjct: 570 ttcagtgcctctaggactttccaccaaggacttggtcgccttgct 613

Score = 234 bits (118), Expect = 3e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
||||||||||||||||||| || || ||||| ||||||||||||| || |||
Sbjct: 45 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 104

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
||| ||||||||||||||||| |||| ||||| ||| || ||||| ||| |||||
Sbjct: 105 tgtgtcaatgcacaactttctactgacttctactacagttcttgcctctctcc 164

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
||||||| ||||||||||||||||| |||||||||||||||||||||
Sbjct: 165 actgtgagatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttctctc 224

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
|| |||||||||||||||||||||||||||||
Sbjct: 225 ctccgcttggttcttccacgattgctttgtcaatg 258

Score = 83.8 bits (42), Expect = 7e-12
Identities = 48/50 (96%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcat 1838
||||| ||||||||||||||||||||||||||||| |||||||||||||
Sbjct: 615 ggtgggcacacaattggacaagcaaggtgcacaaatttcagagcccgcat 664

>gb|FF394030.1| MOODS81TF MOO Vigna unguiculata cDNA 5', mRNA sequence
Length = 786

Score = 246 bits (124), Expect = 8e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 274 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||| ||||||||| || || ||||| ||| |||||||||
Sbjct: 334 aaccccaacagaaactctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
||||||||| ||||||||| || ||||||||| || |||||||||
Sbjct: 394 gagaaagtgtgtccaggagttgtttcctgtgcggatatccttgctattgtgccagagac 453

Query: 1337 tctgttca 1344
|||||||
Sbjct: 454 tctgttca 461

Score = 238 bits (120), Expect = 2e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 466 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||||||| ||||||| ||||||||| ||||||||| |||
Sbjct: 526 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 585

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgcttgtc 1641
|| || ||||| ||||||||| ||||||||| |||||||||
Sbjct: 586 ttcagtgtcttaggactttccaccaaggacttggtcgcttgtc 629

Score = 234 bits (118), Expect = 3e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcataatggggg 630
|||||
Sbjct: 61 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 120

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 121 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 180

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||
Sbjct: 181 actgtgagatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttctctc 240

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 241 ctccgcttggttcttccacgattgctttgtcaatg 274

Score = 180 bits (91), Expect = 4e-41
Identities = 140/155 (90%), Gaps = 1/155 (0%)
Strand = Plus / Plus

Query: 1789 ggtgggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
|||||
Sbjct: 631 ggtggccacacaattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgag 690

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcaggg 1908
|
Sbjct: 691 agcaacatagatacctcattagccaggacaagacaatcaagctgccccagaaacatcaggg 750

Query: 1909 tcaggggacaacaatctggcaccacttgatcttca 1943
|||
Sbjct: 751 tca-gggacaacaatctggcaccgcttgatcttca 784

>gb|FF387818.1| M00C268TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 625

Score = 246 bits (124), Expect = 8e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||| ||||||||| |||||||||
Sbjct: 226 ggatgtgacggttcgattcctttggatgacacgtcaagcttcaccggggagaagaacgca 285

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||||| || ||||||||| || || ||||||| || |||||||||
Sbjct: 286 aaccccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 345

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||||| || || ||||||| || |||||||||
Sbjct: 346 gagaaagtgtgtccaggagttgtttcctgctgcgatatccttgccattgctgccagagac 405

Query: 1337 tctgttca 1344
|||||||
Sbjct: 406 tctgttca 413

Score = 226 bits (114), Expect = 7e-55
Identities = 189/214 (88%)
Strand = Plus / Plus

Query: 571 atggtcttcgttttgttctagattgacaatttgtttggtctgtttgtcctcatatggggg 630
||||||| ||||||| || || ||||||| ||||||||| || |||
Sbjct: 13 atggtcttcgttttgttctagattaactatcagtttggtgctgtttgtcctcgtactgggt 72

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
||| ||||||| ||||| ||||| ||| || ||||| || |||||
Sbjct: 73 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 132

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 133 actgtgagatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttctctc 192

Query: 751 cttcgttgttcttccacgattgctttgtcaatg 784
|| ||||||| ||||||| ||||||| |||||||

Sbjct: 193 ctccgcttgtttcttccacgattgctttgtcaatg 226

Score = 131 bits (66), Expect = 3e-26
Identities = 102/114 (89%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||||| ||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct: 512 ggtgggcacacaattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgag 571

Query: 1849 accaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaaca 1902
| ||||||||| ||| ||||||| ||||| || | | ||||||||| |||||
Sbjct: 572 agcaacatagatacctcatttgccaggacaagacaatcaagctgccccagaaca 625

Score = 97.6 bits (49), Expect = 4e-16
Identities = 64/69 (92%)
Strand = Plus / Plus

Query: 1573 aaaccttaaccaactcatctcaagatttagcgtcttggactttccaccaaggacttgg 1632
||||||||||||||||||||| ||||| || ||||| ||| |||||||||||||||
Sbjct: 442 aaaccttaaccaactcatctctagattcagtgctctaggattttccaccaaggacttgg 501

Query: 1633 cgccttgtc 1641
|||||||
Sbjct: 502 cgccttgtc 510

>gb|FF383796.1| M00B233TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 498

Score = 246 bits (124), Expect = 8e-61
Identities = 172/188 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||||||||| ||||||||||||| |||||||||
Sbjct: 146 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 205

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||
Sbjct: 206 aacccaacagaaattctgtctgtggatatgaagtcattgacagcataaaatcagccgtg 265

Query: 1277 gagaaagtgtgtccaggagttgtttcctgctgcagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 266 gagaaagtgtgtccaggagttgtttcctgtgctggatatccttgccattgctgccagagac 325

Query: 1337 tctgttca 1344

|||||
Sbjct: 326 tctgttca 333

Score = 216 bits (109), Expect = 7e-52
Identities = 148/161 (91%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537

|||||
Sbjct: 338 cttggaggccctagtgtgaatgttaaacttggagaagagatgctagaactgctagccga 397

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

|||||
Sbjct: 398 tctgctgccaacaatggcattcctgcaccttctcaaaccttaaccaactcatctctaga 457

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgcctt 1638

|| || |||||
Sbjct: 458 ttcagtgtcttaggactttccaccaaagacttggctgcctt 498

Score = 178 bits (90), Expect = 1e-40
Identities = 132/146 (90%)
Strand = Plus / Plus

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698

|||||
Sbjct: 1 tgcacaactttctactgacttctactacagttcttgcceaaactcctctccactgtgag 60

Query: 699 atccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 758

|||||
Sbjct: 61 atccacagtgcgaatctgccatatcaaaggagaccgcgatgggtgcttctctccccgctt 120

Query: 759 gttcttccacgattgctttgtcaatg 784
 |||||
Sbjct: 121 gttcttccacgattgctttgtcaatg 146

>dbj|FS240762.1| FS240762 RPSC Glycyrrhiza uralensis cDNA clone KAN050-D13.F 5', mRNA
 sequence
 Length = 554

Score = 244 bits (123), Expect = 3e-60
Identities = 174/191 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||
Sbjct: 246 ggatgtgatggttcaattctactggatgacacatcaagctttacaggggagaagaacgca 305

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 |||||
Sbjct: 306 aaccggaacaggaactcagctcgtgggttcgaagtcacgacaacatcaagtcagccgta 365

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
 |||||
Sbjct: 366 gagaaagtgtgccctggagttgtttcctgcgcgtgatatccttgccatcgctgccagagac 425

Query: 1337 tctgttcagat 1347
 ||
Sbjct: 426 tccgttcagat 436

Score = 178 bits (90), Expect = 1e-40
Identities = 159/182 (87%)
Strand = Plus / Plus

Query: 603 tttggctctgtttgtcctcatatgggggagtgccaatgcacaactttctacaaactttta 662
 |||||
Sbjct: 65 tttggctctctctgtttctcataatggggagtgccaatgcacaactctctacaaactteta 124

Query: 663 ctaccattcatgtccaaacctcttctcctctgtgaaatccacagtgcaatctgccatatc 722
 || |

Sbjct: 125 ctccagttcttgtccaaaactggtttccactgtaaaatccacagtacaatccgccatatac 184

Query: 723 taaggagaccgcgatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaa 782

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 185 aaaggagaccgcgatgggtgcttccctcctccgcttggttcttccatgattgctttgtcaa 244

Query: 783 tg 784

||

Sbjct: 245 tg 246

Score = 137 bits (69), Expect = 5e-28

Identities = 105/117 (89%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 438 cttggaggacctacttggaatgttaaacttggaagaagagacgctaagacggctagccag 497

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctca 1594

||||||| ||||| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 498 tctgctgccaacaacggcatccctcctcccacttctaacctcaaccaactcatctca 554

>gb|FG889628.1| UCRVU08_CCNS10828_b1 Cowpea IT97K-461-4 Mixed Tissue and Conditions

cDNA Library UCRVU08-1-2 Vigna unguiculata cDNA clone

CCNS10828.b1, mRNA sequence

Length = 692

Score = 238 bits (120), Expect = 2e-58

Identities = 171/188 (90%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 257 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 316

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

||||||| || ||||| ||||| || || ||||| ||| ||||| ||||| |||||

Sbjct: 317 aaccccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 376

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcgagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 377 gagaaagtgtgtccaggagttgtttcctgtgcggatatccttgctattgctgccagagac 436

Query: 1337 tctgttca 1344
|||||
Sbjct: 437 tctgttca 444

Score = 238 bits (120), Expect = 2e-58
Identities = 153/164 (93%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 449 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccaa 508

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 509 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 568

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
|| ||
Sbjct: 569 ttcagtgccttaggactttccaccaaggacttggctgccttgtc 612

Score = 226 bits (114), Expect = 7e-55
Identities = 189/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
|||||
Sbjct: 44 atggcttcgttttgttctagattaactttcagtttggttctgtttgtcctcgactgggt 103

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 104 tgtgtcaatgcacaactttctactgacttctactacagtcttgcceaaaactcctctcc 163

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||

Sbjct: 164 actgtgagatccacagtgaatctgccatatcaaaggagaccgcatgggtgcttctctc 223

Query: 751 cttcgcttggtttccacgattgctttgtcaatg 784

|| ||||||||||||||||||||||||||||||||

Sbjct: 224 ctccgcttggtttccacgattgctttgtcaatg 257

Score = 111 bits (56), Expect = 3e-20

Identities = 65/68 (95%)

Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848

||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||

Sbjct: 614 ggtggccacacaattggacaagcaaggtgcacaaatttcagagcccgcatctacaacgag 673

Query: 1849 accaacaat 1856

| |||||

Sbjct: 674 agcaacaat 681

>gb|FF403045.1| M00F734TF M00 Vigna unguiculata cDNA 5', mRNA sequence

Length = 745

Score = 238 bits (120), Expect = 2e-58

Identities = 153/164 (93%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

||||||||||| ||||||||||||||||||||| ||||||||||||||||

Sbjct: 465 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccaa 524

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

||||||| ||||||||| ||||| ||||||||||||||||||||| |||

Sbjct: 525 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 584

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641

|| || ||||| |||||||||||||||||||||

Sbjct: 585 ttcagtgtctaggaactttccaccaaggacttggctgccttgtc 628

Score = 234 bits (118), Expect = 3e-57

Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggettcgttttgttctagattgacaatttgtttggctctgtttgtcctcatatggggg 630
|||||

Sbjct: 61 atggettcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 120

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||

Sbjct: 121 tgtgtcaatgcacaactttctactgacttctactacagtcttgcccaaaactcctctcc 180

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||

Sbjct: 181 actgtgagatccacagtgaatctgccatatcaaaggagacccgcatgggtgcttctctc 240

Query: 751 cttegcttggttcttccacgattgctttgtcaatg 784
||

Sbjct: 241 ctccgcttggttcttccacgattgctttgtcaatg 274

Score = 222 bits (112), Expect = 1e-53
Identities = 170/188 (90%), Gaps = 1/188 (0%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||

Sbjct: 274 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccgggagaagaacgca 333

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|||||

Sbjct: 334 aaccccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 393

Query: 1277 gagaaagtgtgtccaggagttgtttcctgtgcgagatatccttgccatcgctgccagagac 1336
|||||

Sbjct: 394 gagaaagtgtgt-caggggttggtttcctgtgcggatatccttgccattgctgccagagac 452

Query: 1337 tctgttca 1344
|||||

Sbjct: 453 tctgttca 460

Query: 1789 ggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgag 1848
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 630 ggtgggcacacaattggacaagcaaagtgcacaaatttcagagcccgcatctacaacgag 689

>gb|FF392448.1| M00CV65TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 607

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 272 ggatgtgacggttcgattcttttggatgacacgtcaagcttcaccggggagaagaacgca 331

```

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
          |||||
Sbjct: 332 aacccaacagaaattctgctcgtggatatgaagtcattgacagcataaaatcagccgtg 391

```

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgagatatccttgccatcgctgccagagac 1336
 |||||||
 Sbjct: 392 gagaaagtgtgtccaggagttgtttcctgcgagatatcctcgccattgctgccagagac 451

```
Query: 1337 tctgttca 1344
      |||||
Sbjct: 452 tctgttca 459
```

Score = 234 bits (118), Expect = 3e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttggttggtctgtttgtcctcatatggggg 630
|||||||
Sbjct: 59 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 118

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 119 tgtgtcaatgcacaactttctactgacttctactacagttcttgccaaaactcctctcc 178

Query: 691 tctgtgaaatccacagtgcgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||
Sbjct: 179 actgtgagatccacagtgcgaatctgccatatcaaaggagacccgcatgggtgcttctctc 238

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 239 ctccgcttggttcttccacgattgctttgtcaatg 272

Score = 198 bits (100), Expect = 2e-46
Identities = 133/144 (92%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 464 cttggaggccctagtgtgaatgttaaacttggaagaagagatgctagaactgctagccaa 523

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||||
Sbjct: 524 tctgctgccaacaatggcattcctgcaccttcttcaaaccttaaccaactcatctctaga 583

Query: 1598 tttagcgctcttggaactttccacc 1621
||
Sbjct: 584 ttcagtgccttaggaactttccacc 607

>gb|FF399144.1| M00EV84TF M00 Vigna unguiculata cDNA 5', mRNA sequence
Length = 345

Score = 234 bits (118), Expect = 3e-57
Identities = 190/214 (88%)
Strand = Plus / Plus

Query: 571 atggcttcgttttgttctagattgacaatttggttggtctgtttgtcctcatatggggg 630
|||||
Sbjct: 64 atggcttcgttttgttctagattaactatcagtttggttctgtttgtcctcgtactgggt 123

Query: 631 agtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcc 690
|||
Sbjct: 124 tgtgtcaatgcacaactttctactgacttctactacagttcttgcccaaaactcctctcc 183

Query: 691 tctgtgaaatccacagtgaatctgccatatctaaggagacccgcatgggtgcttctctc 750
|||||
Sbjct: 184 actgtgagatccacagtgaatctgccatatcaaaggagacccgcatgggtgcttctctc 243

Query: 751 cttcgcttggttcttccacgattgctttgtcaatg 784
||
Sbjct: 244 ctccgcttggttcttccacgattgctttgtcaatg 277

Score = 89.7 bits (45), Expect = 1e-13
Identities = 63/69 (91%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 277 ggatgtgacggttcgattcttttgatgacacgtcaagcttccccggggagaagaacgca 336

Query: 1217 aacccaac 1225
|||||
Sbjct: 337 aacccaac 345

>gb|G0019707.1| LJMAW92TF JCVI-LJ2 Lotus japonicus cDNA 5', mRNA sequence
Length = 663

Score = 208 bits (105), Expect = 2e-49
Identities = 180/205 (87%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttggttggtctgtttgtcctcatatgggggagtccaat 639
|||||
Sbjct: 71 ttttgttctagattaactatctgtttgtcctctttgtcctcatattgggggagtccaat 130

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699
|| ||||| ||||| || || ||||| ||||| || |||||
Sbjct: 131 gctcaactttctacaaacttctattctagttcttgtccaaacctctttccactgtgaaa 190

Query: 700 tccacagtgcgaatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttg 759
||| ||||| ||||| ||||| | ||||| ||||| |||||
Sbjct: 191 tcctcagtgcgaatccgccatatcaaaggaggctcgcatgggtgcttctctcctccgcttg 250

Query: 760 ttcttccacgattgctttgtcaatg 784
||||| ||||| |||||
Sbjct: 251 ttcttccatgattgcttcgtcaatg 275

Score = 180 bits (91), Expect = 4e-41
Identities = 160/183 (87%)
Strand = Plus / Plus

Query: 1160 tgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 278 tgtgatgggtcagttctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 337

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
||||| ||||| ||||| ||||| || ||||| ||||| || ||||| || |||
Sbjct: 338 cccaacagaaactctgctcgcggatttgatgttattgacaacatcaagtcagcagtagag 397

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 398 gcagcatgccaggagttgtatcctgcgctgatatacctcgccatctctgctagagactct 457

Query: 1340 gtt 1342
|||
Sbjct: 458 gtt 460

Score = 123 bits (62), Expect = 8e-24
Identities = 134/158 (84%)
Strand = Plus / Plus

Query: 1484 ggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaatctgct 1543
||||| ||||||||| || | ||||||||| ||||||||| || ||
Sbjct: 473 ggccccacatggaatgtgaaagtaggaagaagagacgctaaaactgctagccagtcgcc 532

Query: 1544 gctaacaatggcatccctgcaccacattcaaaccttaaccaactcatctcaagatttagc 1603
|| |||| | ||||||||| || || | ||||||| ||||||| || ||
Sbjct: 533 gccaacacaggcatccctgcaccacattctagcttgagccaactcacctcaagttcagt 592

Query: 1604 gctcttggactttccaccaaggacttggcgccttgtc 1641
||||||| ||||| || ||||| || |||||
Sbjct: 593 gctcttggactttccagcaaagacttggttgcatgtc 630

>dbj|AV412875.1| AV412875 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MWM225a08_r 5', mRNA sequence
Length = 282

Score = 208 bits (105), Expect = 2e-49
Identities = 180/205 (87%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggtctgtttgtcctcatatgggggagtgccaat 639
||||||| || || ||||| ||||| ||||||||| |||||||||
Sbjct: 53 ttttgttctagattaactatctgtttgtctctttgtcctcatattggggagtgccaat 112

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699
|| ||||||||| || | || ||||||| ||||| || |||||||
Sbjct: 113 gctcaactttctacaaacttctattctagtcttgtccaaaactcttttccactgtgaaa 172

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
||| ||||||||| ||||||| ||||| | ||||||||| |||||||
Sbjct: 173 tctcagtgcaatccgccatatcaaaggagctcgcatgggtgcttctctcctccgcttg 232

Query: 760 ttcttccacgattgctttgtcaatg 784
||||||| ||||||| |||||||
Sbjct: 233 ttcttccatgattgcttcgtcaatg 257

>dbj|AV771838.1| AV771838 Lotus japonicus Pods (20-30 mm in length) Lotus japonicus
cDNA clone MPD027c11_f 3', mRNA sequence
Length = 430

Score = 202 bits (102), Expect = 1e-47

Identities = 208/242 (85%), Gaps = 1/242 (0%)
Strand = Plus / Minus

Query: 1925 tggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaagaacctcg 1984
|||||
Sbjct: 428 tggcaccacttgaccttcagactccaacctcctttgactaccactacttcaagtacctgg 369

Query: 1985 ttcagaagaagggtctcctccactctgatcagcaactgttcaacggtgggtccaccgact 2044
|||||
Sbjct: 368 ttcagaaccagggcctccgacactccgaccagcaactcttcaacggtgggtccaccgact 309

Query: 2045 ccattgtgctgggtacagcaccaaccgggacaccttctcctctgatttcgccgccgcca 2104
|||
Sbjct: 308 ccaccgtgctgggtacagcaccaaccggagctcatttctcctctgatttcgccagcgcca 249

Query: 2105 -tgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||
Sbjct: 248 ctggtccagatgggagatatcagtcctctcactggatccaacggtgaaatcaggaagaat 189

Query: 2164 tg 2165
||
Sbjct: 188 tg 187

>dbj|BW620524.1| BW620524 Lotus japonicus protoplasts from suspension-cultured cells
Lotus japonicus cDNA clone LjFL1-sab-002-BB11 5', mRNA
sequence
Length = 480

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 211 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 270

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 271 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 330

```

Query: 1340 gtt 1342
        |||
Sbjct: 391  gtt 393

```

```
Query: 586 tctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaatgcacaa 645
          ||||| || || |||| |||| |||| |||| |||| |||| |||| |||| ||||
Sbjct: 10 tctagattaactatctgttttgcctcttcttgccttatattggggagtgctaatgctcaa 69
```

```
Query: 646 ctttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccaca 705
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 70  ctttctacaaacttctattctagttcttctgtccaaaactcttttccactgtgaaatcctcc 129
```

```
Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctcttcgcttgttcttc 765
      ||||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 130 gtgcaatccgccatatcaaaggagctcgcatgggtgcttctctcttcgcttgttcttc 189
```

```
Query: 766  cacgattgctttgtcaatg 784
          || ||||| || |||||
Sbjct: 190  catgattgcttcgtcaatg 208
```

```
Query: 1484  ggcctacatggaatgttaaacttggaagaagagacgctagaactgctagcca 1536
              ||||| ||||||||| || ||||||||||||| |||||||||
Sbjct: 406    ggccccacatggaatgtgaaagtgggaagaagagacgctaaaactgctagcca 458
```

>dbj|BW630489.1| BW630489 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-026-AD06 5', mRNA

sequence
Length = 482

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 145 tgtgatggttcaattctacttggatgacacatcaagcttcaccgggagagaagaatgcaaac 204

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||
Sbjct: 205 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 264

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatataccttgccatcgtgccagagactct 1339
||
Sbjct: 265 gcagcatgcccaggagttgtatcctgcgctgatatacctcgccatctctgctagagactct 324

Query: 1340 gtt 1342
|||
Sbjct: 325 gtt 327

Score = 127 bits (64), Expect = 5e-25
Identities = 100/112 (89%)
Strand = Plus / Plus

Query: 673 tgtccaaacctcttctcctctgtgaaatccacagtgcaatctgccatatctaaggagacc 732
|||||
Sbjct: 31 tgtccaaacctctttccactgtgaaatcctccgtgcaatccgccatatcaaaggagct 90

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 91 cgcattgggtgcttctctccttcgcttgttcttccatgattgcttcgtcaatg 142

Score = 119 bits (60), Expect = 1e-22
Identities = 117/136 (86%)
Strand = Plus / Plus

Query: 1484 ggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaatctgct 1543
||||| |||||||||||| || ||||||||||||||||||| |||||||||||| || ||
Sbjct: 340 ggcacacatggaatgtgaaagttggaagaagagacgctaaaactgctagccagtccgcc 399

Query: 1544 gctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagc 1603
|| ||||| ||||||||||||||||||| || || || || || || || || || || || ||
Sbjct: 400 gccaacacaggcatccctgcacccacttctagcttgagccaactcacctcaaggttcagt 459

Query: 1604 gctcttggactttcca 1619
|||||||||||||||
Sbjct: 460 gctcttggactttcca 475

>dbj|BW629863.1| BW629863 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-024-BE11 5', mRNA
sequence
Length = 471

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctatttgatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||||||||||||||| | ||||||||||||||||||| |||||||| |||||
Sbjct: 276 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 335

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
||||||| ||||||||| ||||||| ||||||||||||||| || ||||| || |||
Sbjct: 336 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 395

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|| || ||||||||||| ||||||| ||||||| ||||| ||||| |||||
Sbjct: 396 gcagcatgcccaggagttgtatcctgcgcgtgatatcctcgccatctctgctagagactct 455

Query: 1340 gtt 1342
|||
Sbjct: 456 gtt 458

Score = 192 bits (97), Expect = 1e-44
Identities = 178/205 (86%)

Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaat 639
|||||

Sbjct: 69 ttttgttctagattaactatctgttttgcctcttctgtcctcatatgggggagtgcta 128

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctctctcctctgtgaaa 699
|||

Sbjct: 129 gctcaactttctacaaacttctattctagttcttgcctccaaactcttttccactgtgaaa 188

Query: 700 tccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
|||

Sbjct: 189 tcctccgtgcaatccgccatatcaaaggaggctcgcatgggtgcttctctcctccgcttg 248

Query: 760 ttcttccacgattgctttgtcaatg 784
|||

Sbjct: 249 ttcttccatgattgcttcgtcaatg 273

>dbj|BW628107.1| BW628107 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-019-CE07 5', mRNA
sequence
Length = 471

Score = 196 bits (99), Expect = 6e-46

Identities = 162/183 (88%)

Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||

Sbjct: 278 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 337

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||||

Sbjct: 338 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 397

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|||

Sbjct: 398 gcagcatgcccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 457

Query: 1340 gtt 1342

|||
Sbjct: 458 gtt 460

Score = 192 bits (97), Expect = 1e-44
Identities = 178/205 (86%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggtctgtttgtcctcatatgggggagtgccaat 639
||||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 71 ttttgttctagattaactatctgtttgtctctttgtcctcatattggggagtgctaata 130

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctctctcctctgtgaaa 699
|| ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 131 gctcaactttctacaaacttctattctagtcttgtccaaaactcttttccactgtgaaa 190

Query: 700 tccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759
||| | ||||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 191 tctccgtgcaatccgccatatcaaaggaggctcgcatgggtgcttctctcctccgcttg 250

Query: 760 ttcttccacattgctttgtcaatg 784
||||||| ||||| |||||
Sbjct: 251 ttcttccatattgcttcgtcaatg 275

>dbj|BW627140.1| BW627140 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-017-AA04 5', mRNA
sequence
Length = 480

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 286 tgtgatggttcaattctacttgatgacacatcaagcttcaccggggagaagaatgcaaac 345

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 346 cccaacagaaactctgctcgcggattcgatgttattgacaacatcaagtcagcagtagag 405

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgtgccagagactct 1339
|| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 406 gcagcatgcccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 465

Query: 1340 gtt 1342
|||
Sbjct: 466 gtt 468

Score = 184 bits (93), Expect = 2e-42
Identities = 177/205 (86%)
Strand = Plus / Plus

Query: 580 ttttgttctagattgacaatttgtttggtctctgtttgtcctcatatgggggagtgccaat 639
||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 79 ttttgttctagattaactatctgtttgtctctttgtcctcatattggggagtgctaata 138

Query: 640 gcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699
|| ||||| ||||| || || ||||| ||||| ||||| |||||
Sbjct: 139 gctcaactttctacaaacttctattctagttctcgtccaaaactcttttccactgtgaaa 198

Query: 700 tccacagtgaatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttg 759
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 199 tcttccgtgcaatccgccatatcaaaggaggctcgcattgggtgcttctctccttcgcttg 258

Query: 760 ttcttccacgattgctttgtcaatg 784
||||| ||||| |||||
Sbjct: 259 ttcttccatgattgcttcgtcaatg 283

>dbj|BW624354.1| BW624354 Lotus japonicus salicylic acid and methyljasmonate treated
cells Lotus japonicus cDNA clone LjFL2-009-BC11 5', mRNA
sequence
Length = 483

Score = 196 bits (99), Expect = 6e-46
Identities = 162/183 (88%)
Strand = Plus / Plus

Query: 1160 tgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 290 tgtgatggttcaattctacttgatgacacaccaagcttcaccggggagaagaatgcaaac 349

Sbjct: 350 cccaacaggaactctgctcgcgattcgatgttattgacaacatcaagtcagcagtagag 409

Sbjct: 410 gcagcatgccaggagttgtatcctgcgctgatatcctcgccatctctgctagagactct 469

Sbjct: 470 gtt 472

Query: 580 ttttgttctagattgacaatttgtttggctctgtttgtcctcatatgggggagtgccaat 639

Query: 640 gcacaacttttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaa 699

Query: 700 tccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttg 759

Query: 760 ttcttcacgattgctttgtcaatg 784

>dbj|BW595840.1| BW595840 Lotus japonicus suspension-cultured cells Lotus japonicus
cDNA clone LjCa-005-DD12 5', mRNA sequence
Length = 485

Identities = 177/203 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
|||||

Sbjct: 283 tcaggggacaacaatttggcaccacttgaccttcagacaccaacctccttcgacaacaac 342

Query: 1969 tacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaac 2028
|||||

Sbjct: 343 tactttaagaacctgggttcaaacaagggcctcctacactctgatcagcaacttttcaac 402

Query: 2029 ggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcctct 2088
|||||

Sbjct: 403 ggtgggtccgccgactccaccgtgcgtgggtacagcaccaacccgagctcattttctct 462

Query: 2089 gatttcgccgcgccatgatcaa 2111
|||||

Sbjct: 463 gatttcgccgcgccatggtcaa 485

Score = 127 bits (64), Expect = 5e-25
Identities = 130/152 (85%)
Strand = Plus / Plus

Query: 1490 acatggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgtaac 1549
|||||

Sbjct: 7 acatggaatgtgaaagtgtgaagaagagacgctaaaactgctagccagtcgccccaac 66

Query: 1550 aatggcatccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctctt 1609
|

Sbjct: 67 acaggcatccctgcacccacttctagcttgagccaactcacctcaaggttcagtgtctt 126

Query: 1610 ggactttccaccaaggacttggctgccttgtc 1641
|||||

Sbjct: 127 ggactttccagcaaagacttgggtgcatgtc 158

>gb|EY976963.1| EST 83 Alfalfa aluminum suppression subtractive library Medicago
sativa cDNA clone E2B11, mRNA sequence
Length = 971

Score = 190 bits (96), Expect = 4e-44
Identities = 147/164 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||| ||| ||||||||||||||| ||||||| ||||| ||
Sbjct: 437 cttggaggcccaacatgggatgtgaaacttggaagaagagatgctagaacagctagtaaa 496

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||| ||||||||||||||| ||||||||||| || |||||||||||||||
Sbjct: 497 tcagctgcaaacatggcatcccagcaccacttcaagcctcaaccaactcatctcaagg 556

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||| ||||||||||||||| ||||||| |||||
Sbjct: 557 tttaatgctcttggactttccaccaaggatttggtcgcattgtc 600

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||||||||||||| | ||||||||||||||| ||||| ||
Sbjct: 245 ggatgtgatggttcaattcttctcggatgacacatcaagcttcaccggagagaaaactgcc 304

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
|| ||||||| || || || ||||||||||| || || ||||| || ||||||| ||
Sbjct: 305 aatcccaacagaaattcggcccgatggattcgaagtgatcgacaaaatcaaatacagcagtg 364

Query: 1277 gagaaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||| | ||||| || || ||||||| ||||| ||||| |||||
Sbjct: 365 gagaaagtatgtccagggtgcagtttcatgtgctgatatcctcgccatcactgctagagac 424

Query: 1337 tctgttcagat 1347
||||||| |||||
Sbjct: 425 tctgttgagat 435

Score = 111 bits (56), Expect = 3e-20
Identities = 71/76 (93%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||||
Sbjct: 170 caatctgccatatcaaaggagacccgcatgggtgcttctcttctacgtttgttcttccac 229

Query: 769 gattgctttgtcaatg 784
|||||||
Sbjct: 230 gattgctttgttaatg 245

Score = 63.9 bits (32), Expect = 6e-06
Identities = 32/32 (100%)
Strand = Plus / Plus

Query: 1789 ggtggtcacacaattggacaagcaaggtgcac 1820
|||||||
Sbjct: 602 ggtggtcacacaattggacaagcaaggtgcac 633

>gb|EH613355.1| EST 02 Alfalfa aluminum suppression subtractive library Medicago
sativa cDNA clone A4 5', mRNA sequence
Length = 748

Score = 190 bits (96), Expect = 4e-44
Identities = 147/164 (89%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 545 cttggaggcccaacatgggatgtgaaacttggaagaagagatgctagaacagctagtaaa 486

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|| |||||
Sbjct: 485 tcagctgcaaacaatggcatccagcaccacttcaagcctcaaccaactcatctcaagg 426

Query: 1598 ttttagcgtcttggactttccaccaaggacttggctgccttgtc 1641
|||||
Sbjct: 425 tttaatgctcttggactttccaccaaggatttggctgcattgtc 382

Score = 149 bits (75), Expect = 1e-31
Identities = 162/191 (84%)
Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 737 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 678

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 677 aatcccaacagaaattcggcccggtgattcgaagtgatcgacaaaatcaaatcagcagtg 618

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 617 gagaaagtatgtccagggtgcagtttcatgtgtgatatcctcgccatcactgctagagac 558

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 557 tctgttgagat 547

Score = 99.6 bits (50), Expect = 1e-16
Identities = 212/266 (79%)
Strand = Plus / Minus

Query: 1900 acatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt 1959
|||||
Sbjct: 269 acatcagggtccggggacaataatttggcacctcttgatcttgcaacaccaacatccttt 210

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
|||||
Sbjct: 209 gacaatcactatttcaagaacctagttgacagtaagggaactactccactccgaccaacaa 150

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcacc 2079
||
Sbjct: 149 ctcttcaatggtggatccactgattccatagtgcatgaatatggcttgtatccaagctct 90

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||
Sbjct: 89 tttctcctctgatttcgtcaccgcccatgatcaagatgggagacattagtcctcctcaccgt 30

Query: 2140 tccaatggagaaatcaggaagaattg 2165

Sbjct: 29 tcaaatggagagataagaaagaattg 4

```
>dbj|BB913062.1| BB913062 Trifolium pratense three week-old plant Trifolium pratense
      cDNA clone RCE12415, mRNA sequence
      Length = 582
```

Score = 190 bits (96), Expect = 4e-44

Strand = Plus / Minus

Query: 1887 aagctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaac 1946

Sbjct: 581 aagctgccccagcacatcagggtcaggggacaacaatttggcacctcttgatcttcagac 522

Query: 1947 tccaaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctcca 2006

Sbjct: 521 tccaacttccttcgacaataactacttcaaaaaccttgттаатааааagggtcttcttca 462

Query: 2007 ctctgatcagcaactgttcaacggtgggtccaccgactccattgtgcgtggctacagcac 2066

Sbjct: 461 ttctgaccaacaacttttcaatggtggctccaccaactccattgttagtggctacagtac 402

Query: 2067 caaccgggacaccttctctctgatttcgccgccgcatgatcaagatgggagacattag 2126

Subject: 401 taatccaagctctttttctttctgattttgctgctgctatgatcaagatgggagacattaa 342

Query: 2127 tcctctcactggctccaatggagaaatcaggaagaattgtagaa 2170

Sbjct: 341 acctcttaccggatccaatggagagatcaggaagaattgcagaa 298

>gb|BI969832.1| GM830009A23A12 Gm-r1083 Glycine max cDNA clone Gm-r1083-3096 3', mRNA
sequence
Length = 678

Score = 180 bits (91), Expect = 4e-41

Identities = 316/392 (80%)

Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||| ||||||||||||||||||||||||| ||| ||||||| ||||| |||||
Sbjct: 585 ggtcatacaattggacaagcaaggtgcacaacctttagagcccgaatctacnnngagagc 526

Query: 1852 aacatagaaaccgcatTTGcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| | | | ||||| | | ||||| || ||||| ||||| |||||
Sbjct: 525 aacatagatagctctTTTgcccgcagtagacaaatctaggtgtccccgaacctcaggatca 466

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctTTGacaactactac 1971
||||||| || | ||||| ||||| || ||||| || ||||| ||||| |||||
Sbjct: 465 ggggacaacaaccttgcaaccttgactTTGCCactccactTTTctTTGacaacctactac 406

Query: 1972 ttcaagaacctcgTtcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 405 ttcaagaacctcattcagaagaagggtctcatccattccgaccaagaactcttcaatggt 346

Query: 2032 gggTccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctctgat 2091
|| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 345 ggtTccactgactccttggTgcgtacctacagcaccaacccggcctcctTTTtcgccgat 286

Query: 2092 ttccgccgcccatgatcaagatgggagacattagTcctctcactggctccaatggagaa 2151
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 285 ttctccgccgcccatgatcaggatgggagacattagTccctcactggctcccgcgagaa 226

Query: 2152 atcaggaagaattgtagaaggattaactaatt 2183
|| ||| |||| | | ||| | |||||
Sbjct: 225 ataagggagaactgcaggagggtcaactaatt 194

Score = 50.1 bits (25), Expect = 0.092
Identities = 25/25 (100%)
Strand = Plus / Minus

Query: 1611 gactttccaccaaggacttggtcgc 1635
||||||| ||||| |||||
Sbjct: 620 gactttccaccaaggacttggtcgc 596

>gb|BI700509.1| sag61f05.y1 Gm-c1082 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1082-1041 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE

;, mRNA sequence
Length = 472

Score = 180 bits (91), Expect = 4e-41
Identities = 282/343 (82%), Gaps = 2/343 (0%)
Strand = Plus / Plus

Query: 1801 attggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaacatagaa 1860
|||||||
Sbjct: 1 attggacaagcaaggtgcacaacctttagagcccgaatctacaacgagaccaacatagat 60

Query: 1861 accgcatttgcaaggactaggcagcaaaagctgccctagaacatcagggtcaggggacaac 1920
|||
Sbjct: 61 agctcttttctcgcgatgagacaatctaggtgtccccgaacctcagggtcaggggacaac 120

Query: 1921 aatctggcaccacttgatcttcaa-actccaaccagctttgacaactactacttcaagaa 1979
|||
Sbjct: 121 aaactagcaccattga-cttcgccactcccaggttctttgacaaccactacttcaagaa 179

Query: 1980 cctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacggtgggtccac 2039
|||||
Sbjct: 180 cctcattcagaagaagggcctcatcattccgaccaacaactcttcaatggtggttccac 239

Query: 2040 cgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctgatttcgccgc 2099
|||||
Sbjct: 240 tgactccatagtgcgtacctacagcaccaaccgggcctcctttttcgccgatttctccgc 299

Query: 2100 cgccatgatcaagatgggagacattagtcctctcactggctcc 2142
|||||
Sbjct: 300 cgccatgatccgatgggagacattagtcctctcactggctcc 342

>gb|BU578183.1| sar49a02.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1074-5404 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 271

Score = 176 bits (89), Expect = 6e-40
Identities = 134/149 (89%)
Strand = Plus / Plus

Query: 630 gagtgcgaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttctc 689

|||||
Sbjct: 1 gagtccaatgcccaactttctacaaacttctactaccattcatggccaaacctcttctc 60

Query: 690 ctctgtgaaatccacagtgcaatctgccatatctaaggagacccgcatgggtgcttctct 749
| |||||

Sbjct: 61 cactgtgaaatccaccagcaatctgccatatcagaagagacccgcatggctgcttctct 120

Query: 750 ccttcgcttggttcttccacgattgctttg 778
||| | | |||||

Sbjct: 121 cctccacctgttcttccaccattgctttg 149

Score = 107 bits (54), Expect = 5e-19
Identities = 99/114 (86%)
Strand = Plus / Plus

Query: 1159 atgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaa 1218
||||| ||||| || ||||| || ||||| ||||| ||

Sbjct: 157 atgtgatgggtcaattctattggatgacacctcgagcttcgccgagagaaaaacgcgaa 216

Query: 1219 ccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagc 1272
||||| ||||| ||||| || ||||| || ||||| ||

Sbjct: 217 ccccaacaagaactctgctcctggataccaggtccttgaccacctaaatcagc 270

>gb|G0258927.1| VBL1_16_M09_E001.g1 Normalized cDNA library from cotyledon and young
leaves of peanut Arachis hypogaea cDNA, mRNA sequence
Length = 616

Score = 174 bits (88), Expect = 2e-39
Identities = 226/272 (83%)
Strand = Plus / Plus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||||| || || || ||||| ||||| || || || ||||| ||

Sbjct: 3 caggggacaacaaccttgccgcttgatctccaaacacccacggccttcgacaacaact 62

Query: 1970 acttcaagaacctcggttcagaagaagggtctctccactctgatcagcaactgttcaacg 2029
||||| ||||| ||||| ||||| || ||||| || ||||| |||||

Sbjct: 63 acttcaggaaccttggttcagaacaagggctgtccactccgaccagcaactcttcaacg 122

Query: 2030 gtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctctg 2089
||||| ||||| || || | ||||| | ||||| | |||||
Sbjct: 123 gtggctccaccgactctatagtcagaggctacgcctccaacccgacctcattctcctctg 182

Query: 2090 atttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatggag 2149
| ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 183 acttcatcagcgccatgatcaagatgggagacattagtcctctcactggatccaacggtg 242

Query: 2150 aaatcaggaagaattgtagaaggattaactaa 2181
||||| ||||| || || ||||| |||||
Sbjct: 243 aaatcaggaagaactgcaggaggatcaactaa 274

>gb|CA852976.1| E14E06_J06_09.ab1 cDNA Peking library 6, 8 day SCN3 Glycine max cDNA
clone E14E06 5', mRNA sequence
Length = 556

Score = 174 bits (88), Expect = 2e-39
Identities = 193/228 (84%)
Strand = Plus / Plus

Query: 1956 ctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatca 2015
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 89 ctttgacaaccactacttcaagaacctcattcagaagaagggtctcatccattccgacca 148

Query: 2016 gcaactgttcaacggtgggtccaccgactccattgtgcgtggctacagcaccaacccggg 2075
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 149 agaactcttcaatggtggttccactgactccttgggtgcgtacctacagcaccaacccggc 208

Query: 2076 caccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcac 2135
| |||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 209 ctcttttttcgccgatttctccgccgcatgatcaggatgggagacattagtcctctcac 268

Query: 2136 tggtccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183
||||| ||||| || ||||| || ||||| ||||| |||||
Sbjct: 269 tggtcccgcggagaaataagggagaactgcaggagggtcaactaatt 316

>gb|CA852554.1| E09B05_C17_03.ab1 cDNA Peking library 6, 8 day SCN3 Glycine max cDNA
clone E09B05 5', mRNA sequence
Length = 539

Score = 174 bits (88), Expect = 2e-39

Identities = 193/228 (84%)
Strand = Plus / Plus

Query: 1956 ctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactctgatca 2015
||||||| ||||||| ||||||| ||||||| |||| || || ||

Sbjct: 67 ctttgacaaccactacttcaagaacctcattcagaagaagggtctcatccattccgacca 126

Query: 2016 gcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccggg 2075
|||| ||||| ||||| ||||| ||||| | ||||| ||||||| |||||||

Sbjct: 127 agaactcttcaatggtggttccactgactccttggtgcgtacctacagcaccaaccggc 186

Query: 2076 caccttctcctctgatcttcgccgccgcatgatcaagatgggagacattagtcctctcac 2135
| |||| | | ||||| ||||||| ||||||| ||||||| ||||||| |||||

Sbjct: 187 ctctttttcgccgatttctccgccgcatgatcaggatgggagacattagtcctctcac 246

Query: 2136 tggtccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183
|||||| ||||||| ||| |||| || || || | |||||||

Sbjct: 247 tggtccccgcggagaaataagggagaactgcaggagggtcaactaatt 294

>gb|AW350788.1| GM210009A20D5 Gm-r1021 Glycine max cDNA clone Gm-r1021-3226 3', mRNA
sequence
Length = 507

Score = 174 bits (88), Expect = 2e-39
Identities = 193/228 (84%)
Strand = Plus / Minus

Query: 1956 ctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactctgatca 2015
||||||| ||||||| ||||||| ||||||| ||||||| |||| || || ||

Sbjct: 444 ctttgacaaccactacttcaagaacctcattcagaagaagggtctcatccattccgacca 385

Query: 2016 gcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccggg 2075
|||| ||||| ||||| ||||| ||||| | ||||| ||||||| |||||||

Sbjct: 384 agaacttttcaatggtggttccactgactccttagtgcgtacctacagcaccaaccggc 325

Query: 2076 caccttctcctctgatcttcgccgccgcatgatcaagatgggagacattagtcctctcac 2135
| |||| | | ||||| ||||||| ||||||| ||||||| ||||||| |||||

Sbjct: 324 ctctttttcgccgatttctccgccgcatgatcaggatgggagacattagtcctctcac 265

Query: 2136 tggtccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183

Score = 163 bits (82), Expect = 9e-36

Identities = 139/158 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 65 cttggtggcccaacttggaacgtgaaacttggaagaagagactccagaacagcaagccaa 124

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 125 tctgctgccaacaatggcatcccacgaccacttcaaaccttaaccaactcatctccaga 184

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgc 1635
|| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 185 ttcaactctcttggactttcctccaaggacttggtcgc 222

Score = 67.9 bits (34), Expect = 4e-07
Identities = 46/50 (92%)
Strand = Plus / Plus

Query: 1295 gttgtttcctgcgcatatccttgccatcgctgccagagactctgttca 1344
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 11 gttgtttcctgtgccgatatccttgccattgctgccagagattctgttca 60

>gb|EY476317.1| METAQ01TF JCVI-MT3 Medicago truncatula cDNA 5', mRNA sequence
Length = 716

Score = 167 bits (84), Expect = 6e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 492 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctagtaaa 551

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 552 tcagctgcaaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 611

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641

Sbjct: 612 |||| |||||||| |||||||||||||||| |||||||| ||||| 655

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 |||||
 Sbjct: 300 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 359

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 || ||||| || || ||||| || || ||||| ||
 Sbjct: 360 aatcccaacaaaaattcgcccggtggattcgaagtatcgacaaaaatcaaatcagcagtg 419

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
 ||||||| ||||||| | ||||| ||||| || ||||||| ||||| |||||||
 Sbjct: 420 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 479

```
Query: 1337 tctgttcagat 1347
      ||||| |||
Sbjct: 480 tctgttgagat 490
```

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

```

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttccac 768
          ||||||||||||| || ||||| ||||||| ||||| || || |||||||||
Sbjct: 225 caatctgccatatcaaaagagactcgcatgggtgcttctctctcgcgttggttcttccac 284

```

```
Query: 769 gattgctttgtcaatg 784
      |||||
Sbjct: 285 gattgctttgttaatg 300
```

Score = 63.9 bits (32), Expect = 6e-06
Identities = 50/56 (89%)

Strand = Plus / Plus

```
Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
          |||
Sbjct: 660 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacga 715
```

>gb|EX530374.1| MTGland_A066_2007-06-28/MTGlandA066_C04_014_1 Medicago truncatula A17
glandular trichome Medicago truncatula cDNA, mRNA
sequence
Length = 1023

Score = 167 bits (84), Expect = 6e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

```
Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
          |||
Sbjct: 487 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 546
```

```
Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
          ||
Sbjct: 547 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 606
```

```
Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
          |||
Sbjct: 607 tttaatgctcttggctttccaccaaggatttggtcgcattgtc 650
```

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

```
Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
          |||
Sbjct: 295 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 354
```

```
Query: 1217 aaccccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
          ||
Sbjct: 355 aatcccaacaaaaattcggcccgatggattcgaagtgatcgacaaaatcaaatcagcagtg 414
```

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||| | ||||| ||||| | ||||||| ||||| ||||| |||||
Sbjct: 415 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 474

Query: 1337 tctgttcagat 1347
||||||| |||||
Sbjct: 475 tctgttgagat 485

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttggttcttccac 768
||||||| ||||| ||||||| ||||||| || || ||||||| |||||
Sbjct: 220 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 279

Query: 769 gattgctttgtcaatg 784
||||||| |||||
Sbjct: 280 gattgctttgttaatg 295

Score = 93.7 bits (47), Expect = 7e-15
Identities = 204/257 (79%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||||| ||||||| || || ||||||| || ||||||| ||
Sbjct: 655 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 714

Query: 1852 aacatagaaaccgcatTTTgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
||||||| || | ||||| | || ||||| | || ||||| || ||
Sbjct: 715 aacatagatacttctTTTgctcgcaaggcaatcagggtgccccaaagacatcnggtcc 774

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactac 1971
||||||| || ||||||| ||||||| || ||||| || ||||||| || ||
Sbjct: 775 ggggacaataatttggcacccttgatcttgcaacaccaacatcctttgacaaccattac 834

Query: 1972 ttcaagaacctcgTTcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
||||||| |||| | | ||||| || ||||||| || || ||||| || || |||||

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||||| | ||||| ||||| | ||||||| ||||| ||||| |||||
Sbjct: 367 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 426

Query: 1337 tctgttcagat 1347
||||||| |||||
Sbjct: 427 tctgttgagat 437

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttccac 768
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 172 caatctgccatatcaaaagagactcgcatgggtgcttctctctctgcgtttgttcttccac 231

Query: 769 gattgctttgtcaatg 784
||||||| |||||
Sbjct: 232 gattgctttgttaatg 247

>gb|CF068375.1| EST669096 MTUS Medicago truncatula cDNA clone MTUS-7C2, mRNA sequence
Length = 776

Score = 167 bits (84), Expect = 6e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 461 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctagtaaa 520

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 521 tcagctgcaaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 580

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
|||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 581 tttaatgctcttggcttttccaccaaggatttggctgcattgtc 624

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 269 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 328

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 329 aatcccaacaaaaattcgcccggtggattcgaaagtgatcgacaaaatcaaactcagcagtg 388

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 389 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 448

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 449 tctgttgagat 459

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttcac 768
|||||||
Sbjct: 194 caatctgccatatcaaaagagactcgcatgggtgcttctctctgcgtttgttcttcac 253

Query: 769 gattgctttgtcaatg 784
|||||||
Sbjct: 254 gattgctttgttaatg 269

Score = 71.9 bits (36), Expect = 3e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851

|||||
Sbjct: 629 ggtcacacaattggacaagcaaggtgcactacattttagagcccacatttacaacgactcc 688

Query: 1852 aacataga 1859

|||||
Sbjct: 689 aacataga 696

>gb|AW268020.1| EST306242 DSIR Medicago truncatula cDNA clone pDSIR-8B8, mRNA
sequence
Length = 702

Score = 167 bits (84), Expect = 6e-37
Identities = 144/164 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 447 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 506

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| |||||
Sbjct: 507 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 566

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgctc 1641
|||||
Sbjct: 567 tttaatgctcttggctttccaccaaggatttggtcgcattgtc 610

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 255 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 314

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 315 aatcccaacaaaaattcggcccgatggattcgaagtgatcgacaaaatcaaatcagcagtg 374

Query: 1956 ctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactctgatca 2015

Query: 2016 gcaactgtttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaaccggg 2075

Query: 2076 caccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcac 2135

Query: 2136 tggctcc 2142

Score = 111 bits (56), Expect = 3e-20
Identities = 65/68 (95%)
Strand = Plus / Minus

Query: 1852 aacataga 1859

>gb|FG998035.1| GLPA295TF JCVI-SOY1 Glycine max cDNA 5', mRNA sequence
Length = 740

Query: 1482 gaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaatctg 1541

Query: 1542 ctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagattta 1601
|||||
Sbjct: 543 ctgccaacaatggcatcccaagaccacttcaaacctcaaccaacttatatccagattta 602

```

Query: 1602 gcgctcttggactttccaccaaggacttggtcgc 1635
          | | | | | | | | | | | | | | | | | |
Sbjct: 603  acactctcggactttccaccaaggacttggtcgc 636

```

Score = 159 bits (80), Expect = 1e-34
Identities = 161/188 (85%)
Strand = Plus / Plus

```
Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
          ||||| || ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 290 tgtgatgggtcgattctacttggatgacacatcaagcttcaccggagagaagaacgcggga 349
```

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|| ||| ||| ||| ||| ||| || | || | ||| ||| ||| |||
Sbjct: 350 cctaacaggaattctgcccgaggatttgaagtgatcgaccaaatcaaatcagctgtggag 409

Query: 1280 aaagtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagactct 1339
 |||
 Sbjct: 410 aaagtgtgtccgggtgtggtttcttgcgctgacattcttgccatcgctgccagagactct 469

```
Query: 1340 gttcagat 1347
      ||| |||
Sbjct: 470  gttgagat 477
```

Score = 121 bits (61), Expect = 3e-23
Identities = 85/93 (91%)
Strand = Plus / Plus

```
Query: 692 ctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttctctcc 751
      |||||  ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 195 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcgatgggtgcttctctcc 254
```

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
| | | | | | | | | | | | | | | | | | | | | |
Sbjct: 255 tacgtttgttcttccacgattgctttgttaatg 287

Score = 87.7 bits (44), Expect = 4e-13
Identities = 62/68 (91%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 647 ggtcatacaattggacaagcaaggtgcacaaccttagagcccgaatctacaacgagagc 706

Query: 1852 aacataga 1859
| | | | | | | |
Sbjct: 707 aacataga 714

>gb|EY477044.1| METAY48TF JCVI-MT3 Medicago truncatula cDNA 5', mRNA sequence
Length = 719

Score = 163 bits (82), Expect = 9e-36
Identities = 139/158 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 494 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctagtaaa 553

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 554 tcagctgcaaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 613

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgc 1635
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 614 tttaatgctcttggctttccaccaaggatttggtcgc 651

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 302 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 361

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 362 aatccaacaaaaattcgcccggtggattcgaagtgatcgacaaaatcaaatacagcagtg 421

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 422 gagaaagtatgtccagggtgcagtttctgtgcgtgacatccttaccatcactgctagagac 481

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 482 tctgttgagat 492

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttcac 768
|||||
Sbjct: 227 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttcac 286

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 287 gattgctttgttaatg 302

Score = 63.9 bits (32), Expect = 6e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||||
Sbjct: 662 ggtcacacaattggacaagcaaggtgcactacatttagagcccacatttacaacga 717

>gb|BG448404.1| NF024B09EC1F1074 Elicited cell culture Medicago truncatula cDNA clone

NF024B09EC 5', mRNA sequence
Length = 673

Score = 155 bits (78), Expect = 2e-33
Identities = 138/158 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| ||||| ||| ||||||||| || ||||| ||||| ||
Sbjct: 481 cttggaggcccaacatgggatgtgaaacttggagaagagatgcaagaacagctagtaaa 540

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||| ||||| ||||| ||||||||| || ||||||||| |||||
Sbjct: 541 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 600

Query: 1598 tttagegctcttggactttccaccaaggacttgggtcgc 1635
||| ||||| ||||||||| |||||
Sbjct: 601 gttaatgctcttggctttccaccaaggatttgggtcgc 638

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| | ||||||||| ||||||||| || ||
Sbjct: 289 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 348

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| ||||| || || || ||||||||| || || ||||| || ||||| |||||
Sbjct: 349 aatcccaacaaaaattcggcccggtgattcgaagtgatcgacaaaatcaaatcagcagtg 408

Query: 1277 gagaaagtgtgtccaggagttgttctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 409 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 468

Query: 1337 tctgttcagat 1347
||||| ||||
Sbjct: 469 tctgttgagat 479

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 214 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 273

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 274 gattgctttgttaatg 289

Score = 48.1 bits (24), Expect = 0.36
Identities = 24/24 (100%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaagg 1815
|||||
Sbjct: 649 ggtcacacaattggacaagcaagg 672

>gb|BF644619.1| NF017G06EC1F1051 Elicited cell culture Medicago truncatula cDNA clone
NF017G06EC 5', mRNA sequence
Length = 684

Score = 155 bits (78), Expect = 2e-33
Identities = 142/164 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 479 cttggaggcccaacatgggatgtgaaacttgaagaagagatgcaagaacagctagtaaa 538

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 539 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaang 598

Query: 1598 tttagcgctcttggactttccaccaaggacttgggtcgcttctgtc 1641
||||
Sbjct: 599 tttaatgctcttggcttttccaccaangatttgggtcgcatctgtc 642

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 287 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 346

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 347 aatcccaacaaaattcggcccgaggattcgaagtgatcgacaaaatcaaatcagcagtg 406

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 407 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 466

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 467 tctgttgagat 477

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttccac 768
|||||||
Sbjct: 212 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 271

Query: 769 gattgctttgtcaatg 784
|||||||
Sbjct: 272 gattgctttgttaatg 287

Score = 58.0 bits (29), Expect = 4e-04
Identities = 29/29 (100%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcac 1820
|||||
Sbjct: 647 ggtcacacaattggacaagcaaggtgcac 675

>gb|CA919059.1| EST636777 MTUS Medicago truncatula cDNA clone MTUS-7C2, mRNA sequence
Length = 802

Score = 151 bits (76), Expect = 3e-32
Identities = 143/164 (87%), Gaps = 1/164 (0%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 754 cttggaggcccaacatgggatgtgaaact-ggaagaagagatgcaagaacagctagtaaa 696

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||
Sbjct: 695 tcagctgcaacaatgacatcccagcaccacttcaagcctcaaccaactcatctcaagg 636

Query: 1598 tttagegctcttggactttccaccaaggacttggcgcttgtc 1641
||||
Sbjct: 635 tttaatgctcttggctttccaccaaggatttggcgcttgtc 592

Score = 117 bits (59), Expect = 5e-22
Identities = 284/359 (79%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 587 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 528

Query: 1852 aacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcagggtca 1911
|||||
Sbjct: 527 aacatagatacttcttggctgcacaaggcaatcagggtgccccagacatcggttcc 468

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactac 1971
|||||
Sbjct: 467 ggggacaataatttggcacccttgatcttgaacaccaacatcctttgacaaccattac 408

```
Query: 1972 ttcaagaacctcgttcagaagaagggtctctccactctgatcagcaactgttcaacggt 2031
          |||||
Sbjct: 407  ttcaagaacctagttgacagtaagggactactccactccgaccaacaactctttaatggt 348
```

Query: 2032 ggggtccaccgactccattgtgctggctacagcaccaaccgggcaccttctcctctgat 2091
 || ||||| |||| ||| | || || | || |||||
 Sbjct: 347 ggatccaccgattccatagtgcacgaatatagcttgatccaagctcttttctcctctgat 288

Query: 2092 ttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatggaga 2150
 |||| | ||||||||||||||||||||| |||| | || |||||||
 Sbjct: 287 ttcgtcaccgccatgatcaagatgggagacattagtcacctcaccggttcaaatggaga 229

```
>gb|AW830120.1| sm23a02.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
      Gm-c1028-4707 5' similar to SW:PERX_BRARA P00434
      PEROXIDASE P7 ;, mRNA sequence
      Length = 573
```

Score = 151 bits (76), Expect = 3e-32
Identities = 154/180 (85%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||||| || ||||| | ||||||||| ||||||||| |||||||||
Sbjct: 232 tgtgatgggtcgattctacttgatgacacatcaagcttcaccggagagaagaacgcggga 291

```
Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
          || ||||| |||| ||||| || || || || || || || || || || || ||
Sbjct: 292 cctaacaggaattctgcccgaggatttgaagtgatcgaccaaatcaaatcagctgtggag 351
```

```
Query: 1280 aaagtgtgtccaggagtgttttctgcgcagatatccttgccatcgctgccagagactct 1339
          |||||
Sbjct: 352 aaagtgtgtccgggtgtggtttcttgcgctgacattcttgccatcgctgccagagactct 411
```

Score = 121 bits (61), Expect = 3e-23
Identities = 85/93 (91%)
Strand = Plus / Plus

Query: 692 cgtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctcc 751

Sbjct: 137 ctgtgaaacgcacagtggaatcggccatatcaaaggagaccgcgatgggtgcttctctcc 196

Score = 75.8 bits (38), Expect = 2e-09
Identities = 87/102 (85%), Gaps = 1/102 (0%)
Strand = Plus / Plus

Query: 1542 ctgctaacaatggcatccctgcaccacttcaaaccttaacc 1583
 ||| ||| ||||| || ||||| ||||| |||||
 Sbjct: 485 ctgccaacgatggcattccaagaccacttc-aaccttaacc 525

Score = 149 bits (75), Expect = 1e-31
Identities = 162/191 (84%)
Strand = Plus / Plus

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 || ||||| || || || ||||| || || || ||||| ||
 Sbjct: 350 aatccaacagaaattcgcccggtgattcgaggtatcgacaaaatcaaacagcagtg 409

Query: 1337 tctgttcagat 1347

Score = 111 bits (56), Expect = 3e-20
Identities = 71/76 (93%)
Strand = Plus / Plus

Score = 93.7 bits (47), Expect = 7e-15
Identities = 83/95 (87%)
Strand = Plus / Plus

Length = 602

Score = 147 bits (74), Expect = 5e-31
Identities = 158/186 (84%)
Strand = Plus / Minus

[illegible]

Query: 2017 caactgttcaacggtgggtccaccgactccattgtgcgtggctacagcaccaaccgggc 2076
 |||||
 Sbjct: 453 gaacttttcaatgggtggttcactgactccttagtggttacctacagcaccaaccggcc 394

```
Query: 2137 ggctcc 2142
      |||||
Sbjct: 333  ggctcc 328
```

Score = 147 bits (74), Expect = 5e-31
Identities = 158/186 (84%)
Strand = Plus / Plus

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 ||||| || || ||||| ||||| || || || ||||| || || |||||
 Sbjct: 358 aacccaatatagaactctgctcgtggattgatgtcatcgacaacataaagacagccgta 417

```
Query: 1337 tctgtt 1342
      |||||
Sbjct: 478 tctgtt 483
```

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||| ||||| | | ||||| || ||||
Sbjct: 142 gggagtaccaatgcacaactttctacaagttttactccaaaacttgccccaaactctct 201

Query: 688 tcctctgtgaaatccacagtgcattctgccatatctaaggagacccgcatgggtgcttct 747
|| | ||||||||||| | || ||||||||| ||||| ||| || |||||||
Sbjct: 202 accacagtgaaatccacactacaaactgccatatcaaaggaggcccgaatgagtgccttct 261

Query: 748 ctccttcgcttggttcttccacgattgctttgtcaatg 784
|||||||||||||||||||||||||||||||||
Sbjct: 262 atccttcgcttggttcttccacgattgctttgtcaatg 298

>gb|C0514259.1| s13dSG76D0500042_157180 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 549

Score = 147 bits (74), Expect = 5e-31
Identities = 158/186 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatgggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||||||||||||||||| ||||| ||||||| |||
Sbjct: 297 ggatgtgatggatcaattctcttggatgacacatcaagctttaccggtgagaagaatgca 356

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| || || ||||||||||||||||| || || || ||||||| || |||||||
Sbjct: 357 aacccaaatagaaactctgctcgtggatttgatgtcatcgacaacataaagacagccgta 416

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||| || || || ||||||||| || || || ||||||||| || ||||||| |||||
Sbjct: 417 gagaacgtatgccccggagttgtctcatgtgccgatatccttgctattgctgccgagac 476

Query: 1337 tctgtt 1342
|||||
Sbjct: 477 tctgtt 482

Score = 137 bits (69), Expect = 5e-28
Identities = 135/157 (85%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||| |||||| | | | ||||| || ||||
Sbjct: 141 gggagtaccaatgcacaactttctacaagttttactccaaaacttgtcccaaactctct 200

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttct 747
|| | ||||||||||| | || |||||||||| | |||| | ||| |||||||||||
Sbjct: 201 accacagtgaaatccacactacaaactgccatatcaaaggaggcccgaatgggtgcttct 260

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784
|||||||||||||||||||||||||||||||||
Sbjct: 261 atccttcgcttggttcttccacgattgctttgtcaatg 297

Score = 58.0 bits (29), Expect = 4e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| || | ||||||| ||||||||||||||||||| |||| | || | ||||| |||
Sbjct: 489 cttggaggtccaacctggaatgtaaaacttggaagaagagatgctaaaacggctagtcaa 548

Query: 1538 t 1538
|
Sbjct: 549 t 549

>gb|AW686470.2| NF041G08NR1F1000 Nodulated root Medicago truncatula cDNA clone
NF041G08NR 5', mRNA sequence
Length = 481

Score = 145 bits (73), Expect = 2e-30
Identities = 136/157 (86%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||||||||||||||||||||||||||||||| | | ||||| || ||||
Sbjct: 118 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgtcccaaactctct 177

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttct 747
|| | ||||||||||| |||| | |||||||||| | |||| | ||| ||||||||| |||

Sbjct: 178 accacagtgaaatccacactgcaaactgccatatcaaaggaggcccgaaatgggtgctct 237

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784

||||| |||||||||||||||||||||||||||||||

Sbjct: 238 atctccgcttggttcttccacgattgctttgtcaatg 274

Score = 123 bits (62), Expect = 8e-24

Identities = 155/186 (83%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||||| ||||||| || ||||||||||||||||||| ||||| ||||||| |||

Sbjct: 274 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 333

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggtattgacaacattaaatcagccgtg 1276

|| || || || ||||| ||||||||||| || || || || ||||||| || |||||||

Sbjct: 334 aatccaaatagaaactccgctcgatggatttgatgtcatcgacaacataaagacagccgta 393

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

||||| || || || || ||||||| || || || || ||||||| ||||| ||||||| |||||

Sbjct: 394 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 453

Query: 1337 tctgtt 1342

|||||

Sbjct: 454 tctgtt 459

>gb|BF639633.1| NF015A12IN1F1097 Insect herbivory Medicago truncatula cDNA clone

NF015A12IN 5', mRNA sequence

Length = 516

Score = 145 bits (73), Expect = 2e-30

Identities = 136/157 (86%)

Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687

||||||||||||||||||||||||||||||||| || || ||||| || |||||

Sbjct: 61 gggagtgccaatgcacaactttctacaaacttttactcaaaaacttgtccaaactctct 120

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagaccgcgatgggtgcttct 747

|| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 121 accacagtgaatccacactgcaaactgccatatcaaaggaggcccgaatgggtgcctct 180

Query: 748 ctcttcgcttggttcttccacgattgctttgtcaatg 784

|||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 181 atctccgcttggttcttccacgattgctttgtcaatg 217

Score = 123 bits (62), Expect = 8e-24
Identities = 155/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 217 ggatgtgatggatcaattctcttagatgacacatcaagctttaccggtgagaagaatgca 276

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|| || || || ||||| ||||| ||||| || || || ||||| || || |||||
Sbjct: 277 aatccaaatagaaactccgctcgtggatttgatgtcatcgacaacataaagacagccgta 336

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336

||||| || || || ||||| || || || ||||| ||||| ||||| |||||
Sbjct: 337 gagaacgtatgccccggagttgtatcatgtgctgatatcctagccattgctgccgagac 396

Query: 1337 tctgtt 1342

|||||
Sbjct: 397 tctgtt 402

Score = 81.8 bits (41), Expect = 3e-11
Identities = 86/101 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

||||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 409 cttggaggtccaacctggaatgtaaaacttggaagaacagatgctaaaacggctagtcaa 468

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaacct 1578

|| ||||| || ||||| ||||| ||||| |||||
Sbjct: 469 tccgctgctaacaactgccatcccgccaccaacttcaaacct 509

>gb|CX530413.1| s13dNF99F02MJ016_246858 Methyl Jasmonate-Elicited Root Cell
Suspension Culture Medicago truncatula cDNA, mRNA
sequence
Length = 585

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 341 aatcccaacaaaaattcggcccgatcgaggttattgacaacattaaatcagccgtg 400

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 401 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 460

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 461 tctgttgagat 471

Score = 113 bits (57), Expect = 7e-21
Identities = 99/113 (87%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||||
Sbjct: 473 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctagtaaa 532

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcat 1590
|| |||||
Sbjct: 533 tcagctgcaacaatgacatcccgacccacttcaagcctcaaccaactcat 585

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttccac 768
|||||||
Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 265

Query: 769 gattgctttgtcaatg 784
|||||||
Sbjct: 266 gattgctttgttaatg 281

>gb|CX529528.1| s13dNF97C05MJ034_245107 Methyl Jasmonate-Elicited Root Cell
Suspension Culture Medicago truncatula cDNA, mRNA
sequence
Length = 545

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||||
Sbjct: 290 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 349

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||
Sbjct: 350 aatcccaacaaaaattcgcccggtggattcgaagtgatcgacaaaatcaaatacagcagtg 409

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||||
Sbjct: 410 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcaactgctagagac 469

Query: 1337 tctgttcagat 1347
|||||||
Sbjct: 470 tctgttgagat 480

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttcac 768
||||||| || ||||| ||||||||| || || |||||||||
Sbjct: 215 caatctgccatatcaaaagagactcgcatgggtgcttctctctgcgttgttcttcac 274

Query: 769 gattgctttgtcaatg 784
||||||| ||||
Sbjct: 275 gattgctttgttaatg 290

Score = 63.9 bits (32), Expect = 6e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctag 1533
||||||| ||||| ||||| ||||||||| || ||||| |||||
Sbjct: 482 cttggaggcccaacatgggatgtgaaacttggaagaagagatgcaagaacagctag 537

>gb|BF647501.1| NF068D03EC1F1029 Elicited cell culture Medicago truncatula cDNA clone
NF068D03EC 5', mRNA sequence
Length = 658

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| || ||||||||| || || ||
Sbjct: 288 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 347

Query: 1217 aaccccaacaggaactctgctcgatggattcgaggttattgacaacattaaatcagccgtg 1276
|| ||||| || || || ||||||||| || || ||||| || ||||| |||||
Sbjct: 348 aatcccaacaaaaattcggcccgatggattcgaagtgatcgacaaaatcaaatcagcagtg 407

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 408 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 467

Query: 1337 tctgttcagat 1347
||||| ||||

Score = 141 bits (71), Expect = 3e-29
Identities = 142/165 (86%), Gaps = 1/165 (0%)
Strand = Plus / Plus

Query: 1538 tctgtgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 540 tcagctgcaaacaatgacatcccagcaccacttcaagcctcaaccaactcatctnaagg 599

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

```
Query:  769  gattgctttgtcaatg  784
          |||||
Sbjct:  273  gattgctttgttaatg  288
```

Score = 141 bits (71), Expect = 3e-29
Identities = 161/191 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 281 ggatgtgatggttcaattcttctc gatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 341 aatcccaacaaaaattcggcccgatggattcgaagtgatcgacaaaatcaaactcagcagtg 400

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 401 gagaaagtatgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 460

Query: 1337 tctgttcagat 1347
|||||
Sbjct: 461 tctgttgagat 471

Score = 107 bits (54), Expect = 5e-19
Identities = 108/125 (86%), Gaps = 1/125 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 473 cttggaggcccaacatgggatgtgaaactnggaagaagagatgcaagaacagctagtaaa 532

Query: 1538 tctgctgctaacaatggcat-ccctgcacccacttcaaaccttaaccaactcatctcaag 1596
|| |||||
Sbjct: 533 tcagctgcaacaatgacatccccagcaccacttcaagcctcaaccaactcatctcaag 592

Query: 1597 attta 1601
||||
Sbjct: 593 gttaa 597

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttggttctccac 768
|||||

Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 265

Query: 769 gattgctttgtcaatg 784

|||||||

Sbjct: 266 gattgctttgttaatg 281

>gb|C0515766.1| s13dSG77F0400043_419681 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 572

Score = 139 bits (70), Expect = 1e-28

Identities = 157/186 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||||

Sbjct: 299 ggatgtgatgatcaattctcttggatgacacatcaagctttaccggtgagaagaatgca 358

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||

Sbjct: 359 aacccaaatagaaactctgctcgtggatttggtgtcatcgacaacataaagacagccgta 418

Query: 1277 gagaaagtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336

|||||

Sbjct: 419 gagaacgtatgccccggagttgtctcatgtgccgatatccttgctattgctgccgcagac 478

Query: 1337 tctgtt 1342

|||||

Sbjct: 479 tctgtt 484

Score = 137 bits (69), Expect = 5e-28

Identities = 135/157 (85%)

Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687

|||||

Sbjct: 143 gggagtaccaatgcacaactttctacaagtttttactccaaaacttgccccaaactctct 202

Query: 688 tcctctgtgaaatccacagtgcaatctgccatatctaaggagacccgcatgggtgcttct 747

Sbjct: 203 accacagtgaatccacactacaaactgccatatcaaaggaggcccgaaatgggtgcttct 262

Query: 748 ctccttcgcttgttcttccacgattgctttgtcaatg 784

|||||
Sbjct: 263 atccttcgcttggtcttccacgattgcttgtcaatg 299

Score = 75.8 bits (38), Expect = 2e-09
Identities = 71/82 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Sbjct: 491 cttggaggtccaacctggaatgtaaaacttgaagaagagatgctaaaacggctagtcaa 550

Query: 1538 tctgctgctaacaatggcatcc 1559

Sbjct: 551 ||||| ||||| 572

```
>gb|AW830346.1| sm33e02.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
      Gm-c1028-5715 5' similar to SW:PERX_BRARA P00434
      PEROXIDASE P7 ;, mRNA sequence
      Length = 459
```

Score = 139 bits (70), Expect = 1e-28
Identities = 136/158 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Sbjct: 160 cttggaggcccaacttgggatgtgaaacttgaagaagagactccaggacggcgaagc 219

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

Sbjct: 220 tctgctgccaacaatgacatcccaagaccacttcaaacctcaaccaacttattttcaga 279

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgc 1635

Sbjct: 280 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 317

Score = 111 bits (56), Expect = 3e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 328 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 387

Query: 1852 aacataga 1859
|||||
Sbjct: 388 aacataga 395

Score = 93.7 bits (47), Expect = 7e-15
Identities = 128/155 (82%)
Strand = Plus / Plus

Query: 1193 agcttcaccggagagaagaacgcaaaccacaacaggaactctgctcgtggattcgaggtt 1252
|||||
Sbjct: 4 agcttcaccggagagaaaaacgcaggacctaacaggaactctgcccgtggttttgaagtg 63

Query: 1253 attgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagat 1312
|| || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Sbjct: 64 atcgatcaaattaagtcagctgtggaaaaagtgtgtccgggtgtggtctcttgcgctgac 123

Query: 1313 atccttgccatcgctgccagagactctgttcagat 1347
|||||
Sbjct: 124 atccttgccatcgctgcaagagactccgttgagat 158

>gb|AW703873.1| sk25b09.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-3186 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 397

Score = 139 bits (70), Expect = 1e-28
Identities = 136/158 (86%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537

|||||
Sbjct: 136 cttggaggcccaacttgggatgtgaaacttgggaagaagagactccaggacggcaagccaa 195

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||

Sbjct: 196 tctgctgccaacaatgacatcccaagaccacttcaaacctcaaccaacttatttccaga 255

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgc 1635
|||||

Sbjct: 256 tttaatgctctcggactttccaccaaagacttggtcgc 293

Score = 111 bits (56), Expect = 3e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||

Sbjct: 304 ggtcacacaattggacaagcaaggtgcacaacctttagagcccgatctacaacgagacc 363

Query: 1852 aacataga 1859
|||||

Sbjct: 364 aacataga 371

Score = 73.8 bits (37), Expect = 6e-09
Identities = 103/125 (82%)
Strand = Plus / Plus

Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|||||

Sbjct: 10 aacaggaactctgcccgtggttttgaagtgatcgatcaaattaagtcagctgtggaaaaa 69

Query: 1283 gtgtgtccaggagtgttttctgcgcagatatccttgccatcgctgccagagactctgtt 1342
|||||

Sbjct: 70 gtgtgtccgggtgtggtctcttgcgctgacatccttgccatcgctgcaagagactccgtt 129

Query: 1343 cagat 1347
|||||

Sbjct: 130 gatat 134

>gb|AI495213.1| sb02b01.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1004-7586 5' similar to TR:Q41326 Q41326 PEROXIDASE
;, mRNA sequence
Length = 448

Score = 139 bits (70), Expect = 1e-28
Identities = 169/202 (83%)
Strand = Plus / Plus

Query: 1985 ttcagaagaaggtctctccactctgatcagcaactgttcaacggtgggtccaccgact 2044
|||||
Sbjct: 4 ttcagaagaaggtctcatccattccgaccaagaactcttcaatggtgggtccactgact 63

Query: 2045 ccattgtgcgtggctacagcaccaacccgggcaccttctcctctgatttcgccgccgcca 2104
|||
Sbjct: 64 ccttagtgcgtacctacagcaccaacccggcctcctttttcgccgatttctccgccgcca 123

Query: 2105 tgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaatt 2164
|||||
Sbjct: 124 tgatcaggatgggagacattagtcacctcactggctcccgaggagaaataagggagaact 183

Query: 2165 gtagaaggattaactaatttga 2186
|||
Sbjct: 184 gcaggagggtcaactaatttga 205

>gb|AW830098.1| sm22c01.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-4633 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 434

Score = 137 bits (69), Expect = 5e-28
Identities = 150/177 (84%)
Strand = Plus / Plus

Query: 1160 tgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
|||||
Sbjct: 258 tgtgatgggtcgattctacttgatgacacatcaagcttcaccggagagaagaacgcggga 317

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|||

Sbjct: 318 cctaacaggaattctgcccgatgtgaagtgatcgaccaaataaatcagctgtggag 377

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
||||||| || || ||||| || || ||||| |||||

Sbjct: 378 aaagtgtgtccgggtgtggtttcttgcgctgacattcttgccatcgctgccagagac 434

Score = 121 bits (61), Expect = 3e-23
Identities = 85/93 (91%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgcgaatcgccatatctaaggagaccgcgatgggtgcttctctcc 751
||||||| ||||| ||| ||||| ||||| ||||| ||||| |||||

Sbjct: 163 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcgatgggtgcttctctcc 222

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784
| || ||||| ||||| ||||| |||||

Sbjct: 223 tacgtttgttcttccacgattgctttgttaatg 255

>gb|AW704238.1| sk18d12.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-2544 5' similar to TR:024336 024336
KOREAN-RADISH ISOPEROXIDASE ;, mRNA sequence
Length = 566

Score = 135 bits (68), Expect = 2e-27
Identities = 158/188 (84%)
Strand = Plus / Plus

Query: 1160 tgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaac 1219
||||||| ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 243 tgtgatgggtcaattctacttgatgacacatcaagcttcaccggagagaaaaacgcagga 302

Query: 1220 cccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggag 1279
|| ||||| ||||| ||||| || || || || || || ||||| |||||

Sbjct: 303 cctaacaggaactctgcccggtgtttgaagtgatcgatcaaattaagtcagctgtggaa 362

Query: 1280 aaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactct 1339
||||||| || || || || ||||| || ||||| ||||| |||||

Sbjct: 363 aaagtgtgtccgggtgtggtctcttgcgctgacatccttgccatcgctgcaagagactcc 422

Query: 1340 gttcagat 1347

Sbjct: 423 gttgagat 430

Score = 129 bits (65), Expect = 1e-25

Identities = 86/93 (92%)

Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgc aatctgccatatctaaggagacccgcatgggtgcttctctcc 751

Sbjct: 148 ctgtgaaacgcacagtggaatcgccatatcaaaggagaccgcgatgggtgcttctctcc 207

Query: 752 ttcgcttggttcttcacgattgctttgtcaatg 784

Sbjct: 208 tacgtttgttcttcacgattgctttgtcaatg 240

Score = 95.6 bits (48), Expect = 2e-15

Identities = 105/124 (84%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Sbjct: 432 cttggaggcccaacttgggatgtgaaacttggagaagagactccaggacggcaagccaa 491

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

Subjet: 492 tctgctgccaacaatgacatccaagaccacttcagacctcaaccaacttattttccaga 551

Query: 1598 tttta 1601

Sbjct: 552 ttta 555

>emb|CU524253.1| CU524253 STSSHWB2Sb_KZ0ACB Theobroma cacao cDNA clone KZ0ACB3Y012FM1,

mRNA sequence

Score = 133 bits (67), Expect = 8e-27

Identities = 229/283 (80%)

Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 243 ctgcccgaaggacaacaggctcaggggacaacaacttggcacccttgatatccagactcc 302

Query: 1950 aaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactc 2009
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 303 aacattttttgacaacaactacttcaagaacctcatcaacaggaggggactcctccactc 362

Query: 2010 tgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtgggtacagcaccaa 2069
|| ||| ||||| || ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 363 cgaccaacacgtgttcaatgggggctccacggattccatcgtgcggggttacagcaacaa 422

Query: 2070 cccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtc 2129
|||| || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 423 cccgagctccttcagtctctgactttgtcaccggcatgatcaagatgggagacatcagtc 482

Query: 2130 tctcactggctccaatggagaaatcaggaagaattgtagaagg 2172
||||||| ||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 483 cctcactggatcaaggggagagatcaggaagaactgcagaagg 525

Score = 58.0 bits (29), Expect = 4e-04

Identities = 101/125 (80%)

Strand = Plus / Plus

Query: 1508 ggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccctgcaccc 1567
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 7 ggaaggagagatgctaggactgctagccaggctgctgccaacaacagcattcctcctcca 66

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
||||| ||| || ||| ||||| || ||||| || ||||| ||||| ||||| |||||

Sbjct: 67 acttctaacttgaacagactcatttctagattcaatgctcttggactttccaccaggac 126

Query: 1628 ttggt 1632
|||||

Sbjct: 127 atggt 131

>dbj|AV771209.1| AV771209 Lotus japonicus Pods (20–30 mm in length) Lotus japonicus

cDNA clone MPD018a07_f 3', mRNA sequence
Length = 375

Score = 133 bits (67), Expect = 8e-27
Identities = 125/143 (87%), Gaps = 1/143 (0%)
Strand = Plus / Minus

Query: 2024 tcaacggtgggtccaccgactccattgtgcgtgggtacagcaccaaccgggcaccttct 2083
 |||
 Sbjct: 339 tcaacggtgggtccaccgactccaccgtgcgtgggtacagcaccaaccgagctcatttt 280

Query: 2084 cctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcca 2143
 |||||
 Sbjct: 279 cctctgatttcgccagcgccatgggtcaagatgggagatatcagtcctctcactggatcca 220

```
Query: 2144 atggagaaat-caggaagaattg 2165
      | ||||| |||||||||
Sbjct: 219 acggtgaaatccaggaagaattg 197
```

>gb|C0516246.1| s13dSG69B0900075_445820 Glandular trichomes *Medicago sativa* cDNA,
mRNA sequence
Length = 516

Score = 131 bits (66), Expect = 3e-26
Identities = 156/186 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
 ||||||| ||||| ||||||||| ||| || ||||| |||
 Sbjct: 162 ggatgtgatggatcaattctcttggatgacacatcaagcttactggtgagaagaatgca 221

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
 ||||| || || ||||| ||||| ||||| || || || ||||| || || |||||
 Sbjct: 222 aacccaatatagaactctgctcgtggatttgatgtcatcgacgacataaagacagccgta 281

Query: 1277 gagaagtggtgccaggagttgtttctgcgcagatatccttgccatcgctgccagagac 1336
 ||||| || || || ||||| || || || ||||| ||||| ||||| |||||
 Sbjct: 282 gagaacgtatgccccggagttgtctcatgtgctgatatccttgctattgctgccgagac 341

Query: 1337 tctgtt 1342
 |||

Sbjct: 342 tctgtt 347

Score = 121 bits (61), Expect = 3e-23
Identities = 133/157 (84%)
Strand = Plus / Plus

Query: 628 gggagtgccaatgcacaactttctacaaacttttactaccattcatgtccaaacctcttc 687
||||| ||||||||||||||||||| ||||||| | | | ||||| || ||||
Sbjct: 6 gggagtaccaatgcacaactttctacaagtttttactccaaaacttgcccaaactctct 65

Query: 688 tcctctgtgaaatccacagtgcgaatctgccatatctaaggagaccgcgcatgggtgcttct 747
|| | |||||||||||| | ||| || ||||||| |||||| |||| |||||||||||||
Sbjct: 66 accacagtgaaatccacactacaaactaccatatcaaaggaggcccgaatgggtgcttct 125

Query: 748 ctctctcgcttggttcttccacgattgctttgtcaatg 784
|||| ||||||||||||||||||||||||||||||||
Sbjct: 126 atctctcgcttggttcttccacgattgctttgtcaatg 162

Score = 103 bits (52), Expect = 7e-18
Identities = 130/156 (83%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| || || ||||||| ||||||||||||||||| |||| ||| ||||| |||
Sbjct: 354 cttggagggtccaaactggaatgtaaaacttggagaagagatgctaaaacggctagtcaa 413

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|| ||||||||| || |||||| ||||| ||||| ||||| || ||| ||||| |||||
Sbjct: 414 tccgctgctaacaactgccatcccagcaccaacttccaacctcaatacactcacctcaatg 473

Query: 1598 tttagcgctcttggactttccaccaaggacttggtc 1633
||||||| |||| ||||||| ||||||| |||||||
Sbjct: 474 tttagcgccgttggtctttccagcaaggatttggtc 509

>gb|BF071209.1| st04h08.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1065-376 5' similar to TR:Q9XFL7 Q9XFL7 PEROXIDASE 6
;, mRNA sequence
Length = 319

Score = 131 bits (66), Expect = 3e-26
Identities = 114/130 (87%)
Strand = Plus / Plus

Query: 1218 accccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtgg 1277
||||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 81 accccaataggatctctgctcgtggatacagaggtcattgactacattagatcatccgtgt 140

Query: 1278 agaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatgctgccagagact 1337
|||| | ||||| |||| | |||| | ||||| ||||| ||||| ||||| |||||
Sbjct: 141 agaatgcgtgtccagtatttgtctcctgcgcagatatgcttgccatagctgccagatact 200

Query: 1338 ctgttcagat 1347
|||||
Sbjct: 201 ctgttcagat 210

Score = 58.0 bits (29), Expect = 4e-04
Identities = 66/77 (85%), Gaps = 1/77 (1%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 212 cttggaggccctagtattgtatgttaaagttggaagatgagacgctagatctgcttgcccta 271

Query: 1538 tctgctgctaacaatgg 1554
|||| || |||||
Sbjct: 272 tctggtg-taacaatgg 287

>gb|EX660929.1| JS1BF51JG Salt stressed *Fragaria vesca* (strain Hawaii-4) cDNA library
Fragaria vesca cDNA clone JS1BF51, mRNA sequence
Length = 758

Score = 129 bits (65), Expect = 1e-25
Identities = 214/263 (81%), Gaps = 3/263 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaactccaaccagctttgacaactac 1968
||||| |||| | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 238 tcaggggacaacaacttggtccacttgatcttcaatctccaacagccttcgacaacaac 297

Query: 1969 tacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttc--- 2025
||||| ||| || || | |||| | ||||||||||||||| ||||||| |||||
Sbjct: 298 tactacaataatcttatcaagaacagagggtctcctccactccgatcagcagttgttcttg 357

Query: 2026 aacggtgggtccaccgactccattgtgcgtgggtacagcaccaacccgggcaccttctcc 2085
|| ||||| ||||||| ||||| ||||||||||||||| || || | ||||| ||| |
Sbjct: 358 aatggtgggtccaccgattccatagtgctgggtacagcagcagccagagcacattcaca 417

Query: 2086 tctgatttcgcgcgcccatgatcaagatgggagacattagtcctctcactgggtccaat 2145
||||| || || ||||| ||||||||||||||| |||| | || ||||||| |||||||
Sbjct: 418 tctgactttgctgccgcaatgatcaagatgggaaacatcaacccgctcactggatccaat 477

Query: 2146 ggagaaatcaggaagaattgtag 2168
||||| || ||||||| |||||
Sbjct: 478 ggagagattaggaagaactgtag 500

Score = 61.9 bits (31), Expect = 2e-05
Identities = 52/59 (88%)
Strand = Plus / Plus

Query: 1574 aaccttaaccaactcatctcaagatttagcgctcttggactttccaccaaggacttggt 1632
||||| ||||| ||||||| ||||| | ||||||| ||||||| ||||||| |||||
Sbjct: 46 aacctaaccagctcatctccagattcaacgctcttggcctttccaccaaggacatggt 104

>gb|DN950706.1| 0st2T_331 Oak tissue culture growing 2 days in hypertonic medium
Quercus robur cDNA 5', mRNA sequence
Length = 852

Score = 129 bits (65), Expect = 1e-25
Identities = 98/109 (89%)
Strand = Plus / Plus

Query: 676 ccaaacctcttctcctctgtgaaatccacagtgcaatctgccatatctaaggagacccgc 735
||||| ||||| || ||||||||||| ||||||||||||||| ||||| |||||
Sbjct: 151 ccaaaactctttccactgtgaaatccaccgtgcaatctgccatatcaaaggaagccga 210

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||||| ||||||| ||||||||||| |||||||||||||||

Sbjct: 211 atgggtgcctctctcctgcgcttggttcttccatgattgctttgtcaatg 259

Score = 101 bits (51), Expect = 3e-17
Identities = 120/143 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
|||||
Sbjct: 466 tggaatgttaaacttggaagaagagatgctaggactgcgagccaggctgctgctaataat 525

Query: 1553 ggcattccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612
|||
Sbjct: 526 agcattcctcctccaacttctaacctaaaccaactcatttctagatttaacaatttgga 585

Query: 1613 ctttccaccaaggacttggtcgc 1635
|||
Sbjct: 586 ctttccactaggacatggtcgc 608

Score = 81.8 bits (41), Expect = 3e-11
Identities = 59/65 (90%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
|||
Sbjct: 622 cacacaattgggcaagcaaggtgtacatccttcagagctcgcatatacaacgagaccaac 681

Query: 1855 ataga 1859
|||
Sbjct: 682 ataga 686

>gb|C0511866.1| s13dSG02H0700064_103632 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 483

Score = 129 bits (65), Expect = 1e-25
Identities = 149/177 (84%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
||||| ||||| ||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 307 gatgggtcaatcctactagatgacacatcaaattttaccggagagaagaacgcactcccc 366

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||| ||||| || ||||| ||| ||||| |||||
Sbjct: 367 aataggaactctgttcgaggattcgatgtcattgacaacataaagacagccgtagagaac 426

Query: 1283 gtgtgtccaggagtgttttctgcgcagatatccttgccatcgctgccagagactct 1339
| ||||| ||||| || || || ||||| ||||| ||||| |||||
Sbjct: 427 atatgtccaggagtgtatcatgtgctgatatcctagccattgctgccacagactct 483

Score = 87.7 bits (44), Expect = 4e-13
Identities = 166/206 (80%), Gaps = 3/206 (1%)
Strand = Plus / Plus

Query: 582 ttgttctagattgacaattt---gtttggctctgtttgtcctcatatgggggagtgccaa 638
||||| ||||| ||||| || ||||| ||| ||| ||||| ||||| |||||
Sbjct: 96 ttgttctagattaacaatgttcagtttggttctattttctcataataggagtgccaa 155

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698
||||| ||||| ||||| ||||| || ||||| || ||||| ||| ||| |
Sbjct: 156 tgcacaactctctacaaacttttactcaaaaactgtccaaactcttccattgtcca 215

Query: 699 atccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 758
| | ||||| || ||||| ||||| | || ||||| ||||| || ||| |||
Sbjct: 216 acgccaagtgaatccgctatatcaaaggaggcacgaatgggtgcttctattctccgatt 275

Query: 759 gttcttccacgattgctttgtcaatg 784
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 276 gttcttccacgattgctttgtcaatg 301

>gb|BF650349.1| NF096E02EC1F1017 Elicited cell culture Medicago truncatula cDNA clone
NF096E02EC 5', mRNA sequence
Length = 474

Score = 129 bits (65), Expect = 1e-25
Identities = 154/184 (83%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 291 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 350

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||||
Sbjct: 351 aatccaacaaaaattcgcccggtggattcgaagtgatcnacaaatcaaatacagcagtg 410

Query: 1277 gagaaagtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagac 1336
|||||
Sbjct: 411 gagaaagtgtgtccagggtgcagtttcatgcgctgacatccttaccatcactgctagagac 470

Query: 1337 tctg 1340
|||
Sbjct: 471 tctg 474

Score = 95.6 bits (48), Expect = 2e-15
Identities = 69/76 (90%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctctccttcgcttgttcttcac 768
|||||
Sbjct: 216 caatctgccatatcaaaagagactcgcatgggtgcttctctctcgcgttgttcttcac 275

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 276 gattgctttgttaatg 291

>gb|BE022178.1| sm68f01.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-9074 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 352

Score = 129 bits (65), Expect = 1e-25
Identities = 86/93 (92%)
Strand = Plus / Plus

Query: 692 ctgtgaaatccacagtgaatctgccatatctaaggagaccgcgatgggtgcttctctcc 751
|||||

Sbjct: 45 ctgtgaaacgcacagtgaatcgccatatcaaaggagaccgcatgggtgcttctctcc 104

Query: 752 ttcgcttggttcttccacgattgctttgtcaatg 784

| | | | | | | | | | | | | | | | | | | | | |

Sbjct: 105 tacgtttgttcttccacgattgctttgtcaatg 137

Score = 60.0 bits (30), Expect = 1e-04

Identities = 54/62 (87%)

Strand = Plus / Plus

Query: 1181 gatgacacatcaagcttcaccggagagaagaacgcaaaccaccaaggaactctgctcgt 1240

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 161 gatgacgcatcaagcttcaccggagagaagacgcaggacctaacaggaactctgcccgt 220

Query: 1241 gg 1242

| |

Sbjct: 221 gg 222

>gb|AW666186.1| sk33d05.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1028-3970 5' similar to SW:PERX_BRARA P00434

PEROXIDASE P7 ;, mRNA sequence

Length = 329

Score = 125 bits (63), Expect = 2e-24

Identities = 120/139 (86%)

Strand = Plus / Plus

Query: 1497 atgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 8 atgtgaaacttggaagaagagactccaggacggcaagccaatctgctgccaacaatgaca 67

Query: 1557 tccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgacttt 1616

| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 68 tcccaagaccacttcaaaccttaaccaacttatttccagatttaatgctctcgacttt 127

Query: 1617 ccaccaaggacttggtcgc 1635

| | | | | | | | | | |

Sbjct: 128 ccaccaagacttggtcgc 146

Score = 111 bits (56), Expect = 3e-20
Identities = 65/68 (95%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 157 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 216

Query: 1852 aacataga 1859
|||||
Sbjct: 217 aacataga 224

>gb|AW685593.1| NF029D05NR1F1000 Nodulated root Medicago truncatula cDNA clone
NF029D05NR 5', mRNA sequence
Length = 677

Score = 117 bits (59), Expect = 5e-22
Identities = 284/359 (79%)
Strand = Plus / Minus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 592 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 533

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtca 1911
|||||
Sbjct: 532 aacatagatacttctttgctcgcaaggcaatcagggtgcccccaagacatcggttcc 473

Query: 1912 ggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactac 1971
|||||
Sbjct: 472 ggggacaataatttggcacccttgatcttgcaacaccaacatcctttgacaaccattac 413

Query: 1972 ttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
|||||
Sbjct: 412 ttcaagaacctagttgacagtaagggtactccactccgaccaacaactctttaatggt 353

Query: 2032 ggggccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctgat 2091
|||
Sbjct: 352 ggatccaccgattccatagtcacgaatatagcttgatccaagctcttttctcctctgat 293

Query: 2092 ttcgccgcccgcgatgatcaagatgggagacattagtcctctcactggctccaatggaga 2150
||||| | ||||||||||||||||||||||||||||||| ||||| || || |||||||||
Sbjct: 292 ttcgtcaccgccgatgatcaagatgggagacattagtcctctcaccggttcaaattggaga 234

Score = 81.8 bits (41), Expect = 3e-11
Identities = 72/81 (88%), Gaps = 1/81 (1%)
Strand = Plus / Minus

Query: 1562 gcacccacttcaaaccttaaccaactcatctcaagatttagcgctc-ttggactttccac 1620
||||||| ||| ||||||||||||||||||| |||| |||| |||| |||||||||
Sbjct: 677 gcacccacttcaagcctcaaccaactcatctcaaggtttaatgctctttggtctttccac 618

Query: 1621 caaggacttggtcgcttctgtc 1641
|||||| |||||||| |||||
Sbjct: 617 caaggatttggtcgcatctgtc 597

>dbj|FS263447.1| FS263447 RPSC Glycyrrhiza uralensis cDNA clone S02198-34-013 5', mRNA
sequence
Length = 146

Score = 113 bits (57), Expect = 7e-21
Identities = 72/77 (93%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||||| ||||||| || || || |||||||||
Sbjct: 70 ggatgtgatggttcaattctactggatgacacatcaagctttacaggggagaagaacgca 129

Query: 1217 aaccccaacaggaactc 1233
||||| |||||||||
Sbjct: 130 aacccgaacaggaactc 146

Score = 107 bits (54), Expect = 5e-19
Identities = 66/70 (94%)
Strand = Plus / Plus

Query: 715 gccatatctaaggagacccgcgatgggtgcttctctccttcgcttggttcttccacgattgc 774
||||||| ||||||| ||||||| ||||| ||||||| ||||||| |||||

|||||
Sbjct: 268 gattgctttgttaatg 283

>gb|EV262518.1| MTYEW71TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 742

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
|||||
Sbjct: 287 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccc 346

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|||
Sbjct: 347 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 406

Query: 1283 gtgtgtccaggagtgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|||
Sbjct: 407 gtatgccccggagtgtatcatgtgctgatatccttgccattgctgccacagactc 462

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
|||||
Sbjct: 202 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 261

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 262 ccacgattgctttgtcaatg 281

Score = 71.9 bits (36), Expect = 3e-08
Identities = 132/164 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||| || | ||||||| |||
Sbjct: 473 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 532

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| | | |||| || ||||| || ||||| ||||||| ||||| |||||
Sbjct: 533 tctgatacgaacactgccatcccaagaccaacttccaaccttaatatatactcacctcaatg 592

Query: 1598 tttagcgcctcttggaactttccaccaaggacttggtcgcttgtc 1641
|||| | |||| ||||||||||||||||||| ||||| |||||
Sbjct: 593 tttagaatgttggctctttccaccaaggacttagtcgcatgtc 636

Score = 63.9 bits (32), Expect = 6e-06
Identities = 62/72 (86%)
Strand = Plus / Plus

Query: 1788 aggtgggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||||||||||||||||||||||| |||| | || | | || ||||||| ||
Sbjct: 637 agtgctcacacaattggacaagcaagggtgtacaacatttaggtacgaatctacaatga 696

Query: 1848 gaccaacataga 1859
|||||||
Sbjct: 697 gaccaacataga 708

>gb|EV260463.1| MTYE803TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 773

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatgggtcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| |||||||| | |||||||||||| || ||||||||||||||||| |||
Sbjct: 310 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccg 369

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||||| || ||||||| || ||||||||||| || | || |||||
Sbjct: 370 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaa 429

Query: 1283 gtgtgtccaggagttgtttcctgcgcgagatatccttgccatcgctgccagagactc 1338
|| || || ||||| || || || ||||| ||||| |||||
Sbjct: 430 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 485

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttctt 764
||||| ||||| ||||| | || || ||||| ||||| |||||
Sbjct: 225 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 284

Query: 765 ccacgattgctttgtcaatg 784
|||||
Sbjct: 285 ccacgattgctttgtcaatg 304

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||| | || ||||| ||||| ||||| || || ||||| ||
Sbjct: 496 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 555

Query: 1538 tctgctgctaacaatggcatccctgcaccacattcaaaccttaaccaactcatctcaaga 1597
||| || ||| || ||||| || ||||| ||||| |||||
Sbjct: 556 tctgatggaacactgccatcccaagaccaactccaaccttaataactcacctcaatg 615

Query: 1598 tttagcgctcttggaactttccaccaaggacttggtcgcttgtc 1641
||| | ||| ||||| ||||| |||||
Sbjct: 616 tttaagaatgttggtctttccaccaaggacttagtcgcattgtc 659

Score = 63.9 bits (32), Expect = 6e-06
Identities = 62/72 (86%)
Strand = Plus / Plus

Query: 1788 agtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847

||||| |||||||||||||||||| ||||||| || || | || ||||||| ||
Sbjct: 660 aggtgctcacacaattggacaagcaaagtgcacaacatttaggtacgaatctacaatga 719

Query: 1848 gaccaacataga 1859

|||||||||||
Sbjct: 720 gaccaacataga 731

>gb|EV258111.1| MTYDG59TF JCVI-MT1 Medicago truncatula cDNA 5', mRNA sequence
Length = 677

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
||||| ||||||||| | ||||||||||||| ||| ||||||||||||||||| |||
Sbjct: 305 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccg 364

Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | |||||||| ||| |||||||| | ||||||||||||| || | || |||||
Sbjct: 365 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 424

Query: 1283 gtgtgtccaggagttgtttctgcgcagatatccttgccatcgctgccagagactc 1338
|| || | |||||||| || || || ||||||||||||| ||||||| |||||
Sbjct: 425 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 480

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||||||| |||||||| ||||| | || || ||||||||| |||| |||||||||
Sbjct: 220 agtgcaatccgccatatcaaggaggcacgaattggtgcttctatcctccgcttgttctt 279

Query: 765 ccacgattgctttgtcaatg 784
|||||||||||
Sbjct: 280 ccacgattgctttgtcaatg 299

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||| || | ||||||| |||
Sbjct: 491 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacaactgctagtcaa 550

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || ||||||| ||| ||||| ||||||| ||||| |||||
Sbjct: 551 tctgatgcgaacactgccatcccaagaccgacttccaaccttaataactcacctcaatg 610

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||| | |||| ||||||||||||||||| ||||| |||||
Sbjct: 611 tttaagaatgttggctctttccaccaaggacttagtcgcattgtc 654

>gb|DW017370.1| EST1226331 MTY Medicago truncatula cDNA clone MTYAS77, mRNA sequence
Length = 793

Score = 111 bits (56), Expect = 3e-20
Identities = 203/252 (80%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||||||||||||||||||||||||| || || | || ||||||| |||
Sbjct: 307 agtgctcacacaattggacaagcaaggtgcacaacatttaggtacgaatctacaatga 366

Query: 1848 gaccaacatagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagg 1907
||||||||||| || | ||||| || || ||||| | ||||| | |||||||
Sbjct: 367 gaccaacatagatacttcttttgctagcacaaaggcaatctaattgcccaaagacatcagg 426

Query: 1908 gtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaacta 1967
||||||||||||||| ||||||| ||||||| || ||||| || |||||||
Sbjct: 427 atcaggggacaacaatttggcacctcttgatctccatactccacttctttgacaactg 486

Query: 1968 ctacttcaagaacctcggttcagaagaaggtctcctccactctgatcagcaactgttcaa 2027
||||| || ||||||| ||||| || ||||||| || || || || || ||||| |||||
Sbjct: 487 ctactacaggaacctgtttcaaaacaaggtcttcttcattcagaccaacaacttttcaa 546

Query: 2028 cgggtgggtccac 2039

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Plus

|||||

[illegible]

Score = 54.0 bits (27), Expect = 0.006
Identities = 84/103 (81%)
Strand = Plus / Plus

[illegible][illegible]

Length = 773

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
||||| ||||||| | |||||||||||| || |||||||||||||||| |||
Sbjct: 311 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgactcccg 370

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||||| || ||||||| || |||||||||||| || | || || |||||
Sbjct: 371 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 430

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|| || || ||||||| || || || |||||||||||||| ||||||| |||||||
Sbjct: 431 gtatgccccgagttgtatcatgtgctgatatccttgccattgctgccacagactc 486

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
||||||| ||||||| |||||| | || || ||||||||| |||| |||||||||
Sbjct: 226 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 285

Query: 765 ccacgattgctttgtcaatg 784
||||||| |||||||
Sbjct: 286 ccacgattgctttgtcaatg 305

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| |||||||||||||||| || | ||||||||| |||
Sbjct: 497 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacaactgctagtcaa 556

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||| ||| |||| || |||||| | || ||||| ||||||| ||||| |||||
Sbjct: 557 tctgatgcgaacactgccatcccaagaccaacttccaaccttaataactcacctcaatg 616

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
|||| | |||| |||||||||||||||| ||||| |||||

Sbjct: 617 ttttaagaatgttggtctttccaccaaggacttagtcgcattgtc 660

Score = 71.9 bits (36), Expect = 3e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||||||||||||||||||||||||| || || | || |||||||| ||
Sbjct: 661 aggtgctcacacaattggacaagcaagggtgcacaacatttagggtacgaatctacaatga 720

Query: 1848 gaccaacataga 1859
|||||||||||
Sbjct: 721 gaccaacataga 732

>gb|C0513179.1| s13dSG23G0900068_129522 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 561

Score = 111 bits (56), Expect = 3e-20
Identities = 169/206 (82%), Gaps = 3/206 (1%)
Strand = Plus / Plus

Query: 582 ttgttctagattgacaattt---gtttggctctgtttgtcctcatatgggggagtgccaa 638
||||||||||| ||||| | |||||| || || || |||||||| |||||||||
Sbjct: 102 ttgttctagattaacaatgttcagtttggttctatttctcctcataataggagtgccaa 161

Query: 639 tgcacaactttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaa 698
||||||||| ||||| ||||||||| | | | ||||| || |||| || ||||| |
Sbjct: 162 tgcacaactctctacgaacttttactccaaaacttgccccaaactctcttccactgtcca 221

Query: 699 atccacagtgcgaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgctt 758
| | |||||||| || ||||| |||||| | || |||||||||||| |||| |||||
Sbjct: 222 acgccaagtgcgaatccgctatatcgaaggaggcacgaatgggtgcttctatcctccgctt 281

Query: 759 gttcttccacgattgctttgtcaatg 784
|||||||||||||||||||
Sbjct: 282 gttcttccacgattgctttgtcaatg 307

Score = 111 bits (56), Expect = 3e-20
Identities = 149/180 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 313 gatgggtcaatcctactagatgacacatcaaattttaccggagagaagaacgcactcccg 372

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||||| || ||||| || || ||||| ||||| || ||||| |||||
Sbjct: 373 aataggaactctgttcgaggatttgatgtcattgacaacataaagacagccgtagagaac 432

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactctgtt 1342
| ||||| ||||| || || || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 433 atatgtccaggagttgtatcatgtgtgatatcctagccattgctgccacataactctgtt 492

Score = 54.0 bits (27), Expect = 0.006
Identities = 54/63 (85%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| | ||||| ||||| ||||| ||||| || || ||||| |||||
Sbjct: 499 cttggaggcccaaactggaatgttaaacttggaagaagagatgccacgactgctagtcaa 558

Query: 1538 tct 1540
|||
Sbjct: 559 tct 561

>gb|C0512465.1| s13dSG100C120008_114444 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 614

Score = 111 bits (56), Expect = 3e-20
Identities = 149/180 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
||||| ||||| ||| | ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 77 gatgggtcaatcctactagatgacacatcaaattttactggagagaagaacgcactcccg 136

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| ||||| ||| ||||| || ||||| || ||| ||| |||||
Sbjct: 137 aataggaactctgttcgaggattcgatgtcattgacaacataaagacagtcgtagagaac 196

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactctgtt 1342
| ||||| ||||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 197 atatgtccaggagttgtatcatgtgctgatatcctagccattgctgccacagactctgtt 256

Score = 87.7 bits (44), Expect = 4e-13
Identities = 134/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||| ||||| ||||| ||||| ||| ||||| |||
Sbjct: 263 cttggtggcccaacctggaatgtaaaacttgggagaagagatgccacgactgctagtcaa 322

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaactcatctcaaga 1597
||||||| |||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 323 tctgctgcgaacactgccatcccagcaccaacttccaaccttaatggactcacctcaatg 382

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||| | ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 383 tttagaatgttggctttccaccaaggacttagtcgcattgtc 426

Score = 71.9 bits (36), Expect = 3e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcactctacaacga 1847
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 427 aggtgctcacacaattggacaagcaaggtgcacaacatttagggctcgaatctacaatga 486

Query: 1848 gaccaacataga 1859
|| |||||
Sbjct: 487 gaacaacataga 498

Score = 69.9 bits (35), Expect = 1e-07
Identities = 59/67 (88%)
Strand = Plus / Plus

Query: 718 atatctaaggagacccgcatgggtgcttctctccttcgcttggttcttccacgattgcttt 777
||||| ||||| | || ||||| ||||| || || ||||| ||||| |||||
Sbjct: 5 atatcaaaggaggcacgaatgggtgcttctattctccgattgttcttccacgattgcttt 64

Query: 778 gtcaatg 784
|||||
Sbjct: 65 gtcaatg 71

>gb|BG456493.1| NF082E02PL1F1017 Phosphate starved leaf Medicago truncatula cDNA
clone NF082E02PL 5', mRNA sequence
Length = 675

Score = 111 bits (56), Expect = 3e-20
Identities = 146/176 (82%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacc 1222
||||| ||||| || ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 280 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcaactccc 339

Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
|| | ||||| || ||||| || ||||| || || || || |||||
Sbjct: 340 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 399

Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|| || | ||||| || || || ||||| ||||| ||||| |||||
Sbjct: 400 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 455

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttggttctt 764
||||||| ||||| ||||| || || || ||||| ||||| |||||
Sbjct: 195 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttggttctt 254

Query: 765 ccacgattgctttgtcaatg 784

Sbjct: 255 ccacgattgctttgtcaatg 274

Score = 71.9 bits (36), Expect = 3e-08

Identities = 87/104 (83%)

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Sbjct: 466 cttggtggcccaacctggaatgtaaaacttgaagaagagatgccacaactgctagtcaa 525

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaa 1581

Sbjct: 526 tctgatgcgaacactgccatcccaagaccaacttccaaccttaa 569

Score = 61.9 bits (31), Expect = 2e-05

Identities = 34/35 (97%)

Query: 1788 aggtgggtcacacaattggacaagcaaggtgcacaa 1822

Subjct: 630 aggtgctcacacaattggacaagcaaggtgcacaa 664

>gb|BG456057.1| NF073F02PL1F1025 Phosphate starved leaf *Medicago truncatula* cDNA

Length = 663

Score = 111 bits (56), Expect = 3e-20

Identities = 146/176 (82%)

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222

Sbjct: 291 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgcactcccg 350

Query: 1223 aacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaa 1282

Sbjct: 351 aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 410

Sbjct: 411 gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 466

Query: 705 agtgcaatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttggttctt 764

Query: 765 ccacgattgctttgtcaatg 784
 |||||

Score = 73.8 bits (37), Expect = 6e-09
Identities = 132/164 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Query: 1538 tctgctgctaacaatggcattccctgcacccattcaaaccttaaccaactcatctcaaga 1597

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```
>gb|DW481567.1| GH_RMIRS_031_E08_R Cotton Normalized Library random primed Gossypium
      hirsutum cDNA, mRNA sequence
      Length = 716
```

Score = 109 bits (55), Expect = 1e-19
Identities = 112/131 (85%)
Strand = Plus / Minus

Query: 1502 aaacttggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccct 1561
|||||
Sbjct: 230 aaacttggaagaagagatgcaagaagtgctagccagctcgcggctaataatggcattccct 171

Query: 1562 gcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||||
Sbjct: 170 gcaccaacttcgaacttgaaccaactcattccaggttcaatgctcttggactttccacc 111

Query: 1622 aaggacttggt 1632
|
Sbjct: 110 agggacttggt 100

Score = 75.8 bits (38), Expect = 2e-09
Identities = 50/54 (92%)
Strand = Plus / Minus

Query: 731 cccgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 499 cccgaatgggtgcttctctgcttcgattgttcttccacgactgctttgtcaatg 446

Score = 56.0 bits (28), Expect = 0.001
Identities = 118/148 (79%)
Strand = Plus / Minus

Query: 1195 cttcaccggagagaagaacgcaaaccaccaaggaactctgctcgtggattcgaggttat 1254
|||||
Sbjct: 408 cttcaccggagagaaaaatgctatcccgaatcggaactcagctcgcggattcgatgttgt 349

Query: 1255 tgacaacattaaatcagccgtggagaaagtgtgtccaggagttgttctcgcgcagatat 1314
|||
Sbjct: 348 tgataacatcaagtacgtgttgagaatgtttgccctggtgtagtttcttgtgctgatat 289

Query: 1315 ccttgccatcgctgccagagactctgtt 1342
| |

Sbjet: 288 cttggccattactgctagagactctgtt 261

>gb|DW481566.1| GH_RMIRS_031_E08_056_F Cotton Normalized Library random primed
Gossypium hirsutum cDNA, mRNA sequence
Length = 716

Score = 109 bits (55), Expect = 1e-19
Identities = 112/131 (85%)
Strand = Plus / Plus

Query: 1502 aaacttggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccct 1561
|||||
Sbjet: 486 aaacttggaagaagagatgcaagaagtgctagccagtctgcggtataataatggcattcct 545

Query: 1562 gcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccacc 1621
|||||
Sbjet: 546 gcaccaacttcgaacttgaaccaactcattccaggttcaatgctcttggactttccacc 605

Query: 1622 aaggacttggt 1632
|
Sbjet: 606 aaggacttggt 616

Score = 75.8 bits (38), Expect = 2e-09
Identities = 50/54 (92%)
Strand = Plus / Plus

Query: 731 cccgcatgggtgcttctctcttcgcttgttcttccacgattgcttgtcaatg 784
|||||
Sbjet: 217 cccgaatgggtgcttctctgcttcgattgttcttccacgactgcttgtcaatg 270

Score = 56.0 bits (28), Expect = 0.001
Identities = 118/148 (79%)
Strand = Plus / Plus

Query: 1195 cttcaccggagagaagaacgcaaaccccaacaggaactctgctcgtggattcgaggttat 1254
|||||
Sbjet: 308 cttcaccggagagaaaaatgctatcccgaatcgaactcagctcgcggattcgatgttgt 367

Query: 1255 tgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatat 1314
||| |||| | |||| | |||| | || | || | || |||| | || ||||
Sbjct: 368 tgataacatcaagtcagctgttgagaatgtttgccctggtgtagtttcttgctgatat 427

Query: 1315 ccttgccatcgctgccagagactctgtt 1342
| | |||| | || |||||||||
Sbjct: 428 cttggccattactgctagagactctgtt 455

>gb|DV443257.1| CV01009B1D06.f1 CV01-normalized library Manihot esculenta cDNA clone
CV01009B1D06.f1, mRNA sequence
Length = 753

Score = 107 bits (54), Expect = 5e-19
Identities = 108/126 (85%)
Strand = Plus / Plus

Query: 1497 atgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556
||||||| ||||| |||| | ||||| || |||| |
Sbjct: 422 atgttaaacttgaagaagagatgctagaactgcaagcctttctgctgcaataatggta 481

Query: 1557 tccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttggaacttt 1616
| ||| | || |||| | |||| | ||||| ||||| | ||||| || ||||
Sbjct: 482 ttctctccaacttctaacctcaaccaactcatctcaagattcaacgctctcggccttt 541

Query: 1617 ccacca 1622
| ||||
Sbjct: 542 caacca 547

Score = 65.9 bits (33), Expect = 2e-06
Identities = 45/49 (91%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttgcttcttccacgattgctttgtcaatg 784
||||||| || | ||||| ||||| ||||| ||||| ||||
Sbjct: 163 atgggtgcttccctcgcttcgcttgcttcttccatgattgctttgttaatg 211

Score = 56.0 bits (28), Expect = 0.001
Identities = 70/84 (83%)
Strand = Plus / Plus

Query: 1256 gacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatatac 1315
||||| || ||||| || || ||||| ||||| ||||| || || || |||||
Sbjct: 310 gacaatataaaatccgcagttgagaaagcttgctcctggagtagtctcatgtgctgatatac 369

Query: 1316 cttgccatcgctgccagagactct 1339
||||||| |||||
Sbjct: 370 cttgccatcgctgctagagactct 393

Score = 54.0 bits (27), Expect = 0.006
Identities = 27/27 (100%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
||||||| |||||
Sbjct: 574 cacacaattggacaagcaaggtgcaca 600

>gb|DY633234.1| Medicago--03-I06.g1 Subtracted medicago cDNA library specific for
UV-B irradiation Medicago truncatula cDNA clone
Medicago--03-I06, mRNA sequence
Length = 290

Score = 105 bits (53), Expect = 2e-18
Identities = 122/145 (84%)
Strand = Plus / Plus

Query: 1901 catcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttg 1960
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 104 catcaggatcaggtgacaacaatttgacacctcttgatcttcagactcctagttcttttg 163

Query: 1961 acaactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaac 2020
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 164 acaacaactacttcaagaaccttggttcagaacaagggtcttctccattcagaccaacaac 223

Query: 2021 tgttcaacgggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 224 tttttaacggcggtccaccaactc 248

>gb|DY633115.1| Medicago--03-I06.b1 Subtracted medicago cDNA library specific for

UV-B irradiation Medicago truncatula cDNA clone
Medicago--03-I06, mRNA sequence
Length = 290

Score = 105 bits (53), Expect = 2e-18
Identities = 122/145 (84%)
Strand = Plus / Minus

Query: 1901 catcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttg 1960
||||| ||||| ||||||| ||||||| ||||||| ||||| | |||
Sbjct: 187 catcaggatcaggtgacaacaatttggcacctcttgatcttcagactcctagttctttg 128

Query: 1961 acaactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaac 2020
||||| ||||||| ||||||| ||||||| ||||||| ||| || |||
Sbjct: 127 acaacaactacttcaagaaccttggttcagaacaagggtcttctccattcagaccaacaac 68

Query: 2021 tgttcaacgggtgggtccaccgactc 2045
| || ||||| ||||||| |||||
Sbjct: 67 tttttaacggcggtccaccaactc 43

>gb|BG359643.1| sac26g07.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1051-3398 5' similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE
;, mRNA sequence
Length = 633

Score = 105 bits (53), Expect = 2e-18
Identities = 120/133 (90%), Gaps = 7/133 (5%)
Strand = Plus / Plus

Query: 1508 ggaagaagagacgc-tagaa-ctgctagcc-aatctgct-gctaacaatggca-tccctg 1562
||||| ||||||| ||||| ||||| || ||||||| ||||||| |||||
Sbjct: 334 ggaagaagagacgcctagaaactgctaaccaatctgcttgctaacaatggcaattcctc 393

Query: 1563 caccacttcaaa-ccttaaccaactcatctcaagatttagcgctcttgactttcca-c 1620
||||| ||||||| ||||||| ||||||| || ||||||| ||||||| |||
Sbjct: 394 caccacttcaaaaccttaaccaactcatctcaagattcaccgctcttgactttccacc 453

Query: 1621 caaggacttggtc 1633
||| |||||||
Sbjct: 454 caaagacttggtc 466

Score = 91.7 bits (46), Expect = 3e-14
Identities = 109/124 (87%), Gaps = 12/124 (9%)
Strand = Plus / Plus

Query: 1162 tgatggttcaattcta-ttggatgacacatcaag--cttcaccggagagaagaa--cgca 1216
|||||
Sbjct: 87 tgatggttcaattctatttggatgacacatcaagnncttcaccggagagaagaanncgca 146

Query: 1217 aaccccaacagg---aactctgctcgtggat--tcgaggttattgaca--acattaaatc 1269
|||||
Sbjct: 147 aaccccaacaggggaacctctgctcgtggatacccgaggtcattgacannacattaaatc 206

Query: 1270 agcc 1273
||||
Sbjct: 207 agcc 210

>gb|GT138697.1| METCC85TF JCVI-MT3 Medicago truncatula cDNA 5', mRNA sequence
Length = 726

Score = 103 bits (52), Expect = 7e-18
Identities = 70/76 (92%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccac 768
|||||
Sbjct: 227 caatctgccatatcaaaagagaccgcgatgggtgcttctcttctgcgtttgttcttccac 286

Query: 769 gattgctttgtcaatg 784
|||||
Sbjct: 287 gattgctttgttaatg 302

Score = 91.7 bits (46), Expect = 3e-14
Identities = 208/262 (79%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
|||||
Sbjct: 410 ggtcacacaattggacaagcaaggtgcactacatttagagccacatttacaacgactcc 469

Query: 1852 aacatagaaaccgcatttgcaaggactaggcagcaagctgccctagaacatcagggtca 1911
 ||||| || | |||| | || |||| | | |||| | |||| || ||
 Sbjct: 470 aacatagatacttcctttgctcgcacaaaggcaatcagggtgccccaaagacatcgggttcc 529

Query: 1972 ttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttcaacggt 2031
||||||| | ||| | ||||| | ||||| | || ||||| |
Sbjct: 590 ttcaagaacctagttagacagtaagggaactactccactccgaccaacaactctttaatggt 649

Score = 77.8 bits (39), Expect = 4e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

```
Query: 1631 gtcgccttgtc 1641
      ||||| |||||
Sbjct: 395 gtcgcattgtc 405
```

```
Query: 1157  ggatgtgatggttcaattctattggatgacacatcaagc 1195
          |||||
Sbjct: 302    ggatgtgatggttcaattctctcgatgacacatcaagc 340
```

Gm-c1028-658 5' similar to TR:P93548 P93548 PEROXIDASE
PRECURSOR ;, mRNA sequence
Length = 286

Score = 103 bits (52), Expect = 7e-18
Identities = 103/120 (85%)
Strand = Plus / Plus

Query: 2023 ttcaacggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttc 2082
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 16 ttcaatggtggttccactgactccatagtgcgtacctacagcaccaacccggcctccttt 75

Query: 2083 tcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctcc 2142
| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 76 ttgccgatttctccgccgcatgatccgatgggagacattagtcctcctcaccggctcc 135

>emb|CU485516.1| CU485516 CUSHIONC_KZOACAC Theobroma cacao cDNA clone KZOACAC4Y017FM1,
mRNA sequence
Length = 540

Score = 101 bits (51), Expect = 3e-17
Identities = 225/283 (79%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 516 ctgcccgaaggacaacaggttcaggggacaacaacttggcacccttgatatccagactcc 457

Query: 1950 aaccagctttgacaactactacttcaagaacctcggttcagaagaagggtctcctccactc 2009
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 456 aacattttttgacaacgattacttcaagaacctcatcaacaggagaggactcctccactc 397

Query: 2010 tgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaa 2069
|| ||| ||||| || ||| ||||| || ||| ||||| || ||||| |||||
Sbjct: 396 cgaccaacagctgttcaatgggggtccacggattccttcgtgcggggttacagcaacaa 337

Query: 2070 cccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtc 2129
|||| || ||||| || ||| || || ||| ||||| ||||| ||||| |||||
Sbjct: 336 cccgagctccttcagttttgactttgtcaccggcatgatcaagatgggagacatcagtc 277

Query: 2130 tctcactggctccaatggagaaatcaggaagaattgtagaagg 2172

>gb|BG454205.1| NF108A01LF1F1001 Developing leaf *Medicago truncatula* cDNA clone
NF108A01LF 5', mRNA sequence
Length = 630

Score = 101 bits (51), Expect = 3e-17
Identities = 144/175 (82%)
Strand = Plus / Plus

Query: 1181 gatgacacatcaagcttcaccggagagaagaacgcaaaccccaacaggaactctgctcgt 1240
|||||

Query: 1241 ggattcgcaggttattgacaacattaaatcagccgtggagaaagtgtgtccaggagtgtt 1300
||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query: 1301 tctgtgcgcagatatccttggccatcgctgccagagactctgttcagattgtaagtg 1355
 |||||
 |||||

Score = 95.6 bits (48), Expect = 2e-15
Identities = 90/104 (86%)
Strand = Plus / Plus

Query: 1475 tagccttgaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagc 1534

Query: 1535 caatctgctgctaacaatggcatccctgcaccacttcaaacct 1578
 ||||| ||||||||| || |||||| ||||| ||||| |||||

Score = 77.8 bits (39), Expect = 4e-10
Identities = 57/63 (90%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
|||||
Sbjct: 556 cacacaattggacaagcaaggtgtacaaatcttagggcacgaatctacaacgagaccaac 615

Query: 1855 ata 1857
|||
Sbjct: 616 ata 618

>gb|BE943474.1| EST423053 MGHG Medicago truncatula cDNA clone pMGHG-15J14, mRNA
sequence
Length = 480

Score = 101 bits (51), Expect = 3e-17
Identities = 138/167 (82%)
Strand = Plus / Plus

Query: 1172 attctattggatgacacatcaagcttcaccggagagaagaacgcaaaccaccaaggaac 1231
|||||
Sbjct: 1 attctactagatgacacatcaaactttaccggagagaagaacgcactcccgaataagaac 60

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
|||||
Sbjct: 61 tctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaacgtatgcccc 120

Query: 1292 ggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
|||||
Sbjct: 121 ggagttgtatcatgtgctgatatccttgccattgctgccacagactc 167

Score = 79.8 bits (40), Expect = 1e-10
Identities = 133/164 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 178 cttgggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 237

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaacttaaccaactcatctcaaga 1597
|||||
Sbjct: 238 tctgatgcgaacactgccatcccaagaccaacttccaaccttaataactcacctcaatg 297

Query: 1598 tttagcgctcttggactttccaccaaggacttggtcgccttgtc 1641
|||| | |||| |||||||||||||||| |||| ||||
Sbjct: 298 tttagaatgttggctttccaccaaggacttagtcgcattgtc 341

Score = 71.9 bits (36), Expect = 3e-08
Identities = 63/72 (87%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
|||| |||||||||||||||||||||||| || || | || |||||| ||
Sbjct: 342 aggtgctcacacaattggacaagcaaggtgcacaacatttaggtacgaatctacaatga 401

Query: 1848 gaccaacataga 1859
||||||||||
Sbjct: 402 gaccaacataga 413

>gb|ES840062.1| UFL_061_05 Cotton fiber 0-10 day post anthesis Gossypium hirsutum
cDNA, mRNA sequence
Length = 1368

Score = 99.6 bits (50), Expect = 1e-16
Identities = 221/278 (79%)
Strand = Plus / Plus

Query: 1906 gggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaac 1965
|||||||||||||| || |||| |||| | || |||||| || ||||||
Sbjct: 204 gggtcaggggacaacaatttgtcaccgcttgacatccagactccaacatattttgacaac 263

Query: 1966 tactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactgttc 2025
| |||||| |||||| | |||| || | |||||| |||| | ||||
Sbjct: 264 aagtacttcaacaacctcatcggaagaggggctgctccactcggatcaagagttgttc 323

Query: 2026 aacgggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcc 2085
|| || | |||||||||||||| | | |||| | |||||| || ||||
Sbjct: 324 aatgggggatccaccgactccattgtaagggttacagtaaaaacccgagctccttcagc 383

Query: 2086 tctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctccaat 2145
|||||| | | |||||| |||||||||||||| |||||| || ||

Sbjct: 384 tctgattttgttacagccatgattaagatgggagacattagtcactcactggatcaaag 443

Query: 2146 ggagaaatcaggaagaattgtagaaggattaactaatt 2183

||||| ||||||||| || |||||| |||||

Sbjct: 444 ggagagatcaggaagaactgcagaagggttaattaatt 481

>gb|BI262826.1| NF091E03EC1F1023 Elicited cell culture Medicago truncatula cDNA clone
NF091E03EC 5', mRNA sequence
Length = 409

Score = 99.6 bits (50), Expect = 1e-16

Identities = 108/128 (84%)

Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

||||||| ||||||||| | ||||||||| ||||||||| || ||

Sbjct: 281 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaactgcc 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|| ||||| || || || || ||||| || || || ||||| || ||||| ||

Sbjct: 341 aatcccaacaaaaattcngcccggtgattcnaagtgatcgacaaaatcaatcagcagtg 400

Query: 1277 gagaaagt 1284

|||||||

Sbjct: 401 gagaaagt 408

Score = 83.8 bits (42), Expect = 7e-12

Identities = 67/76 (88%)

Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggttcttcac 768

||||||| || ||||| ||||||||| || || ||||| ||

Sbjct: 206 caatctgccatatcaaaagagactcgcatgggtgcttctcttntgcgtttgttcttnac 265

Query: 769 gattgctttgtcaatg 784

||||||| ||||

Sbjct: 266 gattgctttgttaatg 281

>gb|AW666202.1| sk33f05.y1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-c1028-3994 5' similar to SW:PERX_BRARA P00434
PEROXIDASE P7 ;, mRNA sequence
Length = 329

Score = 99.6 bits (50), Expect = 1e-16
Identities = 112/133 (84%)
Strand = Plus / Plus

Query: 1497 atgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556
||||| ||||||||||||||||| | || || || ||||||||||||||| ||||||| ||
Sbjct: 8 atgtgaaacttggagaagagactccaggacggcaagccaatctgctgccaacaatgaca 67

Query: 1557 tccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgacttt 1616
||||| ||||||||||||||||| ||||||| || || ||||||| ||||| |||||
Sbjct: 68 tcccaagaccacttcaaacctcaaccaacttatttccagatttaatgctctncaacttt 127

Query: 1617 ccaccaaggactt 1629
||||||| |||||
Sbjct: 128 ccaccaaagactt 140

Score = 71.9 bits (36), Expect = 3e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 1792 ggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagacc 1851
||||||||||||| ||||||| ||||||| ||| ||| ||| ||||||||| |||||
Sbjct: 157 ggtcacacaattgaacaagcaaggtgcacaacctttagaacccaaatctacaacaagacc 216

Query: 1852 aacataga 1859
|||||||
Sbjct: 217 aacataga 224

>gb|G0006531.1| LJGBF85TF JCVI-LJ1 Lotus japonicus cDNA 5', mRNA sequence
Length = 292

Score = 97.6 bits (49), Expect = 4e-16
Identities = 139/165 (84%), Gaps = 3/165 (1%)
Strand = Plus / Plus

Query: 586 tctagattgacaatttgtttggtctgtttgtcctcatatgggggagtgccaatgcacaa 645

||||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 77 tctagattaactatctgttttgcctctctttgtcctcatattggggagtgctaatgctcaa 136

Query: 646 ctttctacaaacttttactaccattcatgtccaaacctcttctcctctgtgaaatccaca 705
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 137 ctttctacaaacttctattctagttcttgcctctctctctctctctctctctctcc 195

Query: 706 gtgcaatctgccatatctaaggagaccgcgcatgggtgcttctctc 750
||||| ||| | ||||| ||||| | ||||| ||||| ||||| ||||| |||||

Sbjct: 196 gtgc-atccg-catatcaaaggagctcgcatgggtgcttctctc 238

>gb|C0511819.1| s13dSG02D0500046_103538 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 468

Score = 97.6 bits (49), Expect = 4e-16
Identities = 118/141 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttgaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 296 tggaatgtaaaacttgaagaagagatgctaaaacggctagtcaatccgctgctaacact 355

Query: 1553 ggcattccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 356 gccatcccagcaccaacttccaacctcaatacactcacctcaatgttttagcgccgttggt 415

Query: 1613 ctttccaccaaggacttggtc 1633
||||||| ||||| |||||

Sbjct: 416 ctttccagcaaggatttggtc 436

>gb|BF648119.1| NF027G10EC1F1083 Elicited cell culture Medicago truncatula cDNA clone
NF027G10EC 5', mRNA sequence
Length = 420

Score = 97.6 bits (49), Expect = 4e-16
Identities = 108/128 (84%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 289 ggatgtgatggttcaattcttctcgatgacacatcaagcttcaccggagagaaaaactgcc 348

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 349 natcccaacaaaaattcgcccggtggattcgaagtgatcgacaaaatcaaatacagcagtg 408

Query: 1277 gagaaagt 1284
| | | | | | | |

Sbjct: 409 gagaaagt 416

Score = 89.7 bits (45), Expect = 1e-13
Identities = 68/76 (89%)
Strand = Plus / Plus

Query: 709 caatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttccac 768
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 214 caatctgccatatcaaaagagactcgcatgggtgcttctcttctgcgtttgttcttccac 273

Query: 769 gattgctttgtcaatg 784
| | | | | | | | | | | |

Sbjct: 274 nattgctttgttaatg 289

>gb|AW309606.1| sf21h05.x1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1028-658 3' similar to TR:P93548 P93548 PEROXIDASE
PRECURSOR ;, mRNA sequence
Length = 419

Score = 97.6 bits (49), Expect = 4e-16
Identities = 102/120 (85%)
Strand = Plus / Minus

Query: 2023 ttcaacggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttc 2082
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 410 ttcaatggtggttcactgactccatagtgcgtaacntacagcaccaacccggcctccttt 351

Query: 2083 tcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactggetcc 2142
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Sbjct: 350 ttgccgatttctccgccgcatgatccgatgggagacattagtcctcctcaccggctcc 291

>gb|C0513848.1| s13dSG73C1100082_156358 Glandular trichomes Medicago sativa cDNA,
mRNA sequence
Length = 629

Score = 95.6 bits (48), Expect = 2e-15
Identities = 135/164 (82%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||||||| ||||||||||||||||| || | ||||||| |||
Sbjct: 162 cttggtggcccaacctggaatgtaaaacttggagaagagatgccacgactgctagtcaa 221

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| |||| | |||||| | |||| | |||||| | |||| | |||||
Sbjct: 222 tctgctgcgaacactgccatcccagcaccaactccaaccttaatgtactcacctcaatg 281

Query: 1598 tttagcgctcttggactttccaccaaggacttggcgccttgtc 1641
|||| | |||| ||||||||||||||||| |||| | |||||
Sbjct: 282 tttaagaatgttggctctttccaccaaggacttagtcgcattgtc 325

Score = 89.7 bits (45), Expect = 1e-13
Identities = 132/161 (81%)
Strand = Plus / Plus

Query: 1900 acatcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt 1959
||||||| ||||||||| || ||||||| ||||||| || ||||| || |||
Sbjct: 438 acatcaggatcaggggacaataatttggcacctcttgatctccatactcccacttctttt 497

Query: 1960 gacaactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaa 2019
||||||| |||| | |||||| | |||| | ||||||| || || | || | |||
Sbjct: 498 gacaactgtactacaggaaccttgttcaaaacaagggtcttcttcattcagaccaacaa 557

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggcta 2060
|| ||||||| ||||||||| |||| | || | |||||||
Sbjct: 558 cttttcaacggcggtccaccaactcaatagtgagtggcta 598

Score = 81.8 bits (41), Expect = 3e-11
Identities = 116/141 (82%)
Strand = Plus / Plus

Query: 1202 ggagagaagaacgcaaaccaccaaggaactctgctcgtggattcgaggttattgacaac 1261
|||||||
Sbjct: 15 ggagagaagaacgcactcccgaataggaactctgttcgaggattcgatgtcattgacaac 74

Query: 1262 attaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagatatccttgcc 1321
|||
Sbjct: 75 ataaagacagatgtagagaacatatgtccaggggtgtatcatgtgctgatatcctagcc 134

Query: 1322 atcgtgccagagactctgtt 1342
||
Sbjct: 135 attgctgccacagactctgtt 155

>gb|AW691930.2| NF050G04ST1F1000 Developing stem Medicago truncatula cDNA clone
NF050G04ST 5', mRNA sequence
Length = 372

Score = 95.6 bits (48), Expect = 2e-15
Identities = 72/80 (90%)
Strand = Plus / Plus

Query: 705 agtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttctt 764
|||||||
Sbjct: 215 agtgcaatccgccatatcaaaggaggcacgaattggtgcttctatcctccgcttgttctt 274

Query: 765 ccacgattgctttgtcaatg 784
|||||||
Sbjct: 275 ccacgattgctttgtcaatg 294

Score = 67.9 bits (34), Expect = 4e-07
Identities = 49/54 (90%)
Strand = Plus / Plus

Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
|||||
Sbjct: 300 gatgggtcaattctactagatgacacatcaaactttaccggagagaagaacgca 353

>emb|AJ548283.1| AJ548283 MTAPHEU Medicago truncatula cDNA clone mtaehac110006d12,
mRNA sequence

Length = 322

Score = 87.7 bits (44), Expect = 4e-13

Identities = 62/68 (91%)

Strand = Plus / Minus

```
Query: 2083 tcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcc 2142
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 191  tcctctgatttcgtcaccgcccatgatcaagatgggagacattagtcctctcactggctca 132
```

Query: 2143 aatggaga 2150

|||||

Sbjct: 131 aatggaga 124

>gb|BF520761.1| EST458234 DSIL Medicago truncatula cDNA clone pDSIL-39G8, mRNA
sequence
Length = 535

Score = 87.7 bits (44), Expect = 4e-13

Identities = 143/176 (81%)

Strand = Plus / Plus

```
Query: 1163 gatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgcaaacccc 1222
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18   gatgggtcaattctactatatgacacttcaaactttaccggagagaagaacgcactgccg 77
```

```
Query: 1223 aacaggaactctgctcgttgattcgaggttattgacaacattaaatcagccgtggagaaa 1282
          || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 78   aataagaactctgttcgaggattcgatgtcattgacaacataaagacggcggtagagaac 137
```

```
Query: 1283 gtgtgtccaggagttgtttcctgcgcagatatccttgccatcgctgccagagactc 1338
          || || || ||||| || || || ||||| ||||| ||||| ||||| |||||
Sbjct: 138  gtatgccccggagttgtatcatgtgctgatatccttgccattgctgccacagactc 193
```

Score = 79.8 bits (40), Expect = 1e-10

Identities = 133/164 (81%)

Strand = Plus / Plus

```
Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
          ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Sbjct: 204 cttggtggcccaacctggaatgtaaaacttggaagaagagatgccacaactgctagtcaa 263

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 264 tctgatgcgaacctgccatcccaagaccaacttccaaccttaataatactcacctcaatg 323

Query: 1598 tttagcgctcttggactttccaccaaggacttggctgccttgtc 1641
||||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 324 tttagaatgttggctctttccaccaaggacttagtcgcattgtc 367

Score = 75.8 bits (38), Expect = 2e-09
Identities = 131/162 (80%)
Strand = Plus / Plus

Query: 1788 aggtggtcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacga 1847
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 368 aggtgctcacacaattggacaagcaaggtgcacaacatttaggtacgaatctacaatga 427

Query: 1848 gaccaacatagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcagg 1907
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 428 gaccaacatagatacttcttttgctagcacaaaggcaatctaattgcccaaagacatcatg 487

Query: 1908 gtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 488 atcaggggacaacaatttggcacctcttgatctccatactcc 529

>emb|FN039861.1| FN039861 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs21P0001M16_R.ab1 2007-08-10, mRNA sequence
Length = 485

Score = 85.7 bits (43), Expect = 2e-12
Identities = 118/143 (82%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Sbjct: 400 tcaggttcaggggacaacaacttagcaccacttgatcttcaaactcctacaaactttgac 341

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||||||||| ||| | | ||||||| || | ||||||| |||||
Sbjct: 340 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 281

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 280 tttaatggtggatccactgactc 258

>emb|FN039860.1| FN039860 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs21P0001M16_F.ab1 2007-08-10, mRNA sequence
Length = 485

Score = 85.7 bits (43), Expect = 2e-12
Identities = 118/143 (82%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaactctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| ||||||||||||| | ||||||||||||||||||| || | |||||||
Sbjct: 85 tcaggttcaggggacaacaacttagcaccacttgatcttcaaactcctacaaactttgac 144

Query: 1963 aactactacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactg 2022
||| || ||||||||||| ||| | | ||||||| || | ||||||| |||||
Sbjct: 145 aacagttatttcaagaaccttgtaacagaaagggtctgcttcattctgatcaacaactc 204

Query: 2023 ttcaacggtgggtccaccgactc 2045
|| || ||||| ||||| |||||
Sbjct: 205 tttaatggtggatccactgactc 227

>gb|EG559283.1| CR03032H04 Root CR03 cDNA library Catharanthus roseus cDNA clone
CR03032H04 5', mRNA sequence
Length = 560

Score = 85.7 bits (43), Expect = 2e-12
Identities = 109/131 (83%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||||||||||||||||| || | ||||| ||||| |||||||||||||
Sbjct: 376 tggaatgtgaaacttggaagaagagatgcaacaactgcaagccaagctgctgctaacaat 435

```
Query: 1553  ggcatccctgcaccacttcaaaccttaaccaactcatctcaagatttagcgctcttggga 1612
           ||| ||| | || ||||| ||||| ||| ||| ||||| | ||||| |||
Sbjct: 436    agcattcctcctcctacttctaaccttaatgcctcgtctccagattcaacgctcttgggt 495
```

```
Query: 1613 ctttcaccaa 1623
          |||||
Sbjct: 496 ctttcaaccaa 506
```

Score = 67.9 bits (34), Expect = 4e-07
Identities = 49/54 (90%)
Strand = Plus / Plus

Query: 731 cccgcatgggtgcttctctccttcgcttggtcttccacgattgctttgtcaatg 784
 |||| |||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 116 ccggaatgggagcctccctccttcgcttggtcttccatgattgctttgtcaatg 169

>gb|DW500373.1| GH_TMIRS_045_H05_F Cotton Normalized Library dT primed Gossypium
hirsutum cDNA, mRNA sequence
Length = 545

Score = 85.7 bits (43), Expect = 2e-12
Identities = 234/295 (79%), Gaps = 2/295 (0%)
Strand = Plus / Plus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaactctggcaccacttgatcttcaaactcc 1949
 ||||| ||||| ||| ||||||||| ||||| ||||| | |||||
 Sbjct: 18 ctgccaagaacaacaggctcaggggacaacaacttgccacctcttgatatccaaactcc 77

```
Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaag-ggtctctccact 2008
           |||  |||||  |||||  |||||  |||||  |||  |||  ||  |||||
Sbjct: 78   aacatcttttgacaacaactacttcaagaacct-aatcagtc aaagagggtcttctccact 136
```

Query: 2009 ctgatcagcaactgttcaacggtgggtccaccgactccattgtgcgtggctacagcacca 2068
 ||||| || ||||| ||||| || ||||| || || || || ||
 Sbjct: 137 ctgatcaacagttgttcaatggtggatccacggattccatcggttcggttacggttaaca 196

```
Query: 2069 acccgggcaccttctcctctgatttcgccgccgcatgatcaagatgggagacattagtc 2128
          ||| || |||| | || | || | ||||| ||||| ||||| ||||| |||||
Sbjct: 197  gcccaagctccttcaattcggaacttgtttctgccatgatcaagatgggagacattagtc 256
```

Query: 2129 ctctcactggctccaatggagaaatcaggaagaattgtagaaggattaactaatt 2183
| ||||| || || ||||| || ||||| || |||||
Sbjct: 257 ccctcactggatcacgtggggagatcaggaagaactgcagaagggtgaactaatt 311

>dbj|CI189311.1| CI189311 Oryza sativa (japonica cultivar-group) root of seedlings
Oryza sativa Japonica Group cDNA clone 035-M100R-G10 3',
mRNA sequence
Length = 520

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 15 tcacaccattggacaagcacgatgcacaaacttcagagctcacatatacaacgaaccaa 74

Query: 1854 catagaaaccgcatttgaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| || ||||| || ||||| ||||| |||||
Sbjct: 75 catcgacagtggctttgcatgagcaggcaatcaggctgccctcgtagctcaggctcagg 134

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||| ||||| || ||||| || ||||| || ||||| |||||
Sbjct: 135 tgacaacaatctggcacctttgatcttcagacgccaaccgtgttcgagaacaactacta 194

Query: 1974 caagaacctcggtcagaagaagggtctcctccactctgatcag 2016
||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 195 caagaacctcgctcgtcaagaaggggtcctcctgcactctgatcag 237

>dbj|CI256090.1| CI256090 Oryza sativa (japonica cultivar-group) Panicles mixture of
one, two, three weeks after flowering and supermix Oryza
sativa Japonica Group cDNA clone 044-M077R-H03 3', mRNA
sequence
Length = 650

Score = 85.7 bits (43), Expect = 2e-12
Identities = 178/223 (79%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 5 tcacaccattggacaagcacgatgcacaaacttcagagctcacatatacaacgaaaccaa 64

Query: 1854 catagaaaccgcatttgcaaggactaggcagcaaagctgccctagaacatcagggtcagg 1913
||| || | ||||| | ||||| | ||||| |||||

Sbjct: 65 catcgacagtggctttgcgatgagcaggcaatcaggctgccctcgtagctcaggctcagg 124

Query: 1914 ggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactactt 1973
||||||| ||||| || ||||| || || || || |||||

Sbjct: 125 tgacaacaatctggcacctttggatcttcagacgccaaccgtgttcgagaacaactacta 184

Query: 1974 caagaacctcgttcagaagaagggtctcctccactctgatcag 2016
||||||| ||||| ||||| ||||| |||||

Sbjct: 185 caagaacctcgtcgtcaagaaggggtcctgcactctgatcag 227

>gb|C0498078.1| G.h.fbr-sw07468 G.h.fbr-sw Gossypium hirsutum cDNA, mRNA sequence
Length = 491

Score = 85.7 bits (43), Expect = 2e-12
Identities = 73/83 (87%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||||| ||||| ||||| || || ||||| |||||

Sbjct: 322 gccatgatcaagatgggagacatcagtcctcactggatcaatgggagagatcaggaag 381

Query: 2161 aattgtagaaggattaactaatt 2183
|| ||||| ||||| |||||

Sbjct: 382 aactgtagaagggttaattaatt 404

>gb|EY707107.1| CS00-C3-701-064-H11-CT.F Sweet orange fruit, development stadium (2
of 6) Citrus sinensis cDNA, mRNA sequence
Length = 837

Score = 83.8 bits (42), Expect = 7e-12
Identities = 123/150 (82%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||||| || ||| || ||||| ||||| ||||| ||||| |||||

Sbjct: 152 cttggaggcccaagctggcaagtaaaactcgggaaggagagatgctagaactgcaagccta 211

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 212 tctgctgctaatacgcgcatctctgctcctacctcaaacttgaatcaactcatctctagg 271

Query: 1598 tttagcgctcttggactttccaccaaggac 1627
|||
Sbjct: 272 ttcaacgctctcggactttccaacaaggac 301

Score = 73.8 bits (37), Expect = 6e-09
Identities = 181/229 (79%)
Strand = Plus / Plus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
|||||
Sbjct: 438 cagggcacaacaacttggcaccgcttgatctgcaaactcctacttgtttgacaacaatt 497

Query: 1970 acttcaagaacctcggtcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
|||||
Sbjct: 498 acttcaggaacctggtcaacagaaagggttgcttcaactctgatcaacagctgttcaatg 557

Query: 2030 gtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctctg 2089
|||||
Sbjct: 558 gtgggtccacagattcacaagtcgcacgtacagtaacaacccgagcaccttcagctctg 617

Query: 2090 atttcgccgccgccatgatcaagatgggagacattagtcctctcactgg 2138
|||||
Sbjct: 618 attttgtcgccggcatgatcaagatgggagatatcagcccactcactgg 666

>gb|FD423297.1| RT00024R_T3_024_F11_31MAY2004_085_ab1 CrUniGene root Catharanthus
roseus cDNA similar to peroxidase, mRNA sequence
Length = 672

Score = 83.8 bits (42), Expect = 7e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgccgccatgatcaagatgggagacattagtcctctcactggc 2139
|||||
Sbjct: 341 ttctactctgattttgctgccgccatgatcaagatgggagatatattagtccttctgactggt 400

```
Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
          || ||||| || | ||||| ||||| || ||| |||
Sbjct: 401 tcaaatggagaggttaggaaaaattgtaggagggttaa 438
```

Score = 46.1 bits (23), Expect = 1.4
Identities = 26/27 (96%)
Strand = Plus / Plus

```
Query: 1795 cacacaattggacaaggaaggtgcaca 1821
      |||||
Sbjct: 56  cacacaattggtcaaggaaggtgcaca 82
```

>gb|FD422675.1| RT00017R_T3_017_E10_31MAY2004_072_ab1 CrUniGene root Catharanthus
roseus cDNA similar to peroxidase, mRNA sequence
Length = 714

Score = 83.8 bits (42), Expect = 7e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcggccatgatcaagatgggagacattagtctctctactggc 2139
||||| ||||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 380 ttctactctgattttgtctgccgccaatgatcaagatgggagatataggctctttagctggt 439

```
Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
          || ||||| || | ||||| ||||| || || |||
Sbjct: 440 tcaaattggagaggttagaaaaaattgtaggagggttaa 477
```

Score = 46.1 bits (23), Expect = 1.4
Identities = 26/27 (96%)
Strand = Plus / Plus

```
Query: 1795  cacacaattggacaaggaaggtgcaca 1821
           |||||
Sbjct: 95    cacacaattggtcaaggaaggtgcaca 121
```

```
>gb|FD422951.1| RT00020R T3 020 G01 31MAY2004 003 ab1 CrUniGene root Catharanthus
```

roseus cDNA similar to peroxidase, mRNA sequence
Length = 708

Score = 83.8 bits (42), Expect = 7e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 376 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 435

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||| || ||||| ||||| || |||||
Sbjct: 436 tcaaatggagaggttaggaaaaattgtaggagggttaa 473

Score = 46.1 bits (23), Expect = 1.4
Identities = 26/27 (96%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcaca 1821
||||| ||||| ||||| |||||
Sbjct: 91 cacacaattggtcaagcaaggtgcaca 117

>gb|FD420140.1| 1_SM-JB_R10-G12_T3__G12_3100394_14_ab1 CrUniGene root Catharanthus
roseus cDNA similar to peroxidase, mRNA sequence
Length = 494

Score = 83.8 bits (42), Expect = 7e-12
Identities = 84/98 (85%)
Strand = Plus / Plus

Query: 2080 ttctcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggc 2139
||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 266 ttctactctgattttgctgccgcccatgatcaagatgggagatattagtcctttgactggt 325

Query: 2140 tccaatggagaaatcaggaagaattgtagaaggattaa 2177
|| ||||| || ||||| ||||| || |||||
Sbjct: 326 tcaaatggagaggttaggaaaaattgtaggagggttaa 363

>gb|DW508346.1| GH_TMIRS_123_D07_F Cotton Normalized Library dT primed Gossypium

hirsutum cDNA, mRNA sequence
Length = 325

Score = 81.8 bits (41), Expect = 3e-11
Identities = 74/85 (87%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||||
Sbjct: 160 gccatgatcaagatgggagacattagtcctctcactggatcacgtgggagatcaggaag 219

Query: 2161 aattgtagaaggattaactaatttg 2185
|| || |||||
Sbjct: 220 aactgcagaagggtgaactaatttg 244

>gb|GT143205.1| METCC85TR JCVI-MT3 Medicago truncatula cDNA 3', mRNA sequence
Length = 534

Score = 79.8 bits (40), Expect = 1e-10
Identities = 61/68 (89%)
Strand = Plus / Minus

Query: 2083 tcctctgatttcgccgcccatgatcaagatgggagacattagtcctctcactggctcc 2142
|||||
Sbjct: 326 tcctctggttcgtcaccgcccatgatcaagatgggagacattagtcctctcactggctcc 267

Query: 2143 aatggaga 2150
|||||||
Sbjct: 266 aatggaga 259

>gb|DR280730.1| 157654 CERES-148 Arabidopsis thaliana cDNA clone 124846 5', mRNA
sequence
Length = 461

Score = 79.8 bits (40), Expect = 1e-10
Identities = 49/52 (94%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||||
Sbjct: 229 cgcatgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 280

Query: 1969 tacttcaagaacctcggtcagaagaagggtctctccactctgatcagcaactgttcaac 2028
 ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 75 tacttcaaaaacctaatccagaataaagggtctctccactctgaccagcagctcttcaat 134

```
Query: 2089 gatttcgcccgcgatgatcaagatgggagacattagtctctcactggctccaatgga 2148
          |||||      ||||||||||||||||| | ||||||||| ||| |||
Sbjct: 195  gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254
```

```
>gb|CN908310.1| 030109ABLC001919HT (ABLC) Braeburn cell culture three days after
subculture Malus x domestica cDNA clone ABLC001919, mRNA
sequence
Length = 627
```

```
Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
          ||||| || ||||| ||||| ||||| ||||| || || || ||||| ||
Sbjct: 15    tcaggagataacaatttggctccacttgaccttcaaaccctacttctttcgacaacaac 74
```

Query: 2029 ggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctct 2088
 |||| | ||||| || | ||| | | ||||| || | | ||||| |||
 Sbjct: 135 ggtggttccaccgattcgatagtgagagcctacagcaacagctacaacgccttcagttct 194

Sbjct: 195 gactttgcgagtgccatgatcaagatgggagacatcaaacctctcactggatccagtggg 254

Query: 2149 gaaatcaggaagaattgtag 2168

|| || |||||

Sbjct: 255 gagattaggaagaattgtag 274

>dbj|AU238571.1| AU238571 RAFL17 Arabidopsis thaliana cDNA clone RAFL17-40-J20 5',
mRNA sequence
Length = 647

Score = 79.8 bits (40), Expect = 1e-10

Identities = 49/52 (94%)

Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784

|||||

Sbjct: 226 cgcatgggtgcttctctccttcgcttgttcttccatgattgtttgtcaatg 277

>emb|FN019009.1| FN019009 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0005I02_R.ab1 2007-08-10, mRNA sequence
Length = 553

Score = 77.8 bits (39), Expect = 4e-10

Identities = 69/79 (87%)

Strand = Plus / Minus

Query: 706 gtgcaatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttgttcttc 765

|||||

Sbjct: 427 gtgcaatctgctatcaataaggaaactcgaatgggtgcttctcttcttcgcctattcttc 368

Query: 766 cacgattgctttgtcaatg 784

|||||

Sbjct: 367 cacgattgctttgtcaatg 349

Score = 75.8 bits (38), Expect = 2e-09

Identities = 110/134 (82%)

Strand = Plus / Minus

Query: 1493 tggaatgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaat 1552

||||||| ||| | ||||||||| || ||||| || ||||||| ||||||| ||||| |
Sbjct: 142 tggaatgtaaaattgggaagaagagatgcaagaacagcaagccaagctgctgcaaacagt 83

Query: 1553 ggcacccctgcacccacttcaaaccttaaccaactcatctcaagatttagcgctcttgga 1612

|||| ||| |||| | | |||||||| | |||||||| | | | | ||| ||||
Sbjct: 82 agcattcctccacctacgtctaaccttaatcgactcatctctagtttcagtgtgttggc 23

Query: 1613 ctttcaccaagga 1626

|||||||||||
Sbjct: 22 ctttcaccaagga 9

Score = 54.0 bits (27), Expect = 0.006
Identities = 60/71 (84%)
Strand = Plus / Minus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291

||||| | |||| | | |||||||||||||||| | | ||||||||| ||
Sbjct: 274 tctgctaggagatttgaagtcattgacaacattaaatctgctgtagagaaagtgtgccct 215

Query: 1292 ggagttgtttc 1302

|| |||||||
Sbjct: 214 ggtgttgtttc 204

>emb|FN019008.1| FN019008 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0005I02_F.ab1 2007-08-10, mRNA sequence
Length = 588

Score = 77.8 bits (39), Expect = 4e-10
Identities = 69/79 (87%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttc 765

|||||||||| | ||||| | | ||||||||||||| ||||| | |||||||
Sbjct: 202 gtgcaatctgctatcaataaggaaactcgaatgggtgcttctcttcttcgcctattcttc 261

Query: 766 cacgattgctttgtcaatg 784

|||||||||||
Sbjct: 262 cacgattgctttgtcaatg 280

Score = 54.0 bits (27), Expect = 0.006
Identities = 60/71 (84%)
Strand = Plus / Plus

Query: 1232 tctgctcgtggattcgaggttattgacaacattaaatcagccgtggagaaagtgtgtcca 1291
||||| | |||| | | ||||||||||||||| | | ||||||||| |
Sbjct: 355 tctgctagaggatttgaagtcattgacaacattaaatctgctgtagagaaagtgtgcct 414

Query: 1292 ggagttgtttc 1302
|| |||||
Sbjct: 415 ggtgtgtttc 425

Score = 52.0 bits (26), Expect = 0.023
Identities = 82/101 (81%)
Strand = Plus / Plus

Query: 1493 tggaatgttaaacttggagaagagacgctagaactgctagccaatctgctgctaacaat 1552
||||||| ||| | ||||||||||| | |||| | ||||| ||||| ||||| |
Sbjct: 487 tggaatgtaaaattgggaagaagagatgcaagaacagcaagccaagctgctgcaaacagt 546

Query: 1553 ggcattccctgcaccacttcaaaccttaaccaactcatctc 1593
|||| ||| |||| | | |||||| | |||||||
Sbjct: 547 agcattctccacctacgtctaaccttantcgactcatctc 587

>emb|FN021689.1| FN021689 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0009N11_R.ab1 2007-08-10, mRNA sequence
Length = 556

Score = 77.8 bits (39), Expect = 4e-10
Identities = 117/143 (81%)
Strand = Plus / Plus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962
||||| |||||||||||| | |||||| ||||||||||||| | | |||||
Sbjct: 84 tcaggttcaggggacaacaacttagcaccacctgatcttcaaactcctacaaactttgac 143

Query: 1963 aactactacttcaagaacctcgttcagaagaagggtctcctccactctgatcagcaactg 2022

||||| ||| ||||||||||||| ||| | | ||||||||| ||| ||| ||||||||| |||||
Sbjct: 144 aacagttatttcaagaaccttgtaacagaaaggtctgcttcattctgatcaacaactc 203

Query: 2023 ttcaacggtgggtccaccgactc 2045

|| || ||||| ||||| |||||
Sbjct: 204 tttaatggtggatccactgactc 226

>emb|FN021688.1| FN021688 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0009N11_F.ab1 2007-08-10, mRNA sequence
Length = 526

Score = 77.8 bits (39), Expect = 4e-10
Identities = 117/143 (81%)
Strand = Plus / Minus

Query: 1903 tcagggtcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgac 1962

||||| ||||||||||||||| | ||||||| ||||||||||||||| || | |||||||
Sbjct: 502 tcagggtcaggggacaacaacttagcaccacctgatcttcaaactcctacaaactttgac 443

Query: 1963 aactactacttcaagaacctcggttcagaagaaggtctcctccactctgatcagcaactg 2022

||| || ||||||||||||| ||| | | ||||||||| || | ||||||||| |||||
Sbjct: 442 aacagttatttcaagaaccttgtaacagaaaggtctgcttcattctgatcaacaactc 383

Query: 2023 ttcaacggtgggtccaccgactc 2045

|| || ||||| ||||| |||||
Sbjct: 382 tttaatggtggatccactgactc 360

>emb|FN034858.1| FN034858 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs13P0012A19_R.ab1 2007-08-10, mRNA sequence
Length = 697

Score = 77.8 bits (39), Expect = 4e-10
Identities = 51/55 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784

||||| ||||||||||||||||||| | ||||||||||||||||| |||||||
Sbjct: 214 acccgaatgggtgcttctctccttcgccttttcttccacgattgcttcgtcaatg 268

Score = 71.9 bits (36), Expect = 3e-08
Identities = 54/60 (90%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853
||||| ||||||||||||||||||| ||||| || ||||| |||||||||||||||
Sbjct: 630 tcacactattggacaagcaaggtgcacaaagtttcagggcacgcatttacaacgagaccaa 689

>emb|FN019751.1| FN019751 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs31P0006L16_F.ab1 2007-08-10, mRNA sequence
Length = 604

Score = 77.8 bits (39), Expect = 4e-10
Identities = 51/55 (92%)
Strand = Plus / Plus

Query: 730 acccgcatgggtgcttctctccttcgcttgttcttcacgattgctttgtcaatg 784
||||| ||||||||||||||||||| | ||||||||||||||||||| |||||||
Sbjct: 211 acccgaatgggtgcttctctccttcgccttttcttcacgattgcttcgtcaatg 265

>gb|FC869557.1| C31102G05EF AbioticR1 Citrus reshni cDNA clone C31102G05, mRNA
sequence
Length = 706

Score = 77.8 bits (39), Expect = 4e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgcatgggtgcttctctccttcgcttgttcttc 765
||||||| || || || ||| | ||||||| || |||||||||||||||||||
Sbjct: 200 gtgcaatctgctatttcaaaagagctcgcatgggcgcctctctccttcgcttgttcttc 259

Query: 766 cagcattgctt 776
|||||||
Sbjct: 260 cagcattgctt 270

Score = 56.0 bits (28), Expect = 0.001
Identities = 122/151 (80%), Gaps = 2/151 (1%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggagaagagacgctagaactgctagccaa 1537
||||| | | | | | | | | | | | | | | | | | | |
Sbjct: 470 cttggaggcccaagctggcaagtaaaactcggaaggagagatgctagaactgcaagccta 529

Query: 1538 tctgctgctaacaatggcatccctgcacc-cacttcaaaccttaaccaactcatctcaag 1596
||||| | | | | | | | | | | | | | | | | | | |
Sbjct: 530 tctgctgctaataagcgcatctctgctcctnacctc-aacttgaatcaactcatctctag 588

Query: 1597 atttagcgctcttggactttccaccaaggac 1627
| | | | | | | | | | | | | | | | | | | |
Sbjct: 589 gttcaacgctctcggactttccaacaaggac 619

Score = 46.1 bits (23), Expect = 1.4
Identities = 101/127 (79%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| | | | | | | | | | | | | | | | | | | |
Sbjct: 278 ggatgcgatggatcagttctactggacgacacatcatctttcactggagagaaaaatgcg 337

Query: 1217 aaccccaacaggaactctgctcgatcgaggttattgacaacattaaatcagccgtg 1276
| | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 338 aatgccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 397

Query: 1277 gagaaag 1283
||||| |
Sbjct: 398 gagaaag 404

>gb|FC870159.1| C31109C09EF AbioticR1 Citrus reshni cDNA clone C31109C09, mRNA
sequence
Length = 735

Score = 77.8 bits (39), Expect = 4e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttgttcttc 765
||||| | | | | | | | | | | | | | | | | | | |

Sbjct: 206 gtgcaatctgctattttcaaaagaggctcgcatgggcgcctctctccttcgcttgttcttc 265

Query: 766 cacgattgctt 776

|||||||||

Sbjct: 266 cacgattgctt 276

Score = 50.1 bits (25), Expect = 0.092

Identities = 91/113 (80%)

Strand = Plus / Plus

Query: 1154 cagggatgtgatgggtcaattctattggatgacacatcaagcttcaccggagagaagaac 1213

||||||| |||| | || |||| |||| ||||||| || |||| ||||||| ||

Sbjct: 561 cagggatgcatggatcagttctactggacgacacatcatctttcactggagagaaaaat 620

Query: 1214 gcaaaccceaacaggaactctgctcgtggattcgaggttattgacaacattaa 1266

|| || |||| | |||| || || ||||||||| || |||||||||

Sbjct: 621 gcgaatgccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaa 673

>gb|FC924498.1| C31806G11EF StrCleopN Citrus reshni cDNA clone C31806G11, mRNA
sequence

Length = 699

Score = 77.8 bits (39), Expect = 4e-10

Identities = 63/71 (88%)

Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagacccgcgcatgggtgcttctctccttcgcttgttcttc 765

||||||||| || || || || | ||||||| || |||||||||||||||||

Sbjct: 211 gtgcaatctgctattttcaaaagaggctcgcatgggcgcctctctccttcgcttgttcttc 270

Query: 766 cacgattgctt 776

|||||||||

Sbjct: 271 cacgattgctt 281

Score = 52.0 bits (26), Expect = 0.023

Identities = 104/130 (80%)

Strand = Plus / Plus

Query: 1154 caggggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaac 1213
 ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||
 Sbjct: 565 caggggatgcatggatcagttctactggacgacacatcatctttcactggagagaaaaat 624

```
Query: 1274  gtggagaaag 1283
           || |||||
Sbjct: 685   gttgagaaag 694
```

Score = 77.8 bits (39), Expect = 4e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

```
Query: 766  cacgattgctt  776
        |||||
Sbjct: 263  cacgattgctt  273
```

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 ||||| | ||| | || ||| || | ||| ||||| |||||
 Sbjct: 473 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 532

Identities = 102/127 (80%)

[illegible]

_____ | | | | | | |

sequence

Identities = 63/71 (88%)

|||||

Identities = 115/142 (80%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | | | | | | | | | | | | | | | |

Sbjct: 476 cttggaggcccaagctggcaagtaaaactcggaaggagagatgctagaactgcaagccta 535

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| | | | | | | | | | | | | | | | |

Sbjct: 536 tctgctgctaataagcggcattccagctcctacctcaaacttgaatcaactcatctctagg 595

Query: 1598 tttagcgctcttggaactttcca 1619
| | | | | | | | | |

Sbjct: 596 ttcaacgctctcggactttcca 617

>gb|FC875071.1| C31503H10EF CEVdCidrol Citrus medica cDNA clone C31503H10, mRNA
sequence
Length = 739

Score = 77.8 bits (39), Expect = 4e-10

Identities = 63/71 (88%)

Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagacccgcatgggtgcttctctccttcgcttgttcttc 765
||||||| | | | | | | | | | | | | | | | |

Sbjct: 203 gtgcaatctgctatttcgaaagaggctcgcatgggcgcctctctccttcgcttgttcttc 262

Query: 766 cacgattgctt 776
|||||||

Sbjct: 263 cacgattgctt 273

Score = 67.9 bits (34), Expect = 4e-07

Identities = 121/150 (80%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | | | | | | | | | | | | | | | |

Sbjct: 473 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 532

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

|||||
Sbjct: 533 tctgctgctaatagcggcattcctcctcctacctaacttgaatcaactcacctctagg 592

Query: 1598 tttagcgctcttggactttccaccaaggac 1627

|||
Sbjct: 593 ttcaacgctctcggactttccaacaaggac 622

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

|||||
Sbjct: 281 ggatgcgatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 340

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276

|||||
Sbjct: 341 gtccccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 400

Query: 1277 gagaaag 1283

|||||
Sbjct: 401 gagaaag 407

>gb|EY867689.1| CL06-C4-500-007-B02-CT.F Rangpur lime root, greenhouse plant Citrus
limonia cDNA, mRNA sequence
Length = 827

Score = 77.8 bits (39), Expect = 4e-10
Identities = 63/71 (88%)
Strand = Plus / Plus

Query: 706 gtgcaatctgccatatctaaggagaccgcgatgggtgcttctctccttcgcttggtcttc 765

|||||
Sbjct: 166 gtgcaatctgctatttcgaaagaggctcgcgatgggcgcctctctccttcgcttggtcttc 225

Query: 766 cacgattgctt 776

|||||
Sbjct: 226 cacgattgctt 236

Score = 67.9 bits (34), Expect = 4e-07
Identities = 121/150 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | ||| | | ||||| | | ||||| ||||| |||||
Sbjct: 436 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 495

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||||| | ||||| | | | | | ||||| | | ||||| ||| |
Sbjct: 496 tctgctgctaataagcggcattcctcctcctacctcaaacttgatcaactcacctctagg 555

Query: 1598 tttagcgctcttggactttccaccaaggac 1627
|| | ||||| ||||| |||||
Sbjct: 556 ttcaacgctctcggactttccaacaaggac 585

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| || ||||| | | ||||| ||||| ||||| ||| |
Sbjct: 244 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 303

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| | | ||||| || || ||||| ||| |
Sbjct: 304 gtcccaatcgtaactccgccgcggattcgaggtcatcgacaacattaagtcgcagtt 363

Query: 1277 gagaaag 1283
|||||
Sbjct: 364 gagaaag 370

>gb|FC325468.1| P00462_C7-H9_M13-F_A09_079.ab1 Onu-Ua-pathc Ulmus americana cDNA,
mRNA sequence
Length = 330

Score = 77.8 bits (39), Expect = 4e-10
Identities = 147/183 (80%)
Strand = Plus / Plus

Query: 1999 ctcctccactctgatcagcaactgttcaacgggtgggtccaccgactccatttgtgcgtggc 2058
|||||
Sbjct: 30 ctcctccactccgatcagcagctgttcaacggcggaatccactgattcgctggtgcgcagc 89

```
Query: 2059  tacagcaccaacccgggcaccttctcctctgatttcgccgcccatgatcaagatggga 2118
              ||||| | | | ||| ||| | || ||||| | | | ||||| |||||
Sbjct: 90     tacagcaacagcgaaggcagcttcacttcgatttcgtggcggcgatgatcaggatggga 149
```

Query: 2119 gacattagtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaac 2178
 ||| | | ||||| ||| ||||| ||| ||||| ||| ||||| |||
 Sbjct: 150 gatatcaaacctctcactggaaacaatggagaaattaggaagaattgcaggaggatcaac 209

```
Query: 2179  taa 2181
      |||
Sbjct: 210   taa 212
```

>gb|EG985866.1| GLE049_D04_013 *Cyamopsis tetragonoloba* (L.) Taub seeds at early
developmental stage *Cyamopsis tetragonoloba* cDNA, mRNA
sequence
Length = 686

Score = 77.8 bits (39), Expect = 4e-10
Identities = 54/59 (91%)
Strand = Plus / Plus

Query: 1151 atgcagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaa 1209
 ||||||||||||||||| ||||| | |||||||||||| ||| |||||||||
 Sbjct: 610 atgcagggatgtgatggttcgattctactagatgacacatcaagtttcagcggagagaa 668

Score = 65.9 bits (33), Expect = 2e-06
Identities = 51/57 (89%)
Strand = Plus / Plus

```

Query: 733 cgc atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatgtaatt 789
          ||||| ||||| ||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 229 cgc atgggtgcttctctgttgcgattgttcttccacgattgtttgttaatgtaatt 285

```

>gb|EG356679.1| P00462 C7-H9 M13-F A09 079 Onu-Ua-pathc Ulmus americana cDNA, mRNA

sequence
Length = 479

Score = 77.8 bits (39), Expect = 4e-10
Identities = 147/183 (80%)
Strand = Plus / Plus

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccgactccattgtgcgtggc 2058
||||| ||||| ||||| || ||||| || || ||||| ||
Sbjct: 52 ctctccactccgatcagcagctgttcaacggcgatccactgattcgctggtgcgcagc 111

Query: 2059 tacagcaccaacccgggcaccttctcctctgatttcgccgccgcatgatcaagatggga 2118
||||| || | ||| |||| | || ||||| || || ||||| |||||
Sbjct: 112 tacagcaacagcgaaggcagcttcacttccgatttcgtggcggcgatgatcaggatggga 171

Query: 2119 gacattagtcctctcactggctccaatggagaaatcaggaagaattgtagaaggattaac 2178
|| || | ||||| || ||||| ||||| || ||||| ||
Sbjct: 172 gatatcaaacctctcactggaacaatggagaaattaggaagaattgcaggaggatcaac 231

Query: 2179 taa 2181
|||
Sbjct: 232 taa 234

>emb|FN034857.1| FN034857 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs13P0012A19_F.ab1 2007-08-10, mRNA sequence
Length = 633

Score = 75.8 bits (38), Expect = 2e-09
Identities = 113/138 (81%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||| ||||| ||||| ||||| ||||| || |||||
Sbjct: 319 ctgcccaagaacctcaggttcaggggacaacaacttggcacctcttgatctccagactcc 260

Query: 1950 aaccagctttgacaactactacttcaagaacctcggtcagaagaagggtctcctccactc 2009
|| ||||| || || |||| || || || || ||||| |||||
Sbjct: 259 tacatactttgacaaccattatttcataaatcttgtaacaaaaagggtctgctccactc 200

Query: 2010 tgatcagcaactgttcaa 2027

||||| || |||||
Sbjct: 199 tgatcagcagctcttcaa 182

Score = 71.9 bits (36), Expect = 3e-08
Identities = 54/60 (90%)
Strand = Plus / Minus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||||||||||||| ||||| || ||||| |||||||||||||||
Sbjct: 418 tcacactattggacaagcaaggtgcacaagtttcagggcacgcatttacaacgagaccaa 359

Score = 50.1 bits (25), Expect = 0.092
Identities = 67/81 (82%)
Strand = Plus / Minus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
||||| ||||||| ||| || ||||| || ||||| || |||||||
Sbjct: 105 atgattaagatgggagactttcgtccccttactggatctaattggcgagatcaggaagaac 46

Query: 2164 tgtagaaggattaactaattt 2184
|| || ||||| |||||||
Sbjct: 45 tgcaggaggatcaactaattt 25

>emb|FN045147.1| FN045147 Petunia axillaris subsp. axillaris pool of root and petal
tissue Petunia axillaris subsp. axillaris cDNA clone
drs21P0009020_F.ab1 2007-08-10, mRNA sequence
Length = 489

Score = 75.8 bits (38), Expect = 2e-09
Identities = 113/138 (81%)
Strand = Plus / Minus

Query: 1890 ctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactcc 1949
||||| ||||| ||||| ||||||||||||||| ||||||| ||||||| || |||||
Sbjct: 318 ctgccaagaacctcaggttcaggggacaacaacttggcacctcttgatctccagactcc 259

Query: 1950 aaccagctttgacaactactacttcaagaacctcgttcagaagaagggtctcctccactc 2009
|| ||||||||| || ||||| || || ||| || ||||||| |||||||
Sbjct: 258 tacatactttgacaaccattatttcataaatcttgtaacaaaaagggtctgctccactc 199

Sbjct: 198 tgatcagcagctcttcaa

Identities = 54/60 (90%)

Strand = Plus / Minus

Objet: 417 tcacactattggacaagcaaggtgcacaagtttcagggcacgcatttacaacgagaccac

Identities = 67/81 (82%)

Strand = Plus / Minus

Sbjct: 104 atgattaagatgggcgacttttcgtccccttactggatctaattggcgagatcaggaagaa

Sbjct: 44 tgcaggaggatcaactaattt

tissue *Petunia axillaris* subsp. *axillaris* cDNA clone

drs31P0006L16 R.ab1 2007-08-10, mRNA sequence

Length = 590

Identities = 113/138 (81%)

Strand = Plus / Minus

[illegible]

Subject: 301 ctgcccagaacctcaggttcaggggacaacaacttggcacctcttgatctccagactcc

Sbjct: 441 tcaggagataacaatttggctccacttgaccttcaaaccctacttctttcgacaacaac 500

Query: 1969 tacttcaagaacctcggttcagaagaagggtctctccactctgatcagcaactgttcaac 2028
||||||| ||||| | ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 501 tacttcaaaaacctaatccagaataaagggtctctccactctgaccagcagctcttcaat 560

Query: 2029 ggtgggtccaccga 2042
||||| |||||

Sbjct: 561 ggtggttccaccga 574

Score = 63.9 bits (32), Expect = 6e-06
Identities = 50/56 (89%)
Strand = Plus / Plus

Query: 1798 acaattggacaagcaagggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||| ||||||||| ||||| ||||| |||||||||
Sbjct: 330 acaattgggcaagcaagggtgcacatcattcagaccccgcatatacaacgagaccaa 385

Score = 50.1 bits (25), Expect = 0.092
Identities = 100/125 (80%)
Strand = Plus / Plus

Query: 1508 ggaagaagagacgctagaactgctagccaatctgctgctaacaatggcatccctgcaccc 1567
||||||||||| || ||||| ||||| | ||||||||| ||||| | ||
Sbjct: 186 ggaagaagagacgcaaggactgcaagccaagccgctgctaacaacaacatccccctcca 245

Query: 1568 acttcaaaccttaaccaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
|| ||||| ||||| ||||||| | ||| || || || ||||| ||||||||| |||
Sbjct: 246 acccgaaacctaaaccagctcatctctacattcagtgctgttggtctttccaccagagac 305

Query: 1628 ttggt 1632
|||||
Sbjct: 306 ttggt 310

>gb|EV227910.1| VV_Pe016c06.b1 Vitis vinifera cv. perlette LibA Vitis vinifera cDNA,
mRNA sequence
Length = 1149

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 284 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 343

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 344 tactacaagaacct 357

>gb|EH047301.1| AS2RM4P1E10.ab1 Roots inoculated with Meloidogyne arenaria (RM)
Arachis stenosperma cDNA 5', mRNA sequence
Length = 725

Score = 75.8 bits (38), Expect = 2e-09
Identities = 164/206 (79%)
Strand = Plus / Plus

Query: 1960 gacaactactacttcaagaacctcggttcagaagaagggtctctccactctgatcagcaa 2019
||||| ||||||| ||||||| | ||| || | ||||||| || || |||||
Sbjct: 80 gacaaccactacttcaacaacctcgtcgaccggaaaggccccctccattccgaccagcaa 139

Query: 2020 ctgttcaacgggtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcacc 2079
|| ||||||| || || || ||||||| || ||||||| | ||||| || |
Sbjct: 140 ctettcaacggaggatctactgactccattgttcgcggtacagctcaaaccctagctct 199

Query: 2080 ttctcctctgatttcgccgccgcatgatcaagatgggagacattagtcctctcactggc 2139
|| | | ||||| ||| ||||||| ||||||| || ||| |||||||
Sbjct: 200 ttttcgccgattttgccagtgccatgatcaagatgggagacataaatccctcactgga 259

Query: 2140 tccaatggagaaatcaggaagaattg 2165
||||| ||||| || || |||||||
Sbjct: 260 tccaaggagagattagaaagaattg 285

>gb|EC991497.1| WIN1142.C21_L14 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1142_L14 3', mRNA sequence
Length = 465

Score = 75.8 bits (38), Expect = 2e-09

Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||
Sbjct: 449 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 390

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 389 tactacaagaacct 376

>gb|EC987303.1| WIN1130.C21_E15 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1130_E15 3', mRNA sequence
Length = 851

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||
Sbjct: 694 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 753

Query: 1969 tacttcaagaacct 1982
|||| |||||||
Sbjct: 754 tactacaagaacct 767

>gb|EC985323.1| WIN1124.C21_I01 Muscat Hamburg pre-veraison berry normalized (WIN11)
Vitis vinifera cDNA clone WIN1124_I01 3', mRNA sequence
Length = 906

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968
||||| ||||||| ||||||| || ||||||| || || ||||| |||||||||
Sbjct: 478 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 537

Query: 1969 tacttcaagaacct 1982
|||| |||||||

Sbjct: 538 tactacaagaacct 551

>gb|CV861937.1| gonad_EST09518 Embryonic gonad cDNA Library Gallus gallus cDNA 5',
mRNA sequence
Length = 1288

Score = 75.8 bits (38), Expect = 2e-09
Identities = 59/66 (89%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||| ||||| || ||| ||||| ||||| |||||
Sbjct: 348 ttgacaccattaaagaagccgtggagagagagtgccaggagttgtttcctgtgcagata 407

Query: 1314 tccttg 1319
|||||
Sbjct: 408 tccttg 413

>gb|CX309187.1| C18022D10Rv Drought2 Citrus reshni cDNA clone C18022D10, mRNA
sequence
Length = 712

Score = 75.8 bits (38), Expect = 2e-09
Identities = 122/150 (81%)
Strand = Plus / Minus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||| ||||| || ||| || ||||| ||||| ||||| ||||| |||||
Sbjct: 516 cttggaggcccaagctggcaagtaaaactcgggaaggagagatgctagaactgcaagccta 457

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
||||| ||||| ||||| || ||| ||||| || ||| ||||| |||||
Sbjct: 456 tctgctgctaataagcggcattcctgctcctacacaaacttgaatcaacccatctctagg 397

Query: 1598 tttagcgctcttggaactttccaccaaggac 1627
|| | ||||| ||||| |||||
Sbjct: 396 ttcaacgctctcggactttccaacaaggac 367

Score = 60.0 bits (30), Expect = 1e-04
Identities = 105/130 (80%)

Strand = Plus / Minus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||||| ||||||| ||||||| ||||||| ||||||| || || ||||||| ||

Sbjct: 230 caggcgacaacaacttggcaccgcttgatctgcaaactcctacttgttttgacaacaatt 171

Query: 1970 acttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
||||| ||||||| || || || ||||||| || ||||||| ||

Sbjct: 170 acttcaggaacctgggtcaacagaaagggttgcttcactctgatcaacagctgttcaatg 111

Query: 2030 gtgggtccac 2039
|||||

Sbjct: 110 gtgggtccac 101

Score = 46.1 bits (23), Expect = 1.4

Identities = 101/127 (79%)

Strand = Plus / Minus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| |||||| ||| |||||| |||| ||||||| || |||| ||||||| || ||

Sbjct: 708 ggatgcgatggatcagttctactggacgacacatcatctttcactggagagaaaaatgcg 649

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
|| |||| | |||||| || || ||||||| || ||||||| || || ||

Sbjct: 648 aatgccaatcgtaactccgcccgcggattcgaggtcatcgacaacattaagtcgcgagtt 589

Query: 1277 gagaaag 1283
|||||

Sbjct: 588 gagaaag 582

>gb|CA105303.1| SCJFHR1C05E10.g HR1 Saccharum officinarum cDNA clone SCJFHR1C05E10
5', mRNA sequence
Length = 857

Score = 75.8 bits (38), Expect = 2e-09

Identities = 80/94 (85%)

Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948

|||||
Sbjct: 402 gctgccctagaacctcaggttcaggtgacaacaatttggcgcctctggaccttcaaacc 461

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982

|||||
Sbjct: 462 caaccgtctttgagaacaactactacaagaacct 495

Score = 44.1 bits (22), Expect = 5.7
Identities = 40/46 (86%)
Strand = Plus / Plus

Query: 2137 ggctccaatggagaaatcaggaagaattgtagaaggattaactaat 2182

|||||
Sbjct: 650 ggctccaatgggcagatcaggaagaactgcagaagggttaactaat 695

>gb|CA102350.1| SCBGHR1058E08.g HR1 Saccharum officinarum cDNA clone SCBGHR1058E08
5', mRNA sequence
Length = 664

Score = 75.8 bits (38), Expect = 2e-09
Identities = 80/94 (85%)
Strand = Plus / Plus

Query: 1889 gctgccctagaacatcagggtcaggggacaacaatctggcaccacttgatcttcaaactc 1948

|||||
Sbjct: 402 gctgccctagaacctcaggttcaggtgacaacaatttggcgcctctggaccttcaaacc 461

Query: 1949 caaccagctttgacaactactacttcaagaacct 1982

|||||
Sbjct: 462 caaccgtctttgagaacaactactacaagaacct 495

>gb|CF205258.1| RR890915I0004_IVa_Ra_B09 Vitis sp. RR890915I Vitis hybrid cultivar
cDNA clone RR890915I0004_IVa_Ra_B09 3', mRNA sequence
Length = 746

Score = 75.8 bits (38), Expect = 2e-09
Identities = 65/74 (87%)
Strand = Plus / Minus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactac 1968

||||| ||||||| ||||||| || ||||||| || || ||||| |||||||
Sbjct: 330 tcaggagacaacaacctggcacctctggatcttcagaccctaccacctttgacaactac 271

Query: 1969 tacttcaagaacct 1982

||||| |||||||
Sbjct: 270 tactacaagaacct 257

>dbj|FS421608.1| FS421608 normalized full-length tobacco cDNA library Nicotiana
tabacum cDNA clone TBK02GR0057_4_D10 5', mRNA sequence
Length = 547

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaat 783
||||| ||||| ||||||| ||||||| | ||||||| |||||||
Sbjct: 281 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 340

Query: 784 g 784
|
Sbjct: 341 g 341

>dbj|FS420315.1| FS420315 normalized full-length tobacco cDNA library Nicotiana
tabacum cDNA clone TBK02GR0054_1_H07 5', mRNA sequence
Length = 572

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaat 783
||||| ||||| ||||||| ||||||| | ||||||| |||||||
Sbjct: 205 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 264

Query: 784 g 784
|
Sbjct: 265 g 265

>gb|ES441310.1| TSH_EST01528 Theobroma cacao-Moniliophthora pernicioso incompatible
interaction library Theobroma cacao cDNA clone RT-052B08

5' similar to class III peroxidase [Gossypium hirsutum]
Length = 320, mRNA sequence
Length = 337

Score = 73.8 bits (37), Expect = 6e-09
Identities = 49/53 (92%)
Strand = Plus / Plus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 117 ccgcatgggtgcttctctcgttcgcttgttcttccatgactgtttgtcaatg 169

>emb|CU488677.1| CU488677 DROUGHTLS_KZOACAF Theobroma cacao cDNA clone
KZOACAF8YE10FM1, mRNA sequence
Length = 501

Score = 73.8 bits (37), Expect = 6e-09
Identities = 49/53 (92%)
Strand = Plus / Plus

Query: 732 ccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaatg 784
|||||
Sbjct: 269 ccgcatgggtgcttctctcgttcgcttgttcttccatgactgtttgtcaatg 321

>gb|FG154278.1| AGN_RNC104xj04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 798

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
|||||
Sbjct: 174 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 233

Query: 784 g 784
|
Sbjct: 234 g 234

Score = 73.8 bits (37), Expect = 6e-09

Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcca 1537
||||| |||| | ||| ||| |||| |||| |||| |||| ||||
Sbjct: 426 cttggagggcctaattgggatgtaaaactcggaagaagagatgccagaacagcaagcca 485

```
Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
          ||| | ||| | ||| ||| | || ||| ||| ||| ||| ||| ||| |||
Sbjct: 486 gctgccgcaaacagtagcattcctcctccaacttctaaccttaaccggctcatctctagc 545
```

```
Query: 1598 tttagcgctcttggactttccaccaagga 1626
          || || ||| ||| ||||| ||||| |||
Sbjct: 546  ttcagtgtgttggcctttccaccaagga 574
```

Score = 48.1 bits (24), Expect = 0.36
Identities = 52/60 (86%), Gaps = 1/60 (1%)
Strand = Plus / Plus

```
Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||||| ||||| ||||| ||||| | ||||| || ||||| ||||| |||||
Sbjct: 596 tcacaccattggacaagcaaagtgactagtttcag-gcacgatatacaacgagaccaa 654
```

>gb|FG173223.1| AGN_RNC126xi04f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 829

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

```

Query: 724 aaggagaccgcgatgggtgcttctctctcttcgcttgttcttccacgattgctttgtcaat 783
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 182 aaggaaaccgatatgggtgcttccctccttcgcttattcttccacgattgcttcgtcaat 241

```

Query: 784 g 784
Sbjct: 242 g 242

Score = 73.8 bits (37), Expect = 6e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
 Sbjct: 434 cttggaggccctaattgggatgtaaaactcggaagaagagatgccagaacagcaagccaa 493

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 494 gctgccgcaaacagtagcattctctccaacttctaaccttaaccggctcatctctagc 553

```
Query: 1598 tttagcgctcttggactttccaccaagga 1626  
          |||||  
Sbjct: 554  ttcagtgtgttggcctttccaccaagga 582
```

Score = 63.9 bits (32), Expect = 6e-06
Identities = 53/60 (88%)
Strand = Plus / Plus

```
Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 604 tcacaccattggacaagcaaggtgcactagtttcagggcacgcataatacaacgagaccaa 663
```

>gb|FG156951.1| AGN_RNC026xe21f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 921

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

```
Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 374 aaggaaaccgatatgggtgcttcctccttcgcctattcttccacgattgcttcgtcaat 433
```

Query: 784 g 784
Sbjct: 434 g 434

Score = 58.0 bits (29), Expect = 4e-04
Identities = 120/149 (80%), Gaps = 1/149 (0%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 625 cttggagggcctaattgggatgtaaaactcggaagaagagatgccaga-cagcaagccaa 683

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
 ||| | ||| | ||| ||| | || ||||| ||||| ||| ||| |||
 Sbjct: 684 gctgccgcaaacagtagcattctctccaacttctaaccttaaccggctcatctctagc 743

Query: 1598 ttttagcgctcttggactttccaccaagga 1626
 || || ||| ||| ||||| ||||| |||||
 Sbjct: 744 ttcagtgtgttggcctttccaccaagga 772

>gb|FG157638.1| AGN_RNC025xk16f1.ab1 AGN_RNC Nicotiana tabacum cDNA 5', mRNA
sequence
Length = 907

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

```
Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttgttcttccacgattgctttgtcaat 783
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 201 aaggaaaccgatatgggtgcttccctccttcgcttattcttccacgattgcttcgtcaat 260
```

Query: 784 g 784
Sbjct: 261 g 261

Score = 73.8 bits (37), Expect = 6e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

Sbjct: 453 cttggaggggcctaattgggatgtaaaactcgaagaagagatgccagaacagcaagccaa 512

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597

Sbjct: 513 gctgccgcgaacagtagcattcctcctccaacttctaaccgttaaccggtcatctctagc 572

Query: 1598 tttagcgctcttggactttccaccaagga 1626

Sbjct: 573 || | | | | | | | | | | | |
ttcagtgtgctgttggcctttccaccaagga 601

Score = 56.0 bits (28), Expect = 0.001
Identities = 52/60 (86%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcattctacaacgagaccaa 1853

[illegible]

```
>dbj|DB920515.1| DB920515 full-length enriched cassava cDNA library Manihot esculenta
      cDNA clone CAS01_002_E19 5', mRNA sequence
      Length = 556
```

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 1497 atgttaaacttggaagaagagacgctagaactgctagccaatctgctgctaacaatggca 1556

Sbjct: 480 atgttaaacttggagaagagatgctagaactgcaagcctttctgctgcaaataatggca 539

Query: 1557 t 1557

Sbjct: 540 t 540

Score = 65.9 bits (33), Expect = 2e-06
Identities = 45/49 (91%)
Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||||| ||| ||||||||||||||| ||||||||| |||
Sbjct: 221 atgggtgcttccctcgcttcgcttggttcttccatgattgctttgttaatg 269

Score = 56.0 bits (28), Expect = 0.001
Identities = 70/84 (83%)
Strand = Plus / Plus

Query: 1256 gacaacattaaatcagccgtggagaaagtgtgtccaggagtgtttcctgcgcagatatac 1315
||||| || ||||| || || ||||||| ||||| ||||| || || || || |||||
Sbjct: 368 gacaatataaaatccgcagttgagaaagcttgctcctggagtagtctcatgtgctgatatac 427

Query: 1316 cttgccatcgctgccagagactct 1339
||||||||||||| |||||||||
Sbjct: 428 cttgccatcgctgctagagactct 451

>gb|EB450877.1| KT7C.108P16F.051219T7 KT7 Nicotiana tabacum cDNA clone KT7C.108P16,
mRNA sequence
Length = 785

Score = 73.8 bits (37), Expect = 6e-09
Identities = 55/61 (90%)
Strand = Plus / Plus

Query: 724 aaggagaccgcgatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaat 783
||||| ||||| ||||||||||| ||||||||| | ||||||||||||||||| |||||
Sbjct: 194 aaggaaaccgcatgggtgcttccctccttcgcctattcttccacgattgcttcgtcaat 253

Query: 784 g 784
|
Sbjct: 254 g 254

Score = 73.8 bits (37), Expect = 6e-09
Identities = 121/149 (81%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
||||||| |||| ||| |||| ||||| ||||||||||| || ||||| || |||||

Sbjct: 446 cttggagggcctaattgggatgtaaaactaggaagaagagatgccagaacagcaagccaa 505

Sbjct: 506 gctgctgcaaatagtagcattcctccccgacttcaaaccttaaccgtctcatctctagc 565

Sbjct: 566 ttcactgctgttggcctttccaccaagga 594

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853

>gb|DY356036.1| Z0_Ec0009K09.f Z0_Ec Zingiber officinale cDNA clone Z0_Ec0009K09
5', mRNA sequence
Length = 628

Query: 2078 ccttctcctctgatttcgccgcccatgatcaagatgggagacattagtctctcactg 2137

Query: 2138 gctccaatggagaaatcaggaagaa 2162
 |||||

>gb|CV005110.1| atr02-9ms3-h07 Atr02 Amborella trichopoda cDNA clone atr02-9ms3-h07
5', mRNA sequence
Length = 515

Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||||

Sbjct: 263 gccatgatcaagatgggtgacatcaaacctctcaccggctctaattggagaaattcgcaag 322

Query: 2161 aattgtagaaggattaactaa 2181
|||||||

Sbjct: 323 aattgtagaaagatcaactaa 343

Score = 71.9 bits (36), Expect = 3e-08

Identities = 87/104 (83%)

Strand = Plus / Plus

Query: 1939 cttcaaactccaaccagctttgacaactactacttcaagaacctcggttcagaagaagggt 1998
|||||||

Sbjct: 101 cttcaaaccccaacggcctttgacaacaagtatttcaagaacctgattaacaagaagggc 160

Query: 1999 ctctccactctgatcagcaactgttcaacgggtgggtccaccga 2042
||

Sbjct: 161 ctctccactctgatcagcagctcttcaatggtgggtccgccga 204

>gb|CN782128.1| EST00224 cqseed Chenopodium quinoa cDNA clone S02D05 5' similar to
peroxidase, putative At5g05340, mRNA sequence
Length = 803

Score = 73.8 bits (37), Expect = 6e-09

Identities = 46/49 (93%)

Strand = Plus / Plus

Query: 736 atgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
|||||||

Sbjct: 238 atgggtgcttctctcctacgtttgttcttccacgattgcttcgtcaatg 286

Score = 46.1 bits (23), Expect = 1.4

Identities = 68/83 (81%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| || || ||||| || || || || ||||| ||||| || |||||
Sbjct: 478 cttggaggaccaacttggaacgtaaagctaggtagaagagatgctaggacagctagccaa 537

Query: 1538 tctgctgctaacaatggcatccc 1560
|| |||| ||||| |||||
Sbjct: 538 tccactgcaaacaatgacatccc 560

>gb|FC869818.1| C31105F02EF AbioticR1 Citrus reshni cDNA clone C31105F02, mRNA
sequence
Length = 630

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctt 776
||||||| || |||||
Sbjct: 51 cgcatgggcctctctccttcgcttgttcttccacgattgctt 94

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| || ||||| || || ||||| || |||||
Sbjct: 102 ggatgcatgatgcatcttctactagacgacacatcatctttcaccggagagaaaaatgca 161

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| || ||||| || || ||||| || || ||||| || || ||
Sbjct: 162 gtccccaatcgtaactccgcccgcgattcgaggtcatcgacaacattaagtccgcagtt 221

Query: 1277 gagaaag 1283
|||||||
Sbjct: 222 gagaaag 228

Score = 54.0 bits (27), Expect = 0.006
Identities = 87/107 (81%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcacccacttcaaactta 1580
||||||| ||||||||| | ||| | || | || ||||| |
Sbjct: 337 ctagaactgcaagccaatctgctgctaataagcggttcctcctctacactcaaactga 396

Query: 1581 accaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
| ||||| ||| || | ||||| ||||||| |||||
Sbjct: 397 atcaactcacctctaggttcaacgctctcggactttccaacaaggac 443

>gb|FC874065.1| C31202A05EF BiotPhyR1 Citrus aurantium cDNA clone C31202A05, mRNA
sequence
Length = 689

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttgttcttccacgattgctt 776
||||||| || ||||||||| ||||||||| |||||||
Sbjct: 228 cgcatgggcctctctccttcgcttgttcttccacgattgctt 271

Score = 56.0 bits (28), Expect = 0.001
Identities = 82/100 (82%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcacccacttcaaactta 1580
||||||| ||||||||| ||||| ||| | || ||||| |
Sbjct: 514 ctagaactgcaagccaatctgctgctaataagcgattcctcctcctacactcaaactga 573

Query: 1581 accaactcatctcaagatttagcgctcttggactttccac 1620
| ||||| ||| || | ||||| |||||||
Sbjct: 574 atcaactcacctctaggttcaacgctctcggactttccac 613

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216

Score = 71.9 bits (36), Expect = 3e-08
Identities = 66/76 (86%)
Strand = Plus / Plus

Query: 2085 ctctgatttcgccgcccgcgatgatcaagatgggagacattagtcctctcactgggtccaa 2144
||||||| || ||||| ||||||||||||| || ||||||| || ||||| |||||
Sbjct: 33 ctctgattttgctgccgcatgatcaagatgggtgatattagtcctcttactgggtccaa 92

Query: 2145 tggagaaatcaggaag 2160
||| ||||| |||||
Sbjct: 93 tggcgaaataaggaag 108

>gb|EY845171.1| CA26-C1-002-040-C02-CT.F Sour orange leaf, field plant Citrus
aurantium cDNA, mRNA sequence
Length = 812

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttggttcttccacgattgctt 776
||||||| || |||||||||||||||||||||||||||||||
Sbjct: 267 cgcattgggcctctctccttcgcttggttcttccacgattgctt 310

Score = 60.0 bits (30), Expect = 1e-04
Identities = 120/150 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| || ||| || || ||||| || || ||||| ||||||||| |||||
Sbjct: 510 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 569

Query: 1538 tctgctgctaacaatggcatccctgcaccacacttcaaaccttaaccaactcatctcaaga 1597
||||||| || ||||| ||| || || || ||||| || || ||||| ||| ||
Sbjct: 570 tctgctgctaatagcggcattcctcctcctacctcaaacttgaatcaactcacctctagg 629

Query: 1598 tttagcgctcttggactttccaccaaggac 1627
| | ||||| ||||||||| |||||
Sbjct: 630 tccaacgctctcggactttccaacaaggac 659

Score = 54.0 bits (27), Expect = 0.006

Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||||| ||||| ||||| |||||
Sbjct: 318 ggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 377

Query: 1217 aacccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || |||||
Sbjct: 378 gtcccaatcgtaactccgccgcggattcgaggtcatcgacaacattaagtccgcagtt 437

Query: 1277 gagaaag 1283
|||||||
Sbjct: 438 gagaaag 444

>gb|EY794850.1| CR05-C3-701-027-F03-CT.F Mandarin fruit, development stadium (2 of
3) Citrus reticulata cDNA, mRNA sequence
Length = 850

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttgttcttccacgattgctt 776
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 235 cgcattgggcctctctccttcgcttgttcttccacgattgctt 278

Score = 61.9 bits (31), Expect = 2e-05
Identities = 88/107 (82%)
Strand = Plus / Plus

Query: 1521 ctagaactgctagccaatctgctgctaacaatggcatccctgcacccacttcaaactta 1580
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 521 ctagaactgcaagccaatctgctgctaataagcgcatcctcctcctacactcaaactga 580

Query: 1581 accaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
| ||||| ||| || || || ||||| ||||| ||||| |||||
Sbjct: 581 atcaactcacctctaggttcaacgctctcgactttccaacaaggac 627

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||| ||||| ||||| ||| |||
Sbjct: 286 ggatgcgatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 345

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || ||| |||
Sbjct: 346 gtccccaatcgtaactccgccgcggattcgaggtcatcgacaacattaagtccgcagtt 405

Query: 1277 gagaaag 1283
|||||||
Sbjct: 406 gagaaag 412

>gb|EY776217.1| CR05-C1-103-015-D05-CT.F Mandarin leaf, infected with Xylella
fastidiosa (stage 2 of 2) Citrus reticulata cDNA, mRNA
sequence
Length = 968

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctctcttcgcttgttcttccacgattgctt 776
||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 225 cgcatgggcgcctctctctcttcgcttgttcttccacgattgctt 268

Score = 54.0 bits (27), Expect = 0.006
Identities = 102/127 (80%)
Strand = Plus / Plus

Query: 1157 ggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaacgca 1216
||||| ||||| ||| ||||| | || ||||| ||| ||||| ||||| ||| |||
Sbjct: 276 ggatgcgatggatcagttctactagacgacacatcatctttcaccggagagaaaaatgca 335

Query: 1217 aaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagccgtg 1276
||||| | ||||| || || ||||| ||||| || ||||| ||||| || ||| |||

Sbjct: 336 gtccccaatcgtaactccgcccgcggattcgaggtcatcgacaacattaagtcgcagtt 395

Query: 1277 gagaaag 1283

|||||||

Sbjct: 396 gagaaag 402

>gb|EY725128.1| CS00-C3-703-086-B09-CT.F Sweet orange fruit, development stadium (4
of 6) Citrus sinensis cDNA, mRNA sequence
Length = 840

Score = 71.9 bits (36), Expect = 3e-08

Identities = 42/44 (95%)

Strand = Plus / Plus

Query: 733 cgcattgggtgcttctctccttcgcttggttcttccacgattgctt 776

||||||| || ||||||||||||||||||||||||||||||||

Sbjct: 210 cgcattgggcctctctccttcgcttggttcttccacgattgctt 253

Score = 67.9 bits (34), Expect = 4e-07

Identities = 121/150 (80%)

Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537

||||||||||| | ||| | || ||||| || || ||||| ||||||||||| |||||

Sbjct: 453 cttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagccaa 512

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597

||||||||||| | ||||| ||| | || || ||||| | || ||||||| ||| ||

Sbjct: 513 tctgctgctaatacgcgcatctctcctctacctcaaacttgaatcaactcacctctagg 572

Query: 1598 tttagcgctcttggactttccaccaaggac 1627

|| | ||||| ||||||||| |||||||

Sbjct: 573 ttcaacgctctcggactttccaacaaggac 602

Score = 54.0 bits (27), Expect = 0.006

Identities = 102/127 (80%)

Strand = Plus / Plus

>gb|CX670039.1| UCRCP01_048_E06_T7 Swingle citrumelo nematode-challenged root cDNA
library - UCRCP01 Citrus x paradisi x Poncirus trifoliata

cDNA clone UCRCP01_048_T7_E06, mRNA sequence
Length = 848

Score = 71.9 bits (36), Expect = 3e-08
Identities = 111/136 (81%)
Strand = Plus / Plus

```
Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 286  caggcgacaacaacttggcaccgcttgatctgcaaactcctacttgttttgacaacaatt 345
```

```
Query: 1970 acttcaagaacctcggtcagaagaagggtctctccactctgatcagcaactgttcaacg 2029
          |||||
Sbjct: 346 acttcaagaacctgggtcaacagaaagggtctctccactctgatcaacagctgttcaatg 405
```

```
Query: 2030  gtgggtccaccgactc 2045
             |||||
Sbjct: 406    gtgggtccactgactc 421
```

Score = 56.0 bits (28), Expect = 0.001
Identities = 88/108 (81%)
Strand = Plus / Plus

```
Query: 1520 gctagaactgctagccaatctgctgctaacaatggcatccctgcaccacttcaaacctt 1579
          |||||
Sbjct: 42    gctagaactgcaagcctatctgctgctaataagcggcattcctgctcctacctcaaacttg 101
```

```
Query: 1580 aaccaactcatctcaagatttagcgctcttggactttccaccaaggac 1627
           || || ||| ||| || | |||| ||||| ||||| |||||
Sbjct: 102  aatcagctcacctctaggttcaacgctctcggactttccaacaaggac 149
```

```
>gb|CX050341.1| UCRCS09_31H06_b Ruby Orange Developing Seed cDNA Library UCRCS09
Citrus sinensis cDNA clone UCRCS09-31H06-P12-1-4.b, mRNA
sequence
Length = 888
```

Score = 71.9 bits (36), Expect = 3e-08
Identities = 42/44 (95%)
Strand = Plus / Minus

Query: 733 cgcatgggtgcttctctccttcgcttggttcttccacgattgctt 776
||||||| || ||||||||||||||||||||||||||||
Sbjct: 512 cgcatgggcgcctctctccttcgcttggttcttccacgattgctt 469

Score = 60.0 bits (30), Expect = 1e-04
Identities = 105/130 (80%)
Strand = Plus / Minus

Query: 1154 cagggatgtgatggttcaattctattggatgacacatcaagcttcaccggagagaagaac 1213
||||||| ||||| ||| ||||| | || ||||||||| ||||||||||||| ||
Sbjct: 175 cagggatgcatggatcagttctactagacgacacatcatctttcaccggagagaaaaat 116

Query: 1214 gcaaaccccaacaggaactctgctcgtggattcgaggttattgacaacattaaatcagcc 1273
||| ||||| | ||||| || || ||||||||||| || ||||||||||| || ||
Sbjct: 115 gcagtcaccaatcgtaactccgccgcggattcgaggtcatcgacaacattaagtccgca 56

Query: 1274 gtggagaaag 1283
|| |||||
Sbjct: 55 gttgagaaag 46

>gb|CV717574.1| UCRCS08_0009D08_f Parent Washington Navel Orange Callus cDNA Library
UCRCS08-1 Citrus sinensis cDNA clone CS_AEa0009D08, mRNA
sequence
Length = 694

Score = 71.9 bits (36), Expect = 3e-08
Identities = 123/152 (80%)
Strand = Plus / Plus

Query: 1476 agcttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagcc 1535
||||||||||| | ||| | || ||||| || || ||||| ||||||||| |||||
Sbjct: 120 agcttggaggcccaagctgggaagtaaaactcggtaggagagatgctagaactgcaagcc 179

Query: 1536 aatctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaa 1595
||||||||||| | ||||| ||| || || ||||||| || ||||||| |||||
Sbjct: 180 aatctgctgctaatagcggcatctctcctcctacctcaaacttgaatcaactcacctcta 239

Query: 1596 gatttagcgctcttggactttccaccaaggac 1627
| || | ||||| ||||||||| |||||
Sbjct: 240 ggttcaacgctctcggactttccaacaaggac 271

Score = 46.1 bits (23), Expect = 1.4
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 2005 cactctgatcagcaactgttcaacgggtgggtccac 2039
||||||| || ||||| |||||
Sbjct: 626 cactctgatcaacagctgttcaatgggtgggtccac 660

>gb|CV093292.1| FAMU_USDA_FP_1315 Vitis shuttleworthii L., grape Vitis shuttleworthii
cDNA clone JLVs077_F09 5', mRNA sequence
Length = 666

Score = 71.9 bits (36), Expect = 3e-08
Identities = 101/120 (84%), Gaps = 2/120 (1%)
Strand = Plus / Plus

Query: 1909 tcaggggacaacaatctggcaccacttgatcttcaaactccaaccagcttt-gacaacta 1967
||||||| ||| || ||||| ||||| || ||||| || |||
Sbjct: 230 tcaggggacaacaacttggccccctctggatcttcaaactcctac-agcttttgagaacaa 288

Query: 1968 ctacttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaa 2027
|||| ||||| || ||||| || ||||| ||||| |||||
Sbjct: 289 ctactacaagaacctgatcaagaagaaggacttctccactctgatcagcagctgttcaa 348

Score = 60.0 bits (30), Expect = 1e-04
Identities = 54/62 (87%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 116 cacacaattgggcaagcaaggtgcacatccttcagggtcgcataataatgagacaaac 175

Query: 1855 at 1856
||
Sbjct: 176 at 177

Score = 50.1 bits (25), Expect = 0.092
Identities = 58/69 (84%)
Strand = Plus / Plus

Query: 2104 atgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaat 2163
|||||
Sbjct: 426 atgatcaagatgggagatatcagccactcactggatcaaacggagagattaggaagaac 485

Query: 2164 tgtagaagg 2172
||
Sbjct: 486 tgcagaagg 494

Score = 48.1 bits (24), Expect = 0.36
Identities = 81/100 (81%)
Strand = Plus / Plus

Query: 1539 ctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaagat 1598
|||||
Sbjct: 6 ctgctgcaaacaacagcatccctcctccaacttcaaacctgaaccaactaatctctagtt 65

Query: 1599 ttagcgctcttggactttccaccaaggacttggctgcctt 1638
|
Sbjct: 66 tccaagctcttggcctctcaaccaggacttgggtgcctt 105

>gb|C0866271.1| Mdfrt3046b02.y1 Mdfrt Malus x domestica cDNA clone Mdfrt3046b02 5'
similar to TR:Q41326 Q41326 PEROXIDASE ;, mRNA sequence
Length = 509

Score = 71.9 bits (36), Expect = 3e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
|||||
Sbjct: 277 gccatgatcaagatgggagacatcaaacctctcactggatccagtggggagattaggaag 336

Query: 2161 aattgtag 2168
|||||
Sbjct: 337 aattgtag 344

Score = 46.1 bits (23), Expect = 1.4
Identities = 90/111 (81%), Gaps = 1/111 (0%)
Strand = Plus / Plus

Query: 1918 aacaatctggcaccacttgatcttcaaactccaaccagctttgacaactactacttcaag 1977
||||| |||| ||||||| ||||||| || || || ||||||| |||||||
Sbjct: 92 aacaatttggtccacttgaccttcaaaccctacttctttcgacaacaactacttcaa 151

Query: 1978 aacctcgttcagaagaagg-gtctcctccactctgatcagcaactgttcaa 2027
||||| | ||||| || | ||||||||||||||| ||||| || |||||
Sbjct: 152 aacctaatccagaataaagagtctcctccactctgaccagcagctcttcaa 202

>gb|C0417575.1| Mdfrt3031k23.y1 Mdfrt Malus x domestica cDNA clone Mdfrt3031k23 5'
similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;, mRNA sequence
Length = 363

Score = 71.9 bits (36), Expect = 3e-08
Identities = 60/68 (88%)
Strand = Plus / Plus

Query: 2101 gccatgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaag 2160
||||||||||||||||||||| | ||||||||||| |||| || | || |||||
Sbjct: 129 gccatgatcaagatgggagacatcaaacctctcactggatccagtggggagattaggaag 188

Query: 2161 aattgtag 2168
|||||||
Sbjct: 189 aattgtag 196

>gb|C0070833.1| GR_Ea28B05.r GR_Ea Gossypium raimondii cDNA clone GR_Ea28B05 3',
mRNA sequence
Length = 857

Score = 71.9 bits (36), Expect = 3e-08
Identities = 48/52 (92%)
Strand = Plus / Plus

Query: 733 cgcatgggtgcttctctccttcgcttggttcttccacgattgctttgtcaatg 784
||||||||||||||||| | ||||||||||| || |||||||||||
Sbjct: 227 cgcatgggtgcttctctcgtccgcttggttcttccatgactgctttgtcaatg 278

>gb|G0566201.1| Mddb5025B21_e2932.g1 Mddb Malus x domestica cDNA 5' similar to
dbj|BAA82306.1| peroxidase [Nicotiana tabacum], mRNA
sequence
Length = 687

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Minus

```
Query: 1794 tcacacaattggacaagcaagggtcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 560   tcacacaattgggcaagcaagggtgtacaactttcagagctgcataatataacgagaccaa 501
```

Query: 1854 cat 1856
 |||
 Sbjct: 500 cat 498

>emb|CU537036.1| CU537036 TISCIVS_KZ0AAQ Theobroma cacao cDNA clone KZ0AAQ5YH15FM1,
mRNA sequence
Length = 744

Score = 69.9 bits (35), Expect = 1e-07
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 |||||
 Sbjct: 463 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 522

```
Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
          ||||| ||||| |||| ||| | || ||||| ||| | || ||||| || |||
Sbjct: 523 gctgctgccaaacagcattctctccaacttctaacttgaacagactcatttctaga 582
```

```
Query: 1598 tttagcgctcttggactttccaccaaggacttggt 1632
          || | ||||| ||||| ||||| |||||
Sbjct: 583  ttcaatgctcttggactttccaccaggacatggt 617
```

Score = 48.1 bits (24), Expect = 0.36
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 633 tcacacaattggactagcaaggtgcaca 660

>emb|CU505430.1| CU505430 PODMEUPA_KZOACAB Theobroma cacao cDNA clone KZOACAB5YF04FM1,
 mRNA sequence
 Length = 769

Score = 69.9 bits (35), Expect = 1e-07
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttgaagaagagacgctagaactgctagccaa 1537
 |||||
Sbjct: 455 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 514

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
 |||||
Sbjct: 515 gctgctgccaacaacagcattcctcctccaacttctaacttgacagactcatttctaga 574

Query: 1598 tttagcgctcttggactttccaccaaggacttgggt 1632
 |||
Sbjct: 575 ttcaatgctcttggactttccaccaggacatgggt 609

Score = 48.1 bits (24), Expect = 0.36
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
 |||||
Sbjct: 625 tcacacaattggactagcaaggtgcaca 652

>emb|CU478688.1| CU478688 COPHAS_KZOAAAL Theobroma cacao cDNA clone KZOAAAL11YB20FM1,
 mRNA sequence
 Length = 642

Score = 69.9 bits (35), Expect = 1e-07
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 458 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 517

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||| ||||| ||| | | ||||| ||| | ||| ||||| || |||
Sbjct: 518 gctgctgccaacaacagcattcctcctccaacttctaacttgaacagactcatttctaga 577

Query: 1598 tttagcgctcttggactttccaccaaggacttggt 1632
|| | ||||||||||||||||||| ||||| |||||
Sbjct: 578 ttcaatgctcttggactttccaccaggacatggt 612

>emb|CU478933.1| CU478933 COPHAS_KZ0AAL Theobroma cacao cDNA clone KZ0AAL12YN22FM1,
mRNA sequence
Length = 744

Score = 69.9 bits (35), Expect = 1e-07
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
||||||| | ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 458 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 517

Query: 1538 tctgctgctaacaatggcatccctgcaccacttcaaaccttaaccaactcatctcaaga 1597
||||||| ||||| ||||| ||| | | ||||| ||| | ||| ||||| || |||
Sbjct: 518 gctgctgccaacaacagcattcctcctccaacttctaacttgaacagactcatttctaga 577

Query: 1598 tttagcgctcttggactttccaccaaggacttggt 1632
|| | ||||||||||||||||||| ||||| |||||
Sbjct: 578 ttcaatgctcttggactttccaccaggacatggt 612

Score = 48.1 bits (24), Expect = 0.36
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 628 tcacacaattggactagcaaggtgcaca 655

>emb|CU480774.1| CU480774 CORTEXS_KZ0AAT Theobroma cacao cDNA clone KZ0AAT11YE09FM1,
mRNA sequence
Length = 703

Score = 69.9 bits (35), Expect = 1e-07
Identities = 125/155 (80%)
Strand = Plus / Plus

Query: 1478 cttggaggccctacatggaatgttaaacttggaagaagagacgctagaactgctagccaa 1537
|||||
Sbjct: 455 cttggaggccccaactgggatgtgaaactcggaaggagagatgctaggactgctagccag 514

Query: 1538 tctgctgctaacaatggcatccctgcacccacttcaaaccttaaccaactcatctcaaga 1597
|||||
Sbjct: 515 gctgctgccaacaacagcattcctcctccaacttctaactgaacagactcatttctaga 574

Query: 1598 tttagcgctcttggactttccaccaaggacttggt 1632
|||
Sbjct: 575 ttcaatgctcttggactttccaccaggacatggt 609

Score = 48.1 bits (24), Expect = 0.36
Identities = 27/28 (96%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcaca 1821
|||||
Sbjct: 625 tcacacaattggactagcaaggtgcaca 652

>dbj|DC895850.1| DC895850 PCC Citrus unshiu cDNA clone PCC0206 5', mRNA sequence
Length = 338

Score = 69.9 bits (35), Expect = 1e-07
Identities = 167/211 (79%)
Strand = Plus / Minus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
|||||
Sbjct: 289 caggcgacaacaacttgccaccgcttgatctgcaaactcctacttgttttgacaacaatt 230

Query: 1970 acttcaagaacctcggttcagaagaagggtctctccactctgatcagcaactgttcaacg 2029
 ||||| ||||| || | |||| | || ||||| |||||
 Sbjct: 229 acttcaggaacctgggtcaacagaaagggtgcttcactctgatcaacagctgttcaatg 170

```
Query: 2030  gtgggtccaccgactccattgtgcgtggctacagcaccaaccgggcaccttctcctctg 2089
               ||||| | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 169    gtgggtccacagattcacaaagtcgcacgtacagtaacaaccggagcaccttcagctctg 110
```

```
Query: 2090 atttcgccgcccatgatcaagatgggaga 2120
      ||| | |||| ||||| ||||| |||||
Sbjct: 109 attttgccgcccatgatcaagatgggaga 79
```

>gb|EX266960.1| 1447232_5_A14_063 PY06 Carica papaya cDNA, mRNA sequence
Length = 1047

Score = 69.9 bits (35), Expect = 1e-07
Identities = 53/59 (89%)
Strand = Plus / Plus

```
Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
      ||||| ||||||| ||||| || ||||| || ||||||| |||||
Sbjct: 684 cacacgattggacaagcaaggtgcacgaatttcagggtcgcataatacaacgagaccaa 742
```

>gb|EX289762.1| 1577761_5_L07_022 PY06 Carica papaya cDNA, mRNA sequence
Length = 1029

Score = 69.9 bits (35), Expect = 1e-07
Identities = 53/59 (89%)
Strand = Plus / Plus

```
Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
          ||||| ||||||||||||||||| || ||||| || ||||| |||||||||||||
Sbjct: 180  cacacgattggacaagcaaggtgcacgaatttcagggtcgcataatacaacgagaccaa 238
```

>gb|EX272151.1| 1452845_5_K11_038 PY06 Carica papaya cDNA, mRNA sequence
Length = 1098

Score = 69.9 bits (35), Expect = 1e-07
Identities = 53/59 (89%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||||||||||||| || ||||| || ||||||| |||||||||||||||
Sbjct: 686 cacacgattggacaagcaaggtgcacgaatttcagggtcgcataatacaacgagaccaa 744

>gb|EB110403.1| 000430AFBC008068HT (AFBC) Royal Gala pre-opened floral bud Malus x
domestica cDNA clone AFBC008068, mRNA sequence
Length = 481

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||| ||||||||||||||||||| ||||| ||||||| ||||| || ||||||| |||||
Sbjct: 217 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcataatacaacgagaccaa 276

Query: 1854 cat 1856
|||
Sbjct: 277 cat 279

>gb|DW157696.1| CLVX9795.b1_E02.ab1 CLV(XYZ) lettuce virosa Lactuca virosa cDNA clone
CLVX9795, mRNA sequence
Length = 440

Score = 69.9 bits (35), Expect = 1e-07
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 2088 tgatttcgccgccgccatgatcaagatgggagacattagtcctctcactggctccaatgg 2147
||||| || ||||||||||||||||||| ||||| || ||| ||||| ||||||||||||||| ||
Sbjct: 198 tgattttgcggccgccatgatcaacatgggtgatattcgtccctcactggctccaacgg 257

Query: 2148 agaaatcaggaagaa 2162
|| |||||||||||
Sbjct: 258 cgagatcaggaagaa 272

>gb|DW145800.1| CLVX10900.b1_H13.ab1 CLV(XYZ) lettuce virosa Lactuca virosa cDNA
clone CLVX10900, mRNA sequence
Length = 453

Score = 69.9 bits (35), Expect = 1e-07
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 2088 tgatttcgccgcccgcctgatcaagatgggagacattagtcctctcactggctccaatgg 2147
||||| || |||||||||||||| ||||| || ||| |||| |||||||||||||| ||
Sbjct: 211 tgattttgcggccgcctgatcaacatgggtgatattcgtccctcactggctccaacgg 270

Query: 2148 agaaatcaggaagaa 2162
|| |||||||||||
Sbjct: 271 cgagatcaggaagaa 285

>gb|C0900249.1| Mddb5025b21.y1 Mddb Malus x domestica cDNA clone Mddb5025b21 5'
similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;, mRNA sequence
Length = 671

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||||||| ||||||||||| |||| |||||||| ||||| || |||||||||||
Sbjct: 344 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcatatataacgagaccaa 403

Query: 1854 cat 1856
|||
Sbjct: 404 cat 406

>gb|C0051719.1| Mdfw2055d05.y1 Mdfw Malus x domestica cDNA clone Mdfw2055d05 5'
similar to TR:Q9XIV9 Q9XIV9 PEROXIDASE ;, mRNA sequence
Length = 537

Score = 69.9 bits (35), Expect = 1e-07
Identities = 56/63 (88%)
Strand = Plus / Plus

Query: 1794 tcacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaa 1853
||||||||||| ||||||||||| |||| |||||||| ||||| || |||||||||||
Sbjct: 93 tcacacaattgggcaagcaaggtgtacaactttcagagctcgcatatataacgagaccaa 152

Query: 1854 cat 1856

|||
Sbjct: 153 cat 155

>gb|CN880015.1| 010418AASA009843HT (AASA) Royal Gala 10 DAFB fruit Malus x
domestica cDNA clone AASA009843, mRNA sequence
Length = 687

Score = 69.9 bits (35), Expect = 1e-07
Identities = 65/75 (86%)
Strand = Plus / Plus

Query: 710 aatctgccatatctaaggagaccgcatgggtgcttctctccttcgcttggttcttccacg 769
||||||| |||| ||||| | ||||||||||||||||||||| | |||||
Sbjct: 168 aatctgccgtatcaaaggaaaagcgcatgggtgcttctctccttcgctccatttccacg 227

Query: 770 attgctttgtcaatg 784
|||||||||||||||
Sbjct: 228 attgctttgtcaatg 242

Score = 67.9 bits (34), Expect = 4e-07
Identities = 55/62 (88%)
Strand = Plus / Plus

Query: 1795 cacacaattggacaagcaaggtgcacaaacttcagagcccgcatctacaacgagaccaac 1854
||||||| ||||||||||||||||| |||| || ||||||||||||| |||||||||
Sbjct: 608 cacacaataggacaagcaaggtgcaccgtcttccgaacccgcatctacaccgagaccaac 667

Query: 1855 at 1856
||
Sbjct: 668 at 669

>gb|GR871114.1| Pq_F_00457 American ginseng Flower cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 519

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313

||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 354 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 413

Query: 1314 tccttg 1319

|||||
Sbjct: 414 tccttg 419

>gb|GR875194.1| Pq_R_02677 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 453

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 354 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 413

Query: 1314 tccttg 1319

|||||
Sbjct: 414 tccttg 419

>gb|GR873483.1| Pq_R_00966 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 494

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||| || ||||| || ||| ||||| ||||| |||||
Sbjct: 292 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 351

Query: 1314 tccttg 1319

|||||
Sbjct: 352 tccttg 357

>gb|GR873276.1| Pq_R_00759 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence

Length = 557

Score = 67.9 bits (34), Expect = 4e-07

Identities = 58/66 (87%)

Strand = Plus / Plus

```
Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
          ||||| ||||| || ||||| || || ||||| ||||| |||||
Sbjct: 341 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 400
```

Query: 1314 tccttg 1319

|||||

Sbjct: 401 tccttg 406

>gb|GR871777.1| Pq_F_01120 American ginseng Flower cDNA Library Panax quinquefolius

cDNA 5', mRNA sequence

Length = 435

Score = 67.9 bits (34), Expect = 4e-07

Identities = 58/66 (87%)

Strand = Plus / Plus

```
Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
          ||||| ||||| || ||||| || || ||||| ||||| |||||
Sbjct: 293 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 352
```

Query: 1314 tccttg 1319

|||||

Sbjct: 353 tccttg 358

>gb|GR874357.1| Pq_R_01840 American ginseng Root cDNA Library Panax quinquefolius

cDNA 5', mRNA sequence

Length = 397

Score = 67.9 bits (34), Expect = 4e-07

Identities = 58/66 (87%)

Strand = Plus / Plus

```
Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
          ||||| ||||| || ||||| || || ||||| ||||| |||||
Sbjct: 315 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 374
```

Query: 1314 tccttg 1319
|||||
Sbjct: 375 tccttg 380

>gb|GR874227.1| Pq_R_01710 American ginseng Root cDNA Library Panax quinquefolius
cDNA 5', mRNA sequence
Length = 415

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||||| || ||||||| || || ||||||| ||||||| |||||||
Sbjct: 67 ttgacaccattaaagaagctgtggagagagagtgccaggagttgtttcctgtgcagata 126

Query: 1314 tccttg 1319
|||||
Sbjct: 127 tccttg 132

>emb|CU507988.1| CU507988 PODSSHWB1Sb_KZOACD Theobroma cacao cDNA clone
KZOACD3YE10FM1, mRNA sequence
Length = 336

Score = 67.9 bits (34), Expect = 4e-07
Identities = 61/70 (87%)
Strand = Plus / Minus

Query: 2103 catgatcaagatgggagacattagtcctctcactggctccaatggagaaatcaggaagaa 2162
||||| ||||||| ||||||| || || ||||||| |||||||
Sbjct: 328 catgatcaagatgggagacatcagtcacctcactggatcaaggggagagatcaggaagaa 269

Query: 2163 ttgtagaagg 2172
|| |||||||
Sbjct: 268 ctgcagaagg 259

>gb|EY664481.1| CS00-C1-101-067-A09-CT.F Sweet orange leaf, infected with Xylella
fastidiosa (stage 1 of 2) Citrus sinensis cDNA, mRNA
sequence
Length = 677

Score = 67.9 bits (34), Expect = 4e-07
Identities = 214/274 (78%)
Strand = Plus / Plus

Query: 1910 caggggacaacaatctggcaccacttgatcttcaaactccaaccagctttgacaactact 1969
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 206 cagggcacaacaacttggcaccgcttgatctgcaaactcctacttcttttgacaacaatt 265

Query: 1970 acttcaagaacctcggttcagaagaagggtctcctccactctgatcagcaactgttcaacg 2029
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 266 acttcaagaacctggtcaacagaaagggtggttcactctgatcaacagctgttcaatg 325

Query: 2030 gtgggtccaccgactccattgtgcgtggctacagcaccaacccgggcaccttctcctctg 2089
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 326 gtgggtccactgattcacaagtcgcgacgtacagtaacaacccgagcaccttcagctctg 385

Query: 2090 atttcgccgccgccatgatcaagatgggagacattagtcctctcactggctccaatggag 2149
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 386 attttggtgctggcatgatcaagatgggagatatcagcccactcactggatcccgcggtg 445

Query: 2150 aaatcaggaagaattgtagaaggattaactaatt 2183
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 446 aaattaggaagaattgcaggaggatcaattaatt 479

>gb|EW712042.1| Ginseng-Feq Contig4 Ginseng F. equiseti subtraction library Panax
quinquefolius cDNA, mRNA sequence
Length = 1030

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 410 ttgacaccattaaagaagctgtggagagagagtgtccaggagttgtttcctgtgcagata 469

Query: 1314 tccttg 1319
|||||
Sbjct: 470 tccttg 475

>gb|EL366609.1| CCES2712.b1_005.ab1 CCE(LMS) endive Cichorium endivia cDNA clone
CCES2712, mRNA sequence
Length = 465

Score = 67.9 bits (34), Expect = 4e-07
Identities = 64/74 (86%)
Strand = Plus / Plus

Query: 2089 gatttcgccgccgcatgatcaagatgggagacattagtcctctcactggctccaatgga 2148
||||||| ||||||||||||||| ||||| || ||| ||||| ||||||| ||||| ||
Sbjct: 267 gatttcgccgccgcatgatcaatatgggtgatattcgtcccctcaccggctccaacggc 326

Query: 2149 gaaatcaggaagaa 2162
|| |||||||||
Sbjct: 327 gagatcaggaagaa 340

>gb|EH664510.1| 11.2E05 Transformed tobacco Lambda Zap II library Nicotiana tabacum
cDNA 5', mRNA sequence
Length = 1034

Score = 67.9 bits (34), Expect = 4e-07
Identities = 54/61 (88%)
Strand = Plus / Plus

Query: 724 aaggagaccgcatgggtgcttctctccttcgcttggttcttcacgattgctttgtcaat 783
||||| ||||| ||||||||||| ||||||||| | ||||| ||||||||| |||||
Sbjct: 206 aaggaaaccgcatgggtgcttccctccttcgcttattcttcnagattgcttcgtcaat 265

Query: 784 g 784
|
Sbjct: 266 g 266

>gb|EC600006.1| PNSSH3G-1469 panax notoginseng subtracted cDNA libraries Panax
notoginseng cDNA 5' similar to secretory peroxidase, mRNA
sequence
Length = 454

Score = 67.9 bits (34), Expect = 4e-07
Identities = 58/66 (87%)
Strand = Plus / Plus

Query: 1254 ttgacaacattaaatcagccgtggagaaagtgtgtccaggagttgtttcctgcgcagata 1313

||||| ||||| || ||||| || ||| ||||||||||||||| |||||
Sbjct: 30 ttgacaccattaaagaagctgtggagagagagtcccaggagttgttcctgtgcagata 89

Query: 1314 tccttg 1319

|||||
Sbjct: 90 tccttg 95

Database: /usr/local/blast/db/blastlibs/est_others

Posted date: Feb 13, 2010 7:48 AM

Number of letters in database: 29,218,461,503

Number of sequences in database: 51,680,690

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 51680690

Number of Hits to DB: 1,226,019,706

Number of extensions: 77420216

Number of successful extensions: 22531408

Number of sequences better than 10.0: 2217

Number of HSP's gapped: 22531246

Number of HSP's successfully gapped: 2762

Length of query: 3867

Length of database: 29,218,461,503

Length adjustment: 24

Effective length of query: 3843

Effective length of database: 27,978,124,943

Effective search space: 107519934155949

Effective search space used: 107519934155949

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 50 (99.1 bits)

S1: 12 (24.3 bits)

S2: 22 (44.1 bits)

BLASTx Output of the Sequence at the Parental Locus of Soybean Event DAS-68416-4 against GenBank Non-redundant Protein Sequences (nr)

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, 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.

Query= 68416_parent_locus
(3867 letters)

Database: /usr/local/blast/db/blastlibs/nr
10,432,217 sequences; 3,559,509,877 total letters

Searching.....done

Sequences producing significant alignments:		Score	E
		(bits)	Value
gb ACU17608.1	unknown [Glycine max]	249	2e-63
gb ACU17865.1	unknown [Glycine max]	242	2e-61
gb AAP76387.1	class III peroxidase [Gossypium hirsutum]	218	4e-54
gb AB077632.1	peroxidase [Medicago truncatula]	217	1e-53
dbj BAA82306.1	peroxidase [Nicotiana tabacum]	212	3e-52
ref XP_002278996.1	PREDICTED: hypothetical protein [Vitis vinif...	211	7e-52
gb AAX44001.2	putative secretory peroxidase [Catharanthus roseus]	209	2e-51
gb AAP42508.1	anionic peroxidase swpb3 [Ipomoea batatas]	209	2e-51
gb ABR23054.1	basic peroxidase swpb4 [Ipomoea batatas]	209	2e-51
gb ACU23245.1	unknown [Glycine max]	208	4e-51
gb ACM47317.1	peroxidase [Capsicum annuum]	205	4e-50
ref XP_002328991.1	predicted protein [Populus trichocarpa] >gi ...	204	5e-50
ref XP_002269918.1	PREDICTED: hypothetical protein [Vitis vinif...	204	5e-50
emb CAD67479.1	peroxidase [Asparagus officinalis]	203	2e-49
ref NP_196153.1	peroxidase, putative [Arabidopsis thaliana] >gi ...	202	3e-49
dbj BAF27413.2	Os11g0112400 [Oryza sativa Japonica Group]	201	8e-49
ref NP_001065568.1	Os11g0112400 [Oryza sativa (japonica cultiva...	201	8e-49
gb EAY79693.1	hypothetical protein OsI_34840 [Oryza sativa Indi...	199	2e-48
ref NP_001065971.1	Os12g0112000 [Oryza sativa (japonica cultiva...	199	2e-48
ref XP_002450132.1	hypothetical protein SORBIDRAFT_05g001000 [S...	199	3e-48
gb ACT35473.1	peroxidase 52 [Brassica rapa]	197	1e-47
ref XP_002441703.1	hypothetical protein SORBIDRAFT_08g000990 [S...	196	2e-47
ref XP_002450133.1	hypothetical protein SORBIDRAFT_05g001010 [S...	196	2e-47
gb ABV24960.2	putative secretory peroxidase [Catharanthus roseus]	196	2e-47
sp P00434.3	PERP7_BRARA RecName: Full=Peroxidase P7; AltName: Fu...	196	2e-47

gb AAD37423.1 AF149281_1 peroxidase 6 [Phaseolus vulgaris]	195	4e-47
ref XP_002520835.1 Peroxidase 52 precursor, putative [Ricinus c...	194	5e-47
ref XP_002319968.1 predicted protein [Populus trichocarpa] >gi ...	193	1e-46
ref NP_001151940.1 peroxidase 52 [Zea mays] >gi 195651251 gb AC...	191	5e-46
ref XP_002489046.1 hypothetical protein SORBIDRAFT_0246s002010 ...	190	1e-45
ref XP_002441702.1 hypothetical protein SORBIDRAFT_08g000980 [S...	190	1e-45
gb AAA96137.1 peroxidase [Stylosanthes humilis]	190	1e-45
gb AAL93151.1 AF485265_1 class III peroxidase [Gossypium hirsutum]	189	2e-45
emb CAD67478.1 peroxidase [Asparagus officinalis]	188	4e-45
gb AAR31108.1 peroxidase precursor [Quercus suber]	188	5e-45
gb AAR31106.1 peroxidase precursor [Quercus suber]	187	1e-44
ref NP_001131000.1 hypothetical protein LOC100192105 [Zea mays]...	186	1e-44
gb AAD43561.1 AF155124_1 bacterial-induced peroxidase precursor ...	185	3e-44
gb ACN33662.1 unknown [Zea mays]	184	6e-44
emb CBI25393.1 unnamed protein product [Vitis vinifera]	184	1e-43
gb ACU23223.1 unknown [Glycine max]	182	3e-43
emb CAA71491.1 peroxidase [Spinacia oleracea]	182	3e-43
gb ABK21858.1 unknown [Picea sitchensis]	180	1e-42
emb CAD67477.1 peroxidase [Asparagus officinalis]	179	2e-42
emb CAA62597.1 korean-radish isoperoxidase [Raphanus sativus]	179	2e-42
gb AC090366.1 peroxidase precursor [Triticum aestivum]	179	2e-42
gb ACN34270.1 unknown [Zea mays]	179	3e-42
gb ACU24215.1 unknown [Glycine max]	178	5e-42
gb AAB48184.1 peroxidase precursor [Linum usitatissimum]	178	5e-42
emb CBI27506.1 unnamed protein product [Vitis vinifera]	177	7e-42
ref XP_002274550.1 PREDICTED: hypothetical protein [Vitis vinif...	177	7e-42
gb ACN42168.1 peroxidase 1 [Sesuvium portulacastrum]	177	9e-42
ref XP_002269058.1 PREDICTED: hypothetical protein [Vitis vinif...	177	1e-41
emb CBI27505.1 unnamed protein product [Vitis vinifera]	177	1e-41
emb CAL25300.1 properoxidase [Picea abies]	176	2e-41
ref XP_002269145.1 PREDICTED: hypothetical protein [Vitis vinif...	175	3e-41
gb ACJ85500.1 unknown [Medicago truncatula]	174	8e-41
emb CAN80097.1 hypothetical protein [Vitis vinifera]	173	2e-40
emb CBI27503.1 unnamed protein product [Vitis vinifera]	172	2e-40
emb CBI27502.1 unnamed protein product [Vitis vinifera]	172	2e-40
ref XP_002269169.1 PREDICTED: hypothetical protein [Vitis vinif...	172	2e-40
gb AA013838.1 AF405326_1 peroxidase 2 [Lupinus albus]	172	2e-40
gb ABA96220.1 Cationic peroxidase 1 precursor, putative, expres...	172	2e-40
tpe CAH69378.1 TPA: class III peroxidase 136 precursor [Oryza s...	172	2e-40
ref XP_002269216.1 PREDICTED: hypothetical protein [Vitis vinif...	172	3e-40
emb CAH10839.1 peroxidase [Picea abies]	172	3e-40
ref XP_002266365.1 PREDICTED: hypothetical protein [Vitis vinif...	172	4e-40
ref NP_001106040.1 plasma membrane-bound peroxidase 2b precurs...	172	4e-40
gb EAY82023.1 hypothetical protein OsI_37207 [Oryza sativa Indi...	171	5e-40
gb ABA91154.1 Cationic peroxidase 1 precursor, putative, expres...	171	5e-40
ref NP_001065566.1 Os11g0112200 [Oryza sativa (japonica cultiva...	171	5e-40
gb EEE67815.1 hypothetical protein OsJ_25569 [Oryza sativa Japo...	171	6e-40
ref NP_001060628.1 Os07g0677200 [Oryza sativa (japonica cultiva...	171	6e-40
tpe CAH69353.1 TPA: class III peroxidase 111 precursor [Oryza s...	171	6e-40

emb	CBI27501.1	unnamed protein product [Vitis vinifera]	170	1e-39
ref	XP_002269266.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
ref	XP_002509730.1	Lignin-forming anionic peroxidase precursor,...	170	1e-39
emb	CBI18066.1	unnamed protein product [Vitis vinifera]	170	1e-39
ref	XP_002268259.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
ref	XP_002299006.1	predicted protein [Populus trichocarpa] >gi ...	170	1e-39
ref	XP_002333334.1	predicted protein [Populus trichocarpa] >gi ...	170	1e-39
ref	XP_002285723.1	PREDICTED: hypothetical protein [Vitis vinif...	170	1e-39
emb	CAA46916.1	peroxidase [Oryza sativa (japonica cultivar-grou...	170	1e-39
ref	XP_002319967.1	predicted protein [Populus trichocarpa] >gi ...	169	2e-39
gb	ABK24123.1	unknown [Picea sitchensis]	169	3e-39
gb	AAA20473.1	peroxidase [Cenchrus ciliaris]	169	3e-39
gb	ABK23423.1	unknown [Picea sitchensis]	168	4e-39
ref	NP_001060629.1	Os07g0677300 [Oryza sativa (japonica cultiva...	168	4e-39
gb	ACJ11762.1	class III peroxidase [Gossypium hirsutum]	168	5e-39
gb	ABK25962.1	unknown [Picea sitchensis]	168	5e-39
gb	EAZ05133.1	hypothetical protein OsI_27326 [Oryza sativa Indi...	168	5e-39
ref	NP_001046400.1	Os02g0240100 [Oryza sativa (japonica cultiva...	168	5e-39
gb	AAC49818.1	peroxidase [Oryza sativa Indica Group]	168	5e-39
dbj	BAD28869.1	putative bacterial-induced peroxidase precursor ...	168	5e-39
ref	XP_002274693.1	PREDICTED: hypothetical protein [Vitis vinif...	167	7e-39
gb	EEC82680.1	hypothetical protein OsI_27324 [Oryza sativa Indi...	167	7e-39
ref	NP_001060626.1	Os07g0676900 [Oryza sativa (japonica cultiva...	167	7e-39
emb	CAH10840.1	peroxidase [Picea abies]	167	7e-39
dbj	BAC83101.1	putative peroxidase precursor [Oryza sativa Japo...	167	7e-39
tpe	CAH69351.1	TPA: class III peroxidase 109 precursor [Oryza s...	167	7e-39
ref	XP_002451848.1	hypothetical protein SORBIDRAFT_04g008620 [S...	167	9e-39
gb	ACN33811.1	unknown [Zea mays]	167	9e-39
gb	ABR18139.1	unknown [Picea sitchensis]	167	9e-39
sp	A2YPX3.2	PER2_ORYSI RecName: Full=Peroxidase 2; Flags: Precur...	167	1e-38
ref	XP_002461208.1	hypothetical protein SORBIDRAFT_02g042850 [S...	166	2e-38
ref	XP_002320417.1	predicted protein [Populus trichocarpa] >gi ...	166	2e-38
ref	NP_001130666.1	hypothetical protein LOC100191769 [Zea mays]...	166	2e-38
ref	NP_200648.1	peroxidase, putative [Arabidopsis thaliana] >gi...	166	2e-38
ref	XP_002338628.1	predicted protein [Populus trichocarpa] >gi ...	166	2e-38
ref	XP_002336344.1	predicted protein [Populus trichocarpa] >gi ...	166	2e-38
emb	CAA71493.1	peroxidase [Spinacia oleracea]	166	2e-38
gb	AAX53172.1	peroxidase [Populus alba x Populus tremula var. g...	166	2e-38
ref	XP_002509738.1	Lignin-forming anionic peroxidase precursor,...	166	3e-38
ref	XP_002453592.1	hypothetical protein SORBIDRAFT_04g008630 [S...	165	4e-38
gb	ACN60163.1	class III peroxidase [Tamarix hispida]	164	8e-38
ref	XP_002450134.1	hypothetical protein SORBIDRAFT_05g001030 [S...	163	1e-37
gb	AAC05277.1	peroxidase FLXPER4 [Linum usitatissimum]	163	1e-37
ref	XP_002269343.1	PREDICTED: hypothetical protein [Vitis vinif...	163	2e-37
gb	EAY85148.1	hypothetical protein OsI_06503 [Oryza sativa Indi...	163	2e-37
ref	XP_002269301.1	PREDICTED: hypothetical protein [Vitis vinif...	162	2e-37
gb	AAD37428.1	AF149278_1 peroxidase 3 precursor [Phaseolus vulga...	162	2e-37
ref	XP_002334243.1	predicted protein [Populus trichocarpa] >gi ...	162	3e-37
ref	XP_002438530.1	hypothetical protein SORBIDRAFT_10g021630 [S...	162	4e-37

ref XP_002281755.1	PREDICTED: hypothetical protein [Vitis vinif...	162	4e-37
ref XP_002437128.1	hypothetical protein SORBIDRAFT_10g021610 [S...	161	5e-37
ref XP_002517727.1	Cationic peroxidase 1 precursor, putative [R...	160	9e-37
ref NP_001057822.1	Os06g0547400 [Oryza sativa (japonica cultiva...	160	9e-37
ref XP_002285724.1	PREDICTED: hypothetical protein [Vitis vinif...	160	1e-36
ref XP_002521867.1	Lignin-forming anionic peroxidase precursor,...	160	1e-36
emb CAH10841.1	peroxidase [Picea abies]	160	1e-36
gb EEE67814.1	hypothetical protein OsJ_25568 [Oryza sativa Japo...	160	1e-36
tpe CAH69352.1	TPA: class III peroxidase 110 precursor [Oryza s...	160	1e-36
ref NP_001060627.1	Os07g0677100 [Oryza sativa (japonica cultiva...	160	1e-36
gb ABD66594.1	peroxidase [Litchi chinensis]	159	2e-36
emb CBI19219.1	unnamed protein product [Vitis vinifera]	159	2e-36
ref XP_002334317.1	predicted protein [Populus trichocarpa] >gi ...	159	2e-36
emb CAN73051.1	hypothetical protein [Vitis vinifera]	159	2e-36
gb EEE67818.1	hypothetical protein OsJ_25573 [Oryza sativa Japo...	159	3e-36
gb EEE56633.1	hypothetical protein OsJ_06032 [Oryza sativa Japo...	159	3e-36
ref XP_002281731.1	PREDICTED: hypothetical protein [Vitis vinif...	159	3e-36
gb EAZ05136.1	hypothetical protein OsI_27329 [Oryza sativa Indi...	159	3e-36
ref NP_001046402.1	Os02g0240500 [Oryza sativa (japonica cultiva...	159	3e-36
ref NP_001060630.1	Os07g0677400 [Oryza sativa (japonica cultiva...	159	3e-36
emb CAA59487.1	peroxidase [Triticum aestivum] >gi 193074375 gb ...	159	3e-36
gb AAB02554.1	cationic peroxidase [Stylosanthes humilis]	159	3e-36
sp P16147.2	PERX_LUPPO RecName: Full=Peroxidase >gi 1345541 emb ...	159	3e-36
dbj BAA77389.1	peroxidase 3 [Scutellaria baicalensis]	159	3e-36
ref XP_002461207.1	hypothetical protein SORBIDRAFT_02g042840 [S...	158	4e-36
gb EEC82684.1	hypothetical protein OsI_27330 [Oryza sativa Indi...	158	4e-36
gb AAW52720.1	peroxidase 6 [Triticum monococcum]	158	4e-36
gb AAQ55292.1	class III peroxidase GvPx2b [Vitis vinifera]	158	4e-36
gb AAF65464.2	AF247700_1 peroxidase POC1 [Oryza sativa Indica Gr...	158	4e-36
ref XP_002311022.1	predicted protein [Populus trichocarpa] >gi ...	158	6e-36
gb EEE67819.1	hypothetical protein OsJ_25574 [Oryza sativa Japo...	158	6e-36
ref NP_001147216.1	LOC100280824 [Zea mays] >gi 195608630 gb ACG...	158	6e-36
ref NP_001060631.1	Os07g0677500 [Oryza sativa (japonica cultiva...	158	6e-36
pdb 1SCH A Chain A, Peanut Peroxidase >gi 1633131 pdb 1SCH B Cha...		158	6e-36
sp P22195.2	PER1_ARAHY RecName: Full=Cationic peroxidase 1; AltN...	158	6e-36
gb ACU22965.1	unknown [Glycine max]	157	7e-36
ref XP_002311955.1	predicted protein [Populus trichocarpa] >gi ...	157	7e-36
gb AAM61588.1	peroxidase [Arabidopsis thaliana]	157	7e-36
ref NP_200647.1	peroxidase, putative [Arabidopsis thaliana] >gi...	157	7e-36
ref XP_002460939.1	hypothetical protein SORBIDRAFT_02g037840 [S...	157	1e-35
ref XP_002334018.1	predicted protein [Populus trichocarpa] >gi ...	157	1e-35
gb EAY85151.1	hypothetical protein OsI_06506 [Oryza sativa Indi...	157	1e-35
emb CAH10842.1	peroxidase [Picea abies]	157	1e-35
emb CBI22007.1	unnamed protein product [Vitis vinifera]	157	1e-35
ref XP_002283995.1	PREDICTED: hypothetical protein [Vitis vinif...	157	1e-35
emb CAN81400.1	hypothetical protein [Vitis vinifera]	157	1e-35
emb CAN63655.1	hypothetical protein [Vitis vinifera]	157	1e-35
gb AAA20472.1	peroxidase [Cenchrus ciliaris]	156	2e-35
gb ACF08096.1	class III peroxidase [Triticum aestivum]	156	2e-35

ref XP_002461211.1	hypothetical protein SORBIDRAFT_02g042870 [S...	156	2e-35
sp Q02200.1 PERX_NICSY	RecName: Full=Lignin-forming anionic pero...	156	2e-35
ref XP_002437129.1	hypothetical protein SORBIDRAFT_10g021620 [S...	155	3e-35
gb AAW52718.1	peroxidase 4 [Triticum monococcum]	155	3e-35
gb ACI03401.1	peroxidase 1 [Litchi chinensis]	155	4e-35
ref XP_002284007.1	PREDICTED: hypothetical protein [Vitis vinif...	155	4e-35
ref XP_002323054.1	predicted protein [Populus trichocarpa] >gi ...	155	4e-35
gb EEC82681.1	hypothetical protein OsI_27325 [Oryza sativa Indi...	155	4e-35
gb EAZ01280.1	hypothetical protein OsI_23303 [Oryza sativa Indi...	155	4e-35
gb AAV89058.1	class III peroxidase [Phelipanche ramosa]	155	4e-35
gb AAW52719.1	peroxidase 5 [Triticum monococcum]	155	4e-35
gb AAC49819.1	peroxidase [Oryza sativa Indica Group]	155	4e-35
dbj BAD97435.1	peroxidase [Pisum sativum]	155	4e-35
ref NP_001057821.1	Os06g0547100 [Oryza sativa (japonica cultiva...	155	4e-35
emb CBI19220.1	unnamed protein product [Vitis vinifera]	155	5e-35
gb ACN30737.1	unknown [Zea mays]	155	5e-35
gb ACG40622.1	peroxidase 2 precursor [Zea mays]	155	5e-35
emb CAN83972.1	hypothetical protein [Vitis vinifera]	154	6e-35
ref XP_002509737.1	Lignin-forming anionic peroxidase precursor,...	154	8e-35
ref XP_002268412.1	PREDICTED: hypothetical protein [Vitis vinif...	154	8e-35
dbj BAD36900.1	peroxidase [Lotus japonicus]	154	8e-35
gb ACN26131.1	unknown [Zea mays]	154	1e-34
gb ACF08094.1	class III peroxidase [Triticum aestivum]	153	1e-34
ref XP_002509733.1	Lignin-forming anionic peroxidase precursor,...	153	1e-34
ref XP_002319407.1	predicted protein [Populus trichocarpa] >gi ...	153	1e-34
dbj BAA77388.1	peroxidase 2 [Scutellaria baicalensis]	153	1e-34
gb ACF08095.1	class III peroxidase [Triticum aestivum]	153	2e-34
gb EAZ01279.1	hypothetical protein OsI_23302 [Oryza sativa Indi...	153	2e-34
ref NP_001046392.1	Os02g0236600 [Oryza sativa (japonica cultiva...	152	2e-34
gb EAZ37287.1	hypothetical protein OsJ_21626 [Oryza sativa Japo...	152	2e-34
gb ABD47726.1	peroxidase [Eucalyptus globulus subsp. globulus]	152	2e-34
ref NP_001057820.1	Os06g0546500 [Oryza sativa (japonica cultiva...	152	2e-34
ref XP_002438534.1	hypothetical protein SORBIDRAFT_10g021650 [S...	152	3e-34
ref NP_001140437.1	hypothetical protein LOC100272496 [Zea mays]...	152	3e-34
gb ACF82414.1	unknown [Zea mays]	152	3e-34
dbj BAF19735.2	Os06g0547100 [Oryza sativa Japonica Group]	152	4e-34
ref XP_002438533.1	hypothetical protein SORBIDRAFT_10g021640 [S...	151	5e-34
gb ACE00594.1	lignin biosynthetic peroxidase [Leucaena leucocep...	151	5e-34
emb CBI19221.1	unnamed protein product [Vitis vinifera]	151	7e-34
ref XP_002451846.1	hypothetical protein SORBIDRAFT_04g008590 [S...	151	7e-34
emb CAL25299.1	properoxidase [Picea abies]	151	7e-34
emb CBI15847.1	unnamed protein product [Vitis vinifera]	150	9e-34
ref XP_002451850.1	hypothetical protein SORBIDRAFT_04g008650 [S...	150	9e-34
ref XP_002276796.1	PREDICTED: hypothetical protein [Vitis vinif...	150	9e-34
gb EAZ22364.1	hypothetical protein OsJ_06022 [Oryza sativa Japo...	150	9e-34
gb EAY85141.1	hypothetical protein OsI_06496 [Oryza sativa Indi...	150	9e-34
tpe CAH69268.1	TPA: class III peroxidase 26 precursor [Oryza sa...	150	9e-34
ref NP_001046393.1	Os02g0236800 [Oryza sativa (japonica cultiva...	150	9e-34
gb ABK22680.1	unknown [Picea sitchensis]	150	1e-33

emb CAN61440.1	hypothetical protein [Vitis vinifera]	150	1e-33
gb AAC31550.1	peroxidase PXC2 precursor [Avena sativa]	150	1e-33
gb AAC31551.1	peroxidase PXC6 precursor [Avena sativa]	150	1e-33
emb CAA71492.1	peroxidase [Spinacia oleracea]	149	3e-33
ref NP_001054096.1	Os04g0651000 [Oryza sativa (japonica cultiva...	149	3e-33
ref XP_002308244.1	predicted protein [Populus trichocarpa] >gi ...	149	3e-33
emb CBI19222.1	unnamed protein product [Vitis vinifera]	148	4e-33
ref XP_002467656.1	hypothetical protein SORBIDRAFT_01g031740 [S...	148	4e-33
gb EEE61812.1	hypothetical protein OsJ_16433 [Oryza sativa Japo...	148	4e-33
gb EEC78144.1	hypothetical protein OsI_17703 [Oryza sativa Indi...	148	4e-33
emb CAJ86184.1	H0212B02.16 [Oryza sativa (indica cultivar-group...	148	4e-33
gb EAZ22372.1	hypothetical protein OsJ_06030 [Oryza sativa Japo...	148	4e-33
ref NP_001046401.1	Os02g0240300 [Oryza sativa (japonica cultiva...	148	4e-33
gb ABK21983.1	unknown [Picea sitchensis]	148	6e-33
ref XP_002461210.1	hypothetical protein SORBIDRAFT_02g042860 [S...	148	6e-33
emb CBI18065.1	unnamed protein product [Vitis vinifera]	147	8e-33
gb ACF08091.1	class III peroxidase [Triticum aestivum]	147	8e-33
gb EAY85149.1	hypothetical protein OsI_06504 [Oryza sativa Indi...	147	8e-33
gb AAW52716.1	peroxidase 2 [Triticum monococcum]	147	8e-33
gb AAA32972.1	peroxidase [Hordeum vulgare]	147	8e-33
emb CBI22008.1	unnamed protein product [Vitis vinifera]	147	1e-32
gb ACD70388.1	class III peroxidase [Triticum aestivum]	147	1e-32
gb ABF48527.1	cell wall peroxidase [Capsicum annuum] >gi 110348...	147	1e-32
gb ACF08092.1	class III peroxidase [Triticum aestivum]	146	2e-32
gb ACN37032.1	unknown [Zea mays]	146	2e-32
sp P27337.1	PER1_HORVU RecName: Full=Peroxidase 1; Flags: Precur...	146	2e-32
gb ABV24961.1	peroxidase [Catharanthus roseus]	146	2e-32
emb CAL25298.1	properoxidase [Picea abies]	146	2e-32
gb ACF08089.1	class III peroxidase [Triticum aestivum]	146	2e-32
ref XP_002467893.1	hypothetical protein SORBIDRAFT_01g036000 [S...	145	3e-32
gb EEC75221.1	hypothetical protein OsI_11488 [Oryza sativa Indi...	145	3e-32
gb ABF95843.1	Peroxidase 52 precursor, putative, expressed [Ory...	145	3e-32
tpe CAH69282.1	TPA: class III peroxidase 40 precursor [Oryza sa...	145	3e-32
ref XP_002531319.1	Peroxidase 2 precursor, putative [Ricinus co...	145	3e-32
ref NP_001147254.1	peroxidase 52 [Zea mays] >gi 195609124 gb AC...	145	3e-32
ref XP_002465306.1	hypothetical protein SORBIDRAFT_01g035990 [S...	145	4e-32
emb CAA39486.1	peroxidase [Triticum aestivum]	145	4e-32
gb ACR36744.1	unknown [Zea mays]	145	5e-32
ref XP_002323056.1	predicted protein [Populus trichocarpa] >gi ...	145	5e-32
gb ACF88317.1	unknown [Zea mays]	145	5e-32
gb AAZ42168.1	lignin peroxidase-like [Cucumis sativus]	145	5e-32
gb AAB48986.1	peroxidase precursor [Medicago truncatula]	144	6e-32
ref XP_002521852.1	Lignin-forming anionic peroxidase precursor,...	144	6e-32
ref NP_001106020.1	plasma membrane-bound peroxidase 3-2 precurs...	144	6e-32
ref XP_002521866.1	Lignin-forming anionic peroxidase precursor,...	144	8e-32
ref XP_002521851.1	Lignin-forming anionic peroxidase precursor,...	144	8e-32
gb EEC75545.1	hypothetical protein OsI_12177 [Oryza sativa Indi...	144	8e-32
ref NP_001050435.1	Os03g0434800 [Oryza sativa (japonica cultiva...	144	8e-32
gb AAU89207.1	peroxidase, putative [Oryza sativa Japonica Group...	144	8e-32

gb ACU21160.1	unknown [Glycine max]	144	8e-32
gb ACF08090.1	class III peroxidase [Triticum aestivum]	144	1e-31
emb CAA59484.1	pox1 [Triticum aestivum]	144	1e-31
gb AAW52715.1	peroxidase 1 [Triticum monococcum]	143	1e-31
ref NP_001042342.1	Os01g0205900 [Oryza sativa (japonica cultiva...	143	1e-31
tpe CAH69245.1	TPA: class III peroxidase 2 precursor [Oryza sat...	143	1e-31
gb ACU20213.1	unknown [Glycine max]	143	2e-31
gb EEC75220.1	hypothetical protein OsI_11487 [Oryza sativa Indi...	143	2e-31
emb CAB99487.1	peroxidase [Hordeum vulgare subsp. vulgare]	143	2e-31
ref NP_001050059.1	Os03g0339300 [Oryza sativa (japonica cultiva...	143	2e-31
emb CAD92857.1	peroxidase [Picea abies]	142	2e-31
gb ACF08086.1	class III peroxidase [Triticum aestivum]	142	2e-31
emb CAN80096.1	hypothetical protein [Vitis vinifera]	142	2e-31
gb AAB97854.1	ferriprotein porphyrin-containing peroxidase [Str...	142	2e-31
emb CAC81821.1	peroxidase [Beta vulgaris]	142	3e-31
gb ACF08083.1	class III peroxidase [Triticum aestivum]	142	3e-31
ref NP_001106019.1	LOC100101533 precursor [Zea mays] >gi 221272...	142	3e-31
ref NP_172906.1	anionic peroxidase, putative [Arabidopsis thali...	142	3e-31
gb ACF70708.1	root peroxidase [Triticum aestivum]	142	4e-31
gb ACF70706.1	root peroxidase [Triticum aestivum]	142	4e-31
ref NP_001050434.1	Os03g0434500 [Oryza sativa (japonica cultiva...	142	4e-31
gb AAU89205.1	peroxidase, putative [Oryza sativa Japonica Group...	142	4e-31
gb EEC70139.1	hypothetical protein OsI_00829 [Oryza sativa Indi...	141	5e-31
ref XP_002319422.1	predicted protein [Populus trichocarpa] >gi ...	141	7e-31
gb ACF70710.1	root peroxidase [Triticum aestivum]	140	9e-31
gb ACF70709.1	root peroxidase [Triticum aestivum]	140	9e-31
gb ACF70705.1	root peroxidase [Triticum aestivum] >gi 194425605...	140	9e-31
gb ACF70701.1	root peroxidase [Triticum aestivum]	140	9e-31
gb AAM76682.1	AF387866_1 peroxidase [Triticum aestivum]	140	9e-31
ref XP_002448660.1	hypothetical protein SORBIDRAFT_06g030940 [S...	140	1e-30
gb AAM65211.1	peroxidase [Arabidopsis thaliana] >gi 42494611 gb...	140	1e-30
gb ACF08087.1	class III peroxidase [Triticum aestivum]	140	1e-30
ref XP_002270068.1	PREDICTED: hypothetical protein [Vitis vinif...	140	1e-30
ref XP_002323055.1	predicted protein [Populus trichocarpa] >gi ...	140	1e-30
gb AAF43956.1	AC012188_33 Strong similarity to an Anionic Peroxi...	140	1e-30
gb AAF63165.1	AC010657_1 T5E21.5 [Arabidopsis thaliana]	140	1e-30
ref NP_172907.1	anionic peroxidase, putative [Arabidopsis thali...	140	1e-30
ref NP_001147443.1	peroxidase 52 [Zea mays] >gi 195611432 gb AC...	140	2e-30
gb ACF08085.1	class III peroxidase [Aegilops ventricosa]	140	2e-30
gb ACF70703.1	root peroxidase [Triticum aestivum]	140	2e-30
gb ACT78791.1	putative peroxidase [Cucumis sativus]	139	2e-30
gb ACD87898.1	class III peroxidase [Aegilops ventricosa]	139	2e-30
gb ACF70707.1	root peroxidase [Triticum aestivum]	139	2e-30
emb CAN61439.1	hypothetical protein [Vitis vinifera]	139	2e-30
gb AAW52717.1	peroxidase 3 [Triticum monococcum] >gi 193074352 ...	139	2e-30
sp Q05855.1	PER1_WHEAT RecName: Full=Peroxidase; AltName: Full=W...	139	2e-30
gb ACF08084.1	class III peroxidase [Triticum aestivum]	139	3e-30
ref XP_002521868.1	Lignin-forming anionic peroxidase precursor,...	139	3e-30
gb ACF70702.1	root peroxidase [Triticum aestivum]	139	3e-30

ref XP_002327780.1 predicted protein [Populus trichocarpa] >gi ...	139	4e-30
gb EEE54081.1 hypothetical protein OsJ_00811 [Oryza sativa Japo...	139	4e-30
gb AAQ55233.1 peroxidase [Orobancha cernua var. cumana]	138	5e-30
emb CAN80051.1 hypothetical protein [Vitis vinifera]	138	6e-30
ref XP_002521850.1 Peroxidase 30 precursor, putative [Ricinus c...	138	6e-30
gb ABR13314.1 putative peroxidase class III [Prunus dulcis]	138	6e-30
ref XP_002530724.1 Peroxidase 53 precursor, putative [Ricinus c...	137	8e-30
emb CAA59485.1 peroxidase [Triticum aestivum]	137	8e-30
gb ABK59095.1 peroxidase 1 [Sesbania rostrata]	137	1e-29
gb AAP42504.1 anionic peroxidase swpa5 [Ipomoea batatas]	137	1e-29
emb CBI27504.1 unnamed protein product [Vitis vinifera]	136	2e-29
emb CBI17443.1 unnamed protein product [Vitis vinifera]	136	2e-29
gb ACU23405.1 unknown [Glycine max]	136	2e-29
ref XP_002521512.1 Peroxidase 72 precursor, putative [Ricinus c...	136	2e-29
ref XP_002275309.1 PREDICTED: hypothetical protein [Vitis vinif...	136	2e-29
ref XP_002531320.1 Cationic peroxidase 1 precursor, putative [R...	136	2e-29
gb ABG49114.1 peroxidase [Dimocarpus longan]	136	2e-29
gb AAP42506.1 anionic peroxidase swpb1 [Ipomoea batatas]	136	2e-29
gb ACU24350.1 unknown [Glycine max]	135	3e-29
gb ACU21179.1 unknown [Glycine max]	135	3e-29
ref XP_002310274.1 predicted protein [Populus trichocarpa] >gi ...	135	3e-29
gb ABR17414.1 unknown [Picea sitchensis]	135	3e-29
gb AAB97853.1 ferriprotein porphyrin-containing peroxidase [Str...	135	3e-29
ref XP_002322726.1 predicted protein [Populus trichocarpa] >gi ...	135	5e-29
gb ACI22425.1 pericarp peroxidase 3 [Litchi chinensis]	134	7e-29
ref XP_002304885.1 predicted protein [Populus trichocarpa] >gi ...	134	9e-29
gb ABR17480.1 unknown [Picea sitchensis]	134	9e-29
gb ABZ80408.1 class III peroxidase [Casuarina glauca]	134	9e-29
gb AAK52085.1 peroxidase [Nicotiana tabacum]	134	9e-29
ref XP_002455406.1 hypothetical protein SORBIDRAFT_03g010250 [S...	134	1e-28
ref XP_002455405.1 hypothetical protein SORBIDRAFT_03g010240 [S...	134	1e-28
gb ACG44598.1 peroxidase 72 precursor [Zea mays]	134	1e-28
ref NP_001136736.1 hypothetical protein LOC100216875 [Zea mays]...	134	1e-28
ref NP_195361.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	134	1e-28
gb ABR23055.1 basic peroxidase swpb5 [Ipomoea batatas]	133	1e-28
gb EAY85142.1 hypothetical protein OsI_06497 [Oryza sativa Indi...	133	1e-28
gb AAC49822.1 peroxidase [Oryza sativa Indica Group]	133	1e-28
gb ACU21377.1 unknown [Glycine max]	133	2e-28
ref NP_001148509.1 peroxidase 72 [Zea mays] >gi 195619908 gb AC...	132	3e-28
gb ABK26974.1 unknown [Picea sitchensis]	132	3e-28
gb AAF63025.1 AF244922_1 peroxidase prx13 precursor [Spinacia ol...	132	3e-28
gb AAM61616.1 putative peroxidase [Arabidopsis thaliana]	132	3e-28
ref NP_179407.1 peroxidase, putative [Arabidopsis thaliana] >gi ...	132	3e-28
emb CBI27500.1 unnamed protein product [Vitis vinifera]	132	3e-28
gb AAP42507.1 anionic peroxidase swpb2 [Ipomoea batatas]	132	3e-28
gb ABV26013.1 peroxidase [Musa acuminata]	132	4e-28
sp Q9LEH3.1 PER15_IPOBA RecName: Full=Peroxidase 15; Short=Prx15...	132	4e-28
ref XP_002300745.1 predicted protein [Populus trichocarpa] >gi ...	131	6e-28
gb ABC60345.1 putative peroxidase [Musa acuminata AAA Group]	131	6e-28

emb CAA66964.1	peroxidase [Arabidopsis thaliana] >gi 1429215 em...	131	6e-28
gb AAR15704.3	peroxidase [Brassica napus]	131	7e-28
gb AAM63684.1	peroxidase, putative [Arabidopsis thaliana]	131	7e-28
ref NP_175117.1	peroxidase, putative [Arabidopsis thaliana] >gi...	131	7e-28
ref NP_001050060.1	Os03g0339400 [Oryza sativa (japonica cultiva...	131	7e-28
sp Q4W1I8.1 PER1_ZINEL	RecName: Full=Basic peroxidase; AltName: ...	131	7e-28
sp Q4W1I9.1 PER2_ZINEL	RecName: Full=Basic peroxidase; AltName: ...	131	7e-28
gb AAF63026.1 AF244923_1	peroxidase prx14 precursor [Spinacia ol...	130	1e-27
ref NP_001046394.1	Os02g0237000 [Oryza sativa (japonica cultiva...	130	1e-27
dbj BAD27600.1	putative bacterial-induced peroxidase precursor ...	130	1e-27
ref NP_201440.1	peroxidase 72 (PER72) (P72) (PRXR8) [Arabidopsi...	130	1e-27
gb ABB45838.1	hypothetical protein [Thellungiella halophila]	130	2e-27
gb AAS00456.1	acid isoperoxidase [Brassica napus]	129	2e-27
emb CBI25854.1	unnamed protein product [Vitis vinifera]	129	3e-27
ref XP_002281048.1	PREDICTED: hypothetical protein [Vitis vinif...	129	3e-27
ref XP_002263033.1	PREDICTED: hypothetical protein [Vitis vinif...	129	4e-27
ref XP_002510443.1	Peroxidase 9 precursor, putative [Ricinus co...	129	4e-27
emb CBI15846.1	unnamed protein product [Vitis vinifera]	128	5e-27
ref XP_002457158.1	hypothetical protein SORBIDRAFT_03g002370 [S...	128	5e-27
ref XP_002455760.1	hypothetical protein SORBIDRAFT_03g024460 [S...	128	5e-27
ref XP_002438468.1	hypothetical protein SORBIDRAFT_10g020100 [S...	128	5e-27
gb ABI37011.1	peroxidase [Oryza sativa]	128	6e-27
emb CBI16459.1	unnamed protein product [Vitis vinifera]	127	8e-27
ref XP_002285642.1	PREDICTED: hypothetical protein [Vitis vinif...	127	8e-27
gb EAY73397.1	hypothetical protein OsI_01277 [Oryza sativa Indi...	127	8e-27
ref NP_001042657.1	Os01g0263300 [Oryza sativa (japonica cultiva...	127	8e-27
emb CBI16466.1	unnamed protein product [Vitis vinifera]	127	1e-26
ref XP_002463385.1	hypothetical protein SORBIDRAFT_02g042880 [S...	127	1e-26
ref XP_002285649.1	PREDICTED: hypothetical protein [Vitis vinif...	127	1e-26
gb ABI97032.1	peroxidase [Solanum tuberosum]	127	1e-26
gb AAU04440.2	secreted peroxidase [Phelipanche ramosa]	127	1e-26
dbj BAG55221.1	peroxidase 2 [Sesbania rostrata]	127	1e-26
ref NP_001151639.1	peroxidase 68 [Zea mays] >gi 195648284 gb AC...	127	1e-26
gb EAY74439.1	hypothetical protein OsI_02330 [Oryza sativa Indi...	127	1e-26
ref XP_002269425.1	PREDICTED: hypothetical protein [Vitis vinif...	126	2e-26
ref NP_001043276.1	Os01g0543100 [Oryza sativa (japonica cultiva...	126	2e-26
dbj BAB89258.1	putative peroxidase ATP6a [Oryza sativa Japonica...	126	2e-26
dbj BAA94962.1	peroxidase [Asparagus officinalis]	125	3e-26
ref NP_179406.1	peroxidase, putative [Arabidopsis thaliana] >gi...	125	5e-26
emb CBI27497.1	unnamed protein product [Vitis vinifera]	124	7e-26
gb AAM28296.1	peroxidase [Ananas comosus]	124	7e-26
gb ABD47725.1	peroxidase [Eucalyptus globulus subsp. globulus]	124	7e-26
gb ACF88307.1	unknown [Zea mays]	124	9e-26
gb EAZ22365.1	hypothetical protein OsJ_06023 [Oryza sativa Japo...	123	2e-25
ref NP_564948.1	peroxidase, putative [Arabidopsis thaliana] >gi...	122	3e-25
emb CAH69540.1	putative peroxidase [Zinnia elegans]	122	4e-25
ref XP_002312356.1	predicted protein [Populus trichocarpa] >gi ...	121	6e-25
dbj BAD43011.1	peroxidase ATP23a [Arabidopsis thaliana]	121	6e-25
emb CAH69535.1	putative peroxidase [Zinnia elegans]	121	8e-25

gb AA013837.1 AF403735_1	extensin peroxidase [Lupinus albus]	121	8e-25
ref XP_002457609.1	hypothetical protein SORBIDRAFT_03g010230 [S...	120	1e-24
emb CAB65334.1	SPI2 protein [Picea abies]	120	1e-24
gb ACF22712.1	peroxidase precursor [Brachypodium distachyon]	120	2e-24
ref XP_002315983.1	predicted protein [Populus trichocarpa] >gi ...	120	2e-24
emb CAM31942.1	hypothetical protein [Lolium perenne]	120	2e-24
ref XP_002438233.1	hypothetical protein SORBIDRAFT_10g010040 [S...	119	2e-24
ref XP_002451847.1	hypothetical protein SORBIDRAFT_04g008600 [S...	119	2e-24
ref NP_190668.2	electron carrier/ heme binding / peroxidase [Ar...	119	3e-24
emb CAB62621.1	peroxidase-like protein [Arabidopsis thaliana] >...	119	3e-24
gb EAZ05138.1	hypothetical protein OsI_27331 [Oryza sativa Indi...	119	3e-24
ref NP_001060632.1	Os07g0677600 [Oryza sativa (japonica cultiva...	119	3e-24
emb CBI27438.1	unnamed protein product [Vitis vinifera]	119	4e-24
ref XP_002270660.1	PREDICTED: hypothetical protein [Vitis vinif...	119	4e-24
emb CAN65777.1	hypothetical protein [Vitis vinifera]	119	4e-24
gb EAY89162.1	hypothetical protein OsI_10658 [Oryza sativa Indi...	118	5e-24
ref NP_001042655.1	Os01g0263000 [Oryza sativa (japonica cultiva...	118	5e-24
ref NP_001049480.1	Os03g0234500 [Oryza sativa (japonica cultiva...	118	5e-24
ref XP_002509732.1	Lignin-forming anionic peroxidase precursor,...	118	5e-24
ref XP_002509731.1	Lignin-forming anionic peroxidase precursor,...	118	5e-24
gb EEC70836.1	hypothetical protein OsI_02331 [Oryza sativa Indi...	118	6e-24
emb CAH55694.1	putative peroxidase [Lolium perenne]	117	8e-24
emb CAH55692.1	putative peroxidase [Festuca pratensis]	117	8e-24
ref NP_001057377.1	Os06g0274800 [Oryza sativa (japonica cultiva...	117	1e-23
ref XP_002509735.1	Lignin-forming anionic peroxidase precursor,...	117	1e-23
gb ACF08088.1	class III peroxidase [Aegilops ventricosa]	116	2e-23
gb ACG43658.1	hypothetical protein [Zea mays]	116	2e-23
gb ACF80021.1	unknown [Zea mays]	116	2e-23
ref NP_001130123.1	hypothetical protein LOC100191217 [Zea mays]...	116	2e-23
ref XP_002304020.1	predicted protein [Populus trichocarpa] >gi ...	115	3e-23
ref XP_002306459.1	predicted protein [Populus trichocarpa] >gi ...	115	4e-23
gb ABF95842.1	Peroxidase 2 precursor, putative, expressed [Oryz...	115	4e-23
emb CAA59486.1	peroxidase [Triticum aestivum]	115	5e-23
dbj BAA01992.1	peroxidase [Nicotiana tabacum]	114	9e-23
ref XP_002529736.1	Peroxidase 27 precursor, putative [Ricinus c...	114	1e-22
gb ACJ84393.1	unknown [Medicago truncatula]	114	1e-22
gb ACU23010.1	unknown [Glycine max]	113	2e-22
ref XP_001751508.1	predicted protein [Physcomitrella patens sub...	112	4e-22
gb AA013839.1 AF405327_1	peroxidase 1 [Lupinus albus]	112	5e-22
gb AAL58444.1 AF455807_1	anionic peroxidase [Nicotiana tomentososi...	112	5e-22
ref XP_002464560.1	hypothetical protein SORBIDRAFT_01g020830 [S...	111	6e-22
gb ACF70704.1	root peroxidase [Triticum aestivum]	111	6e-22
dbj BAD97439.1	peroxidase [Pisum sativum]	111	6e-22
gb AAQ67366.1	POD9 precursor [Gossypium hirsutum]	111	6e-22
ref XP_002309830.1	predicted protein [Populus trichocarpa] >gi ...	111	8e-22
gb EEE59027.1	hypothetical protein OsJ_10774 [Oryza sativa Japo...	111	8e-22
gb AAA34101.1	peroxidase [Nicotiana tabacum]	110	1e-21
sp P11965.1 PERX_TOBAC	RecName: Full=Lignin-forming anionic pero...	110	1e-21
emb CBI28955.1	unnamed protein product [Vitis vinifera]	110	1e-21

ref XP_002274157.1	PREDICTED: hypothetical protein [Vitis vinif...	110	1e-21
sp P15003.1 PER1_SOLLC	RecName: Full=Suberization-associated ani...	110	1e-21
gb EAZ22371.1	hypothetical protein OsJ_06029 [Oryza sativa Japo...	110	2e-21
gb ABK22032.1	unknown [Picea sitchensis]	109	2e-21
ref XP_001783974.1	predicted protein [Physcomitrella patens sub...	108	4e-21
gb EAZ37178.1	hypothetical protein OsJ_21519 [Oryza sativa Japo...	108	4e-21
emb CBI28956.1	unnamed protein product [Vitis vinifera]	108	5e-21
gb ACJ11761.1	class III peroxidase [Gossypium hirsutum]	108	5e-21
dbj BAF08306.2	Os02g0236600 [Oryza sativa Japonica Group]	108	5e-21
gb EAZ01154.1	hypothetical protein OsI_23183 [Oryza sativa Indi...	108	5e-21
tpe CAH69331.1	TPA: class III peroxidase 89 precursor [Oryza sa...	108	5e-21
ref NP_001058379.1	Os06g0681600 [Oryza sativa (japonica cultiva...	108	5e-21
dbj BAD45811.1	putative bacterial-induced peroxidase precursor ...	108	5e-21
ref NP_001057744.1	Os06g0521200 [Oryza sativa (japonica cultiva...	108	5e-21
gb EAZ01158.1	hypothetical protein OsI_23186 [Oryza sativa Indi...	108	7e-21
gb ACJ11766.1	class III peroxidase [Gossypium hirsutum]	108	7e-21
ref XP_002443277.1	hypothetical protein SORBIDRAFT_08g016840 [S...	107	1e-20
emb CAA50597.1	peroxidase [Solanum lycopersicum]	107	1e-20
emb CAB67121.1	peroxidase [Solanum lycopersicum]	107	1e-20
ref XP_002465968.1	hypothetical protein SORBIDRAFT_01g049140 [S...	107	1e-20
gb ACU20287.1	unknown [Glycine max]	107	1e-20
gb EEE65802.1	hypothetical protein OsJ_21515 [Oryza sativa Japo...	107	1e-20
sp P12437.2 PERX_SOLTU	RecName: Full=Suberization-associated ani...	107	1e-20
dbj BAD98313.2	peroxidase [Nicotiana tabacum]	107	1e-20
dbj BAD98314.1	peroxidase [Nicotiana tabacum]	107	1e-20
ref NP_001057745.1	Os06g0521400 [Oryza sativa (japonica cultiva...	107	1e-20
sp P15004.1 PER2_SOLLC	RecName: Full=Suberization-associated ani...	107	1e-20
gb AAA33837.1	anionic peroxidase [Solanum tuberosum] >gi 228610...	107	1e-20
ref XP_002336172.1	predicted protein [Populus trichocarpa] >gi ...	107	1e-20
ref NP_001136722.1	hypothetical protein LOC100216859 [Zea mays]...	107	1e-20
ref XP_002516846.1	Peroxidase 24 precursor, putative [Ricinus c...	106	2e-20
ref NP_001140982.1	hypothetical protein LOC100273061 [Zea mays]...	106	2e-20
gb ABU63712.1	lignin peroxidase [Garcinia mangostana]	106	2e-20
emb CBI25927.1	unnamed protein product [Vitis vinifera]	106	3e-20

>gb|ACU17608.1| unknown [Glycine max]

Length = 320

Score = 249 bits (635), Expect = 2e-63

Identities = 120/124 (96%), Positives = 121/124 (97%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCTNFRARIYNETNI TAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV

Sbjct: 197 QARCTNFRARIYNETNIGTAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

QKKG LHSDQQLFNGGSTDSIVRGYSTNPGTF SDFAAAMIKMGDISPLTGSNGE+RKNC

Sbjct: 257 QKKGFLHSDQQLFNGGSTDSIVRGYSTNPGTFPSDFAAAMIKMGDISPLTGSNGEVRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 213 bits (543), Expect = 1e-52
Identities = 118/165 (71%), Positives = 120/165 (72%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI
Sbjct: 70 VNGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ G PTWNVKLG
Sbjct: 130 RDSVQILGG-----PTWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG
Sbjct: 147 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 191

Score = 145 bits (365), Expect = 5e-32
Identities = 70/71 (98%), Positives = 70/71 (98%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKS VQSAISKETRMGASL
Sbjct: 1 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKS VQSAISKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>gb|ACU17865.1| unknown [Glycine max]
Length = 320

Score = 242 bits (618), Expect = 2e-61
Identities = 117/124 (94%), Positives = 120/124 (96%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRARIYNE+NI+TAFAR RQQSCPRTSGSGDNNLA LDLQTPT FDNYYFKNLV
Sbjct: 197 QARCTNFRARIYNESNIDTAFARARQQSCPRTSGSGDNNLATLDLQPTFEFDNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKGLLHSDQQLFNGGSTDSIVRGYSTNP +FSSDFAAAMIKMGDISPLTGSNGEIRKNC
Sbjct: 257 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPSSFSSDFAAAMIKMGDISPLTGSNGEIRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 208 bits (530), Expect = 4e-51
Identities = 114/165 (69%), Positives = 119/165 (72%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARG+EVIDNIKSAVEK CPGVVSCADILAI
Sbjct: 70 VNGCDGSILLDDTSSFTGEKNANPNRNSARGYEVIDNIKSAVEKACPGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ GGP+WNVK+G
Sbjct: 130 RDSVQIL-----GGPSWNVKVG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANNGIP PTSNLNQLISRFSALGLSTKDLVALSG
Sbjct: 147 RRDARTASQSAANNGIPPPTSNLNQLISRFSALGLSTKDLVALSG 191

Score = 138 bits (347), Expect = 6e-30
Identities = 68/71 (95%), Positives = 69/71 (97%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASL 750
MASFCSRLTICLALFVLI GSANAQLSTNFYYHSCP NFLS+VKSTVQSAISKETRMGASL
Sbjct: 1 MASFCSRLTICLALFVLILGSANAQLSTNFYYHSCP NFLFSTVKSTVQSAISKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LR FFHDCFVN
Sbjct: 61 LRPFFHDCFVN 71

>gb|AAP76387.1| class III peroxidase [Gossypium hirsutum]
Length = 330

Score = 218 bits (556), Expect = 4e-54
Identities = 100/124 (80%), Positives = 116/124 (93%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT+FRARIYNE+NI+ +FA+TRQ++CPRT+GSGDNNLAPLD+QTPTSFDN YFKNL+
Sbjct: 207 QARCTSFARIYNESNIDASFAQTRQRNCPRTTGSGDNNLAPLDIQTPTSFDNNYFKNLI 266

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQQLFNGGSTDSIVRGY +P +F+SDF AAMIKMGDISPLTGS GEIRKNC

Sbjct: 267 SQRGLLHSDQQLFNGGSTDSIVRGYGNPSSFNDFVAAMIKMGDISPLTGSRGEIRKNC 326

Query: 2167 RRIN 2178

RR+N

Sbjct: 327 RRVN 330

Score = 196 bits (499), Expect = 1e-47
Identities = 107/169 (63%), Positives = 117/169 (69%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNANPNRNS+RGF+V+DNIKSAVE VCPGVVSCADILAIAA

Sbjct: 80 VNGCDGSVLLDDTSSFTGEKNANPNRNSRGRFDVVDNIKSAVENVCPGVVSCADILAIAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W VKLG

Sbjct: 140 RDSVEI-----LGGPKWAVKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDAR+ASQSAANNGIP PTSNLN+L SRF+ALGLST+DLVALSG I

Sbjct: 157 RRDARSASQSAANNGIPPPTSNLNRLTSRFNALGLSTRDLVALSGAHTI 205

Score = 100 bits (248), Expect = 2e-18
Identities = 51/75 (68%), Positives = 58/75 (77%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRM 738
+K+ AS S+ + L L V + GS NAQLSTNFY SCPNL S+VKSTV SAI+KE RM

Sbjct: 7 TKMGSASSFSKFCLTLLLLVDVLGSTNAQLSTNFYSKSCPNLLSTVKSTVTSAINKEARM 66

Query: 739 GASLLRLLFFHDCFVN 783

GASLLRLLFFHDCFVN

Sbjct: 67 GASLLRLLFFHDCFVN 81

>gb|AB077632.1| peroxidase [Medicago truncatula]
Length = 322

Score = 217 bits (552), Expect = 1e-53
Identities = 104/124 (83%), Positives = 112/124 (90%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNETNI A A TRQ +CP+ SGSGDNNLAPLDLQTP+SFDN YFKNLV

Sbjct: 199 QARCTNFRARIYNETNINAAXASTRQSNCPKASGSGDNNLAPLDLQTPSSFDNYYFKNLV 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGBISPLTGSNGEIRKNC 2166
Q KGLLHSDQQLFNGGST+SIV GYST+P +FSSDFAAAMIKMGI PLTGSNGEIRKNC

Sbjct: 259 QNKGLLHSDQQLFNGGSTNSIVSGYSTSPSSFSSDFAAAMIKMGNIKPLTGSNGEIRKNC 318

Query: 2167 RRIN 2178

R+ N

Sbjct: 319 RKTN 322

Score = 188 bits (478), Expect = 4e-45

Identities = 105/169 (62%), Positives = 112/169 (66%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNANPNRNSARGF+VIDNIK+AVE VCPGVVSCADILAI

Sbjct: 72 VNGCDGSILLDDTSSFTGEKNANPNRNSARGFDVIDNIKTAVENVCPGVVSCADILAI 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
DSV I+ G PTWNVKLG

Sbjct: 132 ADSVAILGG-----PTWNVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDA+TASQSAAN IPAPTSNLN L S FSA+GLS+KDLV LSG I

Sbjct: 149 RRDAKTASQSAANTAIPAPTSNLNTLTSMFSAVGLSSKDLVTLGAHTI 197

Score = 100 bits (249), Expect = 1e-18

Identities = 52/68 (76%), Positives = 58/68 (85%), Gaps = 1/68 (1%)

Frame = +1

Query: 583 CSRLT-ICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
CSRLT I L L VLI GSANAQLSTNFY +CP L ++VKST+Q+AISKE RMGAS+LRL

Sbjct: 6 CSRLTMISLVLSVLIIGSANAQLSTNFYSKTCPKLSTTVKSTLQTAISKEARMGASILRL 65

Query: 760 FFHDCFVN 783

FFHDCFVN

Sbjct: 66 FFHDCFVN 73

>dbj|BAA82306.1| peroxidase [Nicotiana tabacum]

Length = 321

Score = 212 bits (540), Expect = 3e-52
Identities = 102/125 (81%), Positives = 110/125 (88%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT+FRARIYNETN ++ +FARTRQ +CPR+SGSGDNNLAPLDLQTP FDN YFKNL
Sbjct: 197 QARCTSFARIYNETNLDASFARTRQSNCPRSSGSGDNNLAPLDLQTPNKFDNYYFKNL 256

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V KKGLLHSDQQLFNGGS DSIV YS NP +FSSDF AMIKMGDI PLTGSNGEIRKN
Sbjct: 257 VDKKGLLHSDQQLFNGGSADSI VTSYNNPSSFSDFVTAMIKMGDIRPLTGSNGEIRKN 316

Query: 2164 CRRIN 2178
CRR+N
Sbjct: 317 CRRLN 321

Score = 187 bits (476), Expect = 7e-45
Identities = 105/169 (62%), Positives = 113/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEK A PN NSARGFEVIDNIKSAVEKVCPGVVSCADILA+ A
Sbjct: 70 VNGCDGSLLDDTSSFTGEKRAAPNVNSARGFEVIDNIKSAVEKVCPGVVSCADILAVTA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP WNVKLG
Sbjct: 130 RDSVVI-----LGGPNWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTASQSAAN+GIP TSNLN+LIS FSA+GLSTKD+VALSG I
Sbjct: 147 RRDSRTASQSAANS GIPPATSNLNLRISSFSAVGLSTKDMVALSGAHTI 195

Score = 91.3 bits (225), Expect = 8e-16
Identities = 46/71 (64%), Positives = 53/71 (74%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS + L L+ GS++AQLST FY SCP L+ +VKS VQSAI+KETRMGASL
Sbjct: 1 MASLKINAIVLFILVSLIGSSAQLSTGFYSKSCP KLYQTVKSAVQSAINKETRMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>ref|XP_002278996.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 321

Score = 211 bits (536), Expect = 7e-52
Identities = 98/124 (79%), Positives = 112/124 (90%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI+ +FA+TRQ +CPR SGSGDNNLAPLDLQTPT+F+N Y+KNL+
Sbjct: 198 QARCTSFARIYNETNIDNSFAKTRQSNCPRASGSGDNNLAPLDLQTPTAFENNYKNLI 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQLFNGGSTDSIVR YS + F++ F A MIKMGDISPLTGSNGEIRKNC
Sbjct: 258 KKKGLLHSDQQLFNGGSTDSIVRKYSNSRSNFNAHFVAGMIKMGDISPLTGSNGEIRKNC 317

Query: 2167 RRIN 2178
RR+N
Sbjct: 318 RRVN 321

Score = 184 bits (466), Expect = 1e-43
Identities = 100/169 (59%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGS+LLDDTSSF GEKNA PN NS RGF+V+D+IKS VE CPGVVSCAD+LAI 1330
Sbjct: 71 VNGCDGSVLLDDTSSFIGEKNAAPNANSVRGFDVDDIKSKVETACPGVVSCADVLAI 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGP+WNVKLG
Sbjct: 131 RDSVVIL-----GGPSWNVKLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF ALGLST+DLVAL+G+ I
Sbjct: 148 RRDARTASQAAANNSIPPPTSNLNQLISRFAQALGLSTRDLVALAGSHTI 196

Score = 90.1 bits (222), Expect = 2e-15
Identities = 46/72 (63%), Positives = 56/72 (77%), Gaps = 1/72 (1%)
Frame = +1

Query: 571 MASFCSRLTIC-LALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
MAS S + I +AL +L GS+ AQLST++Y SCP LF +VKS V+SA++KE RMGAS
Sbjct: 1 MASPSSYMAIVTMALLILFLGSSTAQLSTDYYSQSCP KLFPTVKS AVKSAVAKEARMGAS 60

Query: 748 LLRLFFHDCFVN 783

LLRLFFHDCFVN
Sbjct: 61 LLRLFFHDCFVN 72

>gb|AAx44001.2| putative secretory peroxidase [Catharanthus roseus]
Length = 318

Score = 209 bits (533), Expect = 2e-51
Identities = 101/125 (80%), Positives = 113/125 (90%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRARIYNETN ++ A A+TR+ +CPR SGS DNNLAPLDLQTP +FDN Y+KNL
Sbjct: 194 QARCTNFRARIYNETNNLDAALAQTRRSNCPRPSGSRDNNLAPLDLQTPRAFDNNYYKNL 253

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V ++GLLHSDQQLFNGGSTDSIVR YS NP +F+SDFAAAMIKMGDISPLTGSNG+IRKN
Sbjct: 254 VNRRGLLHSDQQLFNGGSTDSIVRSYSGNPASFASDFAAAMIKMGDISPLTGSNGQIRKN 313

Query: 2164 CRRIN 2178
CRRIN
Sbjct: 314 CRRIN 318

Score = 191 bits (484), Expect = 8e-46
Identities = 106/169 (62%), Positives = 114/169 (67%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEK A PN NSARGFEV+DNIKSAVE VCPGVVSCADILAIAA
Sbjct: 67 VNGCDGSILLDDTSSFTGEKRAAPNFNSARGFEVVDNIKSAVENVCPGVVSCADILAIAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSVQI+ GGP+WNVKLG
Sbjct: 127 RDSVQIL-----GGPSWNVKLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA TASQ+AANN IP PTSNLN L+SRF+ALGLST DLVALSG+ I
Sbjct: 144 RRDATTASQAAANNSIPPPTSNLNALVSRFNLGLSTNDLVALSGSHTI 192

Score = 85.1 bits (209), Expect = 6e-14
Identities = 42/61 (68%), Positives = 52/61 (85%), Gaps = 1/61 (1%)
Frame = +1

Query: 604 LALFVL-IWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
L +F+L + GS++AQLST++Y SCPN+F++VKS V SAI KE RMGASLLRLFFHDCFV

Sbjct: 8 LGIFLLFLIGSSSAQLSTDYYSKSCPNTVKSQVHSAILKEARMGASLLRLFFHDCFV 67

Query: 781 N 783
N

Sbjct: 68 N 68

>gb|AAP42508.1| anionic peroxidase swpb3 [Ipomoea batatas]
Length = 320

Score = 209 bits (533), Expect = 2e-51
Identities = 100/124 (80%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNE+NI+++FA++R+ +CPR SGSGDNNLAPLDLQTP FDN Y+ NLV
Sbjct: 197 QARCTNFRARIYNESNIDSSFAQSRKGNCPRASGSGDNNLAPLDLQTPIKFDNNYYVNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS VRGYSTNP F SDFAAAMIKMGGDI PLTG+NGEIRKNC
Sbjct: 257 NKKGLLHSDQQLFNGVSTDSTVRGYSTNPSKFKSDFAAAMIKMGGDIKPLTGNGEIRKNC 316

Query: 2167 RRIN 2178
RR N
Sbjct: 317 RRRN 320

Score = 184 bits (467), Expect = 7e-44
Identities = 103/169 (60%), Positives = 113/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEK A PN SARGFEVID IKSAREKVCPCGVVSCADILAI+
Sbjct: 70 VNGCDGSILLDDTSSFTGEKRAAPNFQSARGFEVIDQIKSAVEKVCPCGVVSCADILAI 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP+WNVKLG
Sbjct: 130 RDS-----TVTLGGPSWNVKLG 146

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IPAPTSNLN+LIS FSA+GLST D+V LSG+ I
Sbjct: 147 RRDARTASQAAANSIPAPTSNLNRLISSFSAVGLSTNDMVVLGSHTI 195

Score = 82.8 bits (203), Expect = 3e-13
Identities = 42/71 (59%), Positives = 48/71 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MA LT L +++ G +AQLS FY SCP LF +V S V+SAI KE RMGASL
Sbjct: 1 MAVSVKALTAVLLCVLVLVGGCSAQLSPGFYSKSCPQLFQTVNSVVRSAIQKEARMGASL 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 61 LRLFFHDCFVN 71

>gb|ABR23054.1| basic peroxidase swpb4 [Ipomoea batatas]
Length = 320

Score = 209 bits (532), Expect = 2e-51
Identities = 100/124 (80%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRARIYNE+NI+++FA++R+ +CPR SGSGDNNLAPLDLQTP FDN Y+ NLV
Sbjct: 197 QARCTNFRARIYNESNIDSSFAQSRKGNCPRASGSGDNNLAPLDLQTPIKFDNYYVNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS VRGYSTNP F SDFAAAMIKMGDI PLTG+NGEIRKNC
Sbjct: 257 NKKGLLHSDQQLFNGVSTDSTVRGYSTNPSKFRSDFAAAMIKMGIKPLTGNGEIRKNC 316

Query: 2167 RRIN 2178
RR N
Sbjct: 317 RRRN 320

Score = 182 bits (462), Expect = 3e-43
Identities = 102/169 (60%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGEK A PN SARGFEVID IKSAREKVCPGVVSCADILAIA+
Sbjct: 70 VNGCDGSILLDDTSSFTGEKRAAPNFQSARGFEVIDQIKSAVEKVCPGVVSCADILAIAS 129

Query: 1331 RDSVQIVSGGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP+WNVKLG
Sbjct: 130 RDS-----TVTLGGPSWNVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRDAR ASQ+AANN IPAPTSNLN+LIS FSA+GLST D+V LSG+ I
Sbjct: 147 RRDARAASQAAANNSIPAPTSNLNRLISSFSAVGLSTNDMVVLSGSHTI 195

Score = 80.5 bits (197), Expect = 1e-12
Identities = 40/62 (64%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+ L + VL+ G +AQLS FY SCP LF +V S V+SAI KE RMGASLLRLLFFHDCF
Sbjct: 11 VLLCVLVLV-GGCSAQLSPGFYSKSCPRLFQTVNSVVRSAIQKEARMGASLLRLLFFHDCF 69

Query: 778 VN 783
VN
Sbjct: 70 VN 71

>gb|ACU23245.1| unknown [Glycine max]
Length = 326

Score = 208 bits (530), Expect = 4e-51
Identities = 95/124 (76%), Positives = 111/124 (89%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FRARIYNE+NI+++FAR RQ CPRTSGSGDNNLAP+D TPT FDN+YFKNL+
Sbjct: 203 QARCTTFRARIYNESNIDSSFARMRQSRCPRTSGSGDNNLAPIDFATPTFFDNHYFKNLI 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
QKKG +HSDQ+LFNGGSTDS+V YSTNP +F +DF+AAMI+MGDISPLTGS GEIR+NC
Sbjct: 263 QKKGFIHSDQQLFNGGSTDSLVTYSTNPASFFADFSAAIRMGDISPLTGSRGIRENC 322

Query: 2167 RRIN 2178
RR+N
Sbjct: 323 RRVN 326

Score = 200 bits (509), Expect = 1e-48
Identities = 111/165 (67%), Positives = 116/165 (70%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTSSFTGEKNA PNRNSARGFEVID IKSAREKVCPGVVSCADILAI
Sbjct: 76 VNGCDGSILLDDTSSFTGEKNAGPNRNSARGFEVIDQIKSAVEKVCPGVVSCADILAI 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I L GPTW+VKLG
Sbjct: 136 RDSVEI-----LRGPTWDVKLG 152

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+RTASQSAANNIP PTSNLNLISRF+ LGLSTKDLVALSG
Sbjct: 153 RRDRTASQSAANNIPRPTSNLNLISRFNTLGLSTKDLVALSG 197

Score = 100 bits (248), Expect = 2e-18
Identities = 53/77 (68%), Positives = 57/77 (74%), Gaps = 6/77 (7%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS-----ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKET 732
MAS CS I LAL VL+ G+ AN L TNFYY SCP LF +VK TV+SAISKET
Sbjct: 1 MASSCSSSMITLALLVLVLGTNTSSANANPTLHTNFYSSCPKLFDTVKRTVESAIKET 60

Query: 733 RMGASLLRLFFHDCFVN 783
RMGASLLRLFFHDCFVN
Sbjct: 61 RMGASLLRLFFHDCFVN 77

>gb|ACM47317.1| peroxidase [Capsicum annuum]
Length = 324

Score = 205 bits (521), Expect = 4e-50
Identities = 100/125 (80%), Positives = 108/125 (86%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETN-IETAFARTQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT+FRARIYNETN I+++FA TRQ++CPR SGSGDNNLAPLDLQTPT FDN YFKNL
Sbjct: 200 QARCTSFARIYNETNNIDSSFATTRQRNCPRNSGSGDNNLAPLDLQTPTKFDNNYFKNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
V K+GLLHSDQQLFNGGS DSIV YS NP +FSSDF AMIKMGD PLTGSNGEIRKN
Sbjct: 260 VSKRGLLHSDQQLFNGGSADSIVTSYSNNPSSFSSDFVTAMIKMGDNRP LTGSNGEIRKN 319

Query: 2164 CRRIN 2178
CR N
Sbjct: 320 CRTRN 324

Score = 184 bits (468), Expect = 6e-44
Identities = 104/169 (61%), Positives = 109/169 (64%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEK A PN NS RGFEVIDNIKSAVEK CPGVVSCADILAI A
Sbjct: 73 VNGCDGSLLDDTSSFTGEKRAAPNVNSVRGFEVIDNIKSAVEKACPGVVSCADILAITA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP WNVKLG
Sbjct: 133 RDSVVI-----LGGPNWNVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ AAN+ IP PTSNLNQLIS FSA+GLST D+VALSG I
Sbjct: 150 RRDARTASQGAANSSIPPTSNLNQLISSFSAVGLSTTDMVALSGAHTI 198

Score = 89.4 bits (220), Expect = 3e-15
Identities = 44/60 (73%), Positives = 51/60 (85%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
L + L+ S++AQLSTNFY SCP LF +VKSTVQSAI++ETRMGASLLRLFFHDCFVN
Sbjct: 15 LVVVNLLIVSSSAQLSTNFYSKCPKLFQTVKSTVQSAINRETRMGASLLRLFFHDCFVN 74

>ref|XP_002328991.1| predicted protein [Populus trichocarpa]
gb|EEE77576.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 204 bits (520), Expect = 5e-50
Identities = 96/124 (77%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRARIYNET I+++ A+TR+ +CPRTSGSGDNNLAPLDLQTPT F+N Y+KNL+
Sbjct: 199 QARCTNFRARIYNETTIDSSLAQTRRSNCPRTSGSGDNNLAPLDLQTPTRFENNYKNI 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQQLFNGGSTDSIV YS+N TF SDF A MIKMGDI PLTGS GEIR NC
Sbjct: 259 NRRGLLHSDQQLFNGGSTDSIVSTYSSNENTFRSDFVAGMIKMGDIRPLTGSRGEIRNNC 318

Query: 2167 RRIN 2178
RRIN
Sbjct: 319 RRIN 322

Score = 194 bits (493), Expect = 7e-47
Identities = 107/169 (63%), Positives = 116/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGEKNA PN+NSARGFEVIDNIKSAVEK CPGVVSCADILAIAA
Sbjct: 72 VNGCDGSLLDDTSSFTGEKNAAPKNNSARGFEVIDNIKSAVEKACPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP W+VKLG
Sbjct: 132 RDSTVI-----LGGPEWDVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF+ALGLST+D+VALSG+ I
Sbjct: 149 RRDARTASQAAANNSIPRPTSNLNLISRFNALGLSTRDMVALSGSHTI 197

Score = 87.8 bits (216), Expect = 9e-15
Identities = 43/70 (61%), Positives = 52/70 (74%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
+SF + L +L GS+NAQLS +FY SCP+L S+VK VQSAI+KE RMGAS+L
Sbjct: 4 SSFSKAIVTLAILVMSMGSSNAQLSIDFYKSCPHLLSTVKPVVQSAINKEARMGASIL 63

Query: 754 RLFFHDCFVN 783
RLFFHDCFVN
Sbjct: 64 RLFFHDCFVN 73

>ref|XP_002269918.1| PREDICTED: hypothetical protein [Vitis vinifera]
sp|A7NY33.1|PER4_VITVI RecName: Full=Peroxidase 4; Flags: Precursor
emb|CBI15844.1| unnamed protein product [Vitis vinifera]
Length = 321

Score = 204 bits (520), Expect = 5e-50
Identities = 94/124 (75%), Positives = 110/124 (88%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FRARIYNETNI+++FA+TRQ SCP SGSGDNNLAPLDLQTPT+FDNYY+KNL+
Sbjct: 198 QARCTSFARIYNETNIDSSFAKTRQASCPSASGSGDNNLAPLDLQTPTTFDNYYYKNLI 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L+NGGSTDS V+ Y NP TF+SDF A MIKMGGDI+PLTGS GEIRK+C
Sbjct: 258 NQKGLLHSDQVLYNGGSTDSTVKTYVNNPKTFTSDFVAGMIKMGDITPLTGSEGEIRKSC 317

Query: 2167 RRIN 2178
++N
Sbjct: 318 GKVN 321

Score = 165 bits (417), Expect = 5e-38
Identities = 92/169 (54%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD S+LLDDTSSFTGE+ A PN+NS RG VIDNIKS VE VCPGVVSCADI+AIAA
Sbjct: 71 VNGCDASVLLDDTSSFTGEQTAVPNKNSIRGLNVIDNIKSQVESVCPGVVSCADIIAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG
Sbjct: 131 RDSVVI-----LGGPDWDVKLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD++TAS S ANN IP PTS+L+ LIS+F A GLST+D+VALSG I
Sbjct: 148 RRDSKTASLSGANNIPPTSSLSNLISKFQAQGLSTRDMVALSGAHTI 196

Score = 90.5 bits (223), Expect = 1e-15
Identities = 44/70 (62%), Positives = 54/70 (77%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLL 753
+S S + + L + L GS++AQLSTNFY +CP +F +VKS VQSA+SKE RMGASLL
Sbjct: 3 SSSFSIVVVALGVLALFAGSSSAQLSTNFYSKTCPKVFDTVKSGVQSAVSKERRMGASLL 62

Query: 754 RLFFHDCFVN 783
RLFFHDCFVN
Sbjct: 63 RLFFHDCFVN 72

>emb|CAD67479.1| peroxidase [Asparagus officinalis]
Length = 320

Score = 203 bits (516), Expect = 2e-49
Identities = 95/124 (76%), Positives = 109/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA +YN+T+I+ FA+TRQ +CP TSGSGDNNLAPLDLQTP +FDN YFKNLV
Sbjct: 197 QARCTNFRAHVYNDTIDATFAKTRQSNCPSTSGSGDNNLAPLDLQTPVAFDNYYFKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQ+F+GGST+S V YST+P T+SSDF AAMIKMGDISPLTG +GEIRKNC
Sbjct: 257 SKKGLLHSDQQVFSGGSTNSQVSTYSTSPSTWSSDFVAAAMIKMGDISPLTGKSGEIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKTN 320

Score = 169 bits (427), Expect = 3e-39
Identities = 92/169 (54%), Positives = 107/169 (63%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDTSSFTGEKNA PN+ S RGF+VID IK+AVE+ CPGVVSCADILA+ A
Sbjct: 70 VNGCDGSLLDDTSSFTGEKNAIPNKGSVRGFDVIDKIKTAVEQACPGVVSCADILAVTA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV ++ G PTWNVKLG
Sbjct: 130 RDSVLLGG-----PTWNVKLG 146

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+RTASQS ANN IP PTS+L+ LIS+FSA GLS K++VAL G I
Sbjct: 147 RRDSRTASQSGANNIPPTSSLSNLISKFSAQGLSAKEMVALVGAHTI 195

Score = 80.1 bits (196), Expect = 2e-12
Identities = 42/73 (57%), Positives = 52/73 (71%)
Frame = +1

Query: 565 LTMASFC SRLTICLALFVLIWGSANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGA 744
+ +SF S I L + + +++AQL+ NFY SCP LF ++KS VQSAIS E RMGA
Sbjct: 1 MASSSFKSLAPISLVSYV--RASSAQLTPNFYSSSCTLPFTIKSVVQSAISSEKRMGA 58

Query: 745 SLLRLFFHDCFVN 783
SLLRLFFHDCFVN
Sbjct: 59 SLLRLFFHDCFVN 71

>ref|NP_196153.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9FLC0.1|PER52_ATH RecName: Full=Peroxidase 52; Short=Atperox P52; AltName: Full=ATP49;
Flags: Precursor
dbj|BAB09977.1| peroxidase [Arabidopsis thaliana]
gb|AAL38746.1| putative peroxidase [Arabidopsis thaliana]
Length = 324

Score = 202 bits (513), Expect = 3e-49
Identities = 97/124 (78%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFRARIYNETNI AFA TRQ++CPR SGSGD NLAPLD+ T SFDN YFKNL+
Sbjct: 201 QSRCTNFRARIYNETNINAAFATTRQRTCPRASGSGDGNLAPLDVTTAASFDNYYFKNLM 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNGGSTDSIVRGYS NP +F+SDF AAMIKMGDISPLTGS+GEIRK C
Sbjct: 261 TQRGLLHSDQQLFNGGSTDSIVRGYSNPNSSFNSDFTAAMIKMGDISPLTGSNGEIRKVC 320

Query: 2167 RRIN 2178
R N
Sbjct: 321 GRTN 324

Score = 187 bits (476), Expect = 7e-45
Identities = 104/169 (61%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGE+NA PNRNSARGF VIDNIKSAVEK CPGVVSCADILAI AA
Sbjct: 74 VNGCDGSILLDDTSSFTGEQNAAPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAI AA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 134 RDSV-----VALGGPNWNVKVG 150

Query: 1511 RRDARTASQAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AA N+ IPAPTS+L+QLIS FSA+GLST+D+VALSG I
Sbjct: 151 RRDARTASQAAANSNIPAPTSLSQLISSFSAVGLSTRDMVALSGAHTI 199

Score = 78.2 bits (191), Expect = 7e-12
Identities = 38/66 (57%), Positives = 50/66 (75%), Gaps = 4/66 (6%)
Frame = +1

Query: 598 ICLALFVLIWGSAN----AQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
+ L + +L+ G N AQL+TNFY SCPNL S+V++ V+SA++ E RMGAS+LRLFF
Sbjct: 10 LVLVVTLLLQGDNNYVVEAQLTTFYSTSCP NLSTVQTAVKSAVNSEARMGASILRLFF 69

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 70 HDCFVN 75

>dbj|BAF27413.2| Os11g0112400 [Oryza sativa Japonica Group]
Length = 136

Score = 201 bits (510), Expect = 8e-49
Identities = 93/124 (75%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA +RQ CPR+SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 13 QARCTNFRAHIYNETNIDSGFAMSRQSGCPRSSGSGDNNLAPLDLQTPTVFENNYK NLV 72

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 73 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 132

Query: 2167 RRIN 2178
RRIN
Sbjct: 133 RRIN 136

>ref|NP_001065568.1| Os11g0112400 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69372.1| TPA: class III peroxidase 130 precursor [Oryza sativa (japonica
cultivar-group)]
gb|ABA91159.1| Peroxidase 52 precursor, putative, expressed [Oryza sativa (japonica
cultivar-group)]
gb|EAZ00524.1| hypothetical protein OsI_22542 [Oryza sativa Indica Group]
gb|EAZ17186.1| hypothetical protein OsJ_32693 [Oryza sativa Japonica Group]
dbj|BAH01350.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 324

Score = 201 bits (510), Expect = 8e-49
Identities = 93/124 (75%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA +RQ CPR+SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 201 QARCTNFRAHIYNETNIDSGFAMSRQSGCPRSSGSGDNNLAPLDLQTPTVFENYYKNLV 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 261 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 320

Query: 2167 RRIN 2178
RRIN
Sbjct: 321 RRIN 324

Score = 166 bits (419), Expect = 3e-38
Identities = 94/169 (55%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID IKSAVE +CPGVVSCADILAI AA
Sbjct: 74 VQGCDASLLDDTASFTGEKMANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAI AA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 134 RDSVAI-----LGGPSWDVKVG 150

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG+ I
Sbjct: 151 RRDSRTASLSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGSHTI 199

Score = 75.5 bits (184), Expect = 5e-11
Identities = 35/75 (46%), Positives = 56/75 (74%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETR 735
+++ T ++ CS L + + + + + G ++AQLS +FY +SCP +F +VK +QSAI+ E R
Sbjct: 1 MAQPTSSARCS-LVVMVVVLAVAGGSSAQLSPSFYSYSCPGVFDVAVKCGMQSAIANEKR 59

Query: 736 MGASLLRLFFHDCFV 780
+GAS++RLFFHDCFV
Sbjct: 60 IGASIVRLFFHDCFV 74

>gb|EAY79693.1| hypothetical protein OsI_34840 [Oryza sativa Indica Group]
Length = 329

Score = 199 bits (507), Expect = 2e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA RQ CPR SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 206 QARCTNFRAHIYNETNIDSGFAMRRQSGCPRNSGSGDNNLAPLDLQTPTVFENNYKLV 265

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 266 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 325

Query: 2167 RRIN 2178
RRIN
Sbjct: 326 RRIN 329

Score = 166 bits (421), Expect = 2e-38
Identities = 94/169 (55%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID IKSAVE +CPGVVSCADILAIAA
Sbjct: 79 VQGCDASLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVETICPGVVSCADILAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 139 RDSVAI-----LGGPSWDVKVG 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG+ I
Sbjct: 156 RRDSRTASLSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGSHTI 204

Score = 70.1 bits (170), Expect = 2e-09
Identities = 31/61 (50%), Positives = 47/61 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCF 777
+ + + + + G + AQLS +FY SCP +F++VK +QSAI++E R+GAS++RLFFHDCF
Sbjct: 19 VVVVVVLAVAGGSWAQLSPSFYSFSCPGVFNAVKRGMQSAIAREKRIGASIVRLFFHDCF 78

Query: 778 V 780
V
Sbjct: 79 V 79

>ref|NP_001065971.1| Os12g0112000 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69377.1| TPA: class III peroxidase 135 precursor [Oryza sativa (japonica
cultivar-group)]
gb|ABA96259.1| Peroxidase 52 precursor, putative, expressed [Oryza sativa (japonica
cultivar-group)]
dbj|BAF28990.1| Os12g0112000 [Oryza sativa Japonica Group]
gb|EAZ19424.1| hypothetical protein OsJ_34981 [Oryza sativa Japonica Group]
dbj|BAG91443.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 327

Score = 199 bits (507), Expect = 2e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYNETNI++ FA RQ CPR SGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 204 QARCTNFRAHIYNETNIDSGFAMRRQSGCPRNSGSGDNNLAPLDLQTPTVFENNYKLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y ++ TF +DF MIKMGDI+PLTGSNGEIRKNC
Sbjct: 264 VKKGLLHSDQELFNGGATDALVQSYISSQSTFFADFVTGMIKMGDITPLTGSNGEIRKNC 323

Query: 2167 RRIN 2178
RRIN
Sbjct: 324 RRIN 327

Score = 164 bits (415), Expect = 8e-38
Identities = 93/169 (55%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDDT+SFTGEK ANPN S RGFEVID I KSAVE +CPGVVSCADILAI AA
Sbjct: 77 VQGCDASLLDDTASFTGEKTANPNNGSVRGFEVIDAIKSAVE TICPGVVSCADILAI AA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 137 RDSVAI-----LGGPSWDVKVG 153

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A LS KD+VALSG+ I
Sbjct: 154 RRDSRTASLSGANNIPPTSGLANLTSLFAAQALSQKDMVALSGSHTI 202

Score = 72.8 bits (177), Expect = 3e-10
Identities = 32/63 (50%), Positives = 49/63 (77%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L + + + + G + AQLS +FY +SCP +F++VK +QSAI++E R+GAS++RLFFHD
Sbjct: 15 LVVMVVVLAVAGGSWAQLSPSFYSYSCPGVFNAVKRGMQSAIAREKRIGASIVRLFFHD 74

Query: 772 CFV 780
CFV
Sbjct: 75 CFV 77

>ref|XP_002450132.1| hypothetical protein SORBIDRAFT_05g001000 [Sorghum bicolor]
gb|EES09120.1| hypothetical protein SORBIDRAFT_05g001000 [Sorghum bicolor]
Length = 331

Score = 199 bits (505), Expect = 3e-48
Identities = 93/124 (75%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCTNFRA +YN+TNI+ FARTRQ CPRTSGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 208 QARCTNFRAHVYNDTNIDGTFARTRQSGCPRTSGSGDNNLAPLDLQTPTVFENNY YKNLV 267

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD+ V+ Y ++ TF SDF MIKMGDI+PLTGSNG+IRKNC
Sbjct: 268 CKKGLLHSDQELFNGGATDAQVQSYISSQSTFFSDFVTGMIKMGDITPLTGSNGQIRKNC 327

Query: 2167 RRIN 2178
R IN
Sbjct: 328 RMIN 331

Score = 160 bits (404), Expect = 1e-36
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDT+SF GEK A PN S RGFVID +KSAVEKVCPGVVSCADILAIAA
Sbjct: 81 VQGCASLLDDTASFQGEKMATPNNGSVRGFEVIDAVKSAVEKVCPGVVSCADILAIAA 140

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 141 RDSVVI-----LGGPSWDVKVG 157

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 158 RRDSTTASFSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 206

Score = 82.8 bits (203), Expect = 3e-13
Identities = 39/74 (52%), Positives = 55/74 (74%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRM 738
+K + + S L + L L ++ G+++AQLST+FY SCP ++ SVKS +QSAI+ E RM
Sbjct: 8 TKCSSSCSASGLALLLLVLMAGTSSAQLSTSFYSSSCPGVYDSVKSAIQSAIATEQRM 67

Query: 739 GASLLRLFFHDCFV 780
GAS++RLFFHDCFV
Sbjct: 68 GASIVRLFFHDCFV 81

>gb|ACT35473.1| peroxidase 52 [Brassica rapa]
Length = 306

Score = 197 bits (500), Expect = 1e-47
Identities = 93/124 (75%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RCTNFR R+YNETNI AFA RQ+SCPR +GSGD NLAPLD+ + +FDN YFKNLV
Sbjct: 183 QSRCTNFRTRVYNETNINAAAFATLRQRSCPRAGSGDGNLAPLDVNSANTFDNSYFKNLV 242

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGSTDSIV GYS NP +FSSDF AAMIKMGDISPLTGS+GEIRK C
Sbjct: 243 AQRGLLHSDQQLFNGGSTDSIVTGYSNNPSSFSSDFTAAMIKMGDISPLTGSSGEIRKVC 302

Query: 2167 RRIN 2178
R N

Sbjct: 303 GRTN 306

Score = 189 bits (481), Expect = 2e-45
Identities = 104/169 (61%), Positives = 115/169 (68%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTSSFTGE+NANPNRNSARGF VIDNIK+AVE CPGVVSCADILAI AA
Sbjct: 56 VNGCDGSILLDDTSSFTGEQNANPNRNSARGFNVIDNIKTAVEAACPGVVSCADILAI AA 115

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 116 RDSVVL-----LGGPNWNVKVG 132

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IPAPTS+L+QLIS FSA+GLST+D+VALSG I
Sbjct: 133 RRDARTASQAAANNIPAPTSSLSQLISSFSAVGLSTRDMVALSGAHTI 181

Score = 75.9 bits (185), Expect = 4e-11
Identities = 34/48 (70%), Positives = 41/48 (85%)
Frame = +1

Query: 640 AQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
AQL+TNFY SCPNL S+V+STV+SA+ + R GAS+LRLFFHDCFVN
Sbjct: 10 AQLTTNFYSTSCP NLSTVRSTVKS AVDSQPRTGASILRLFFHDCFVN 57

>ref|XP_002441703.1| hypothetical protein SORBIDRAFT_08g000990 [Sorghum bicolor]
gb|EES15541.1| hypothetical protein SORBIDRAFT_08g000990 [Sorghum bicolor]
Length = 328

Score = 196 bits (498), Expect = 2e-47
Identities = 92/123 (74%), Positives = 105/123 (85%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFRA IYN+TNI+ +FAR+RQ CPRTSGSGDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 206 ARCTNFRAHIYNDTNIDGSFARSRSVCPRTS GSGDNNLAPLDLQTPTVFENNYK NLVY 265

Query: 1990 KKGLLHSDQQLFN GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKG+LHSDQ+LFN GGSTD+ V+ Y ++ F +DF MIKMGDI PLTGSNGEIRKNCR
Sbjct: 266 KKGILHSDQELFN GGSTDAQVQSYVSSQSAFFADFVTGMIKMGDIMPLTGSNGEIRKNCR 325

Query: 2170 RIN 2178
RIN

Sbjct: 326 RIN 328

Score = 164 bits (415), Expect = 8e-38
Identities = 95/169 (56%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+QGCD S+LLDDT SF GEK ANPN SARGFEVID IKS AV+KVCPCGVVSCADILAI
Sbjct: 78 VQGCDASLLDDTPSFQGEKMANPNNGSARGFEVIDAIKSAVDKVCPCGVVSCADILAI 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 138 RDSVVI-----LGGPSWDVKVG 154

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 155 RRDSRTASFSGANNIPPTSGLVNLTSLFAAQGLSQKDMVALSGAHTI 203

Score = 77.4 bits (189), Expect = 1e-11
Identities = 36/61 (59%), Positives = 50/61 (81%), Gaps = 2/61 (3%)
Frame = +1

Query: 604 LALFVLI--WGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCF 777
L L VL+ G+++AQL T+FY HSCP ++ +V+S +Q+AI+++E RMGAS+LRLFFHDCF
Sbjct: 18 LLLLVLLAGTGTSSAQLCTSFYSHSCPGVYDAVRSVLQAAIAREQRMGASILRFFHDCF 77

Query: 778 V 780
V
Sbjct: 78 V 78

>ref|XP_002450133.1| hypothetical protein SORBIDRAFT_05g001010 [Sorghum bicolor]
gb|EES09121.1| hypothetical protein SORBIDRAFT_05g001010 [Sorghum bicolor]
Length = 328

Score = 196 bits (498), Expect = 2e-47
Identities = 89/124 (71%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYN+T+I +AFA+TRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNL+
Sbjct: 205 QARCTNFRAHIYNDTDINSAFAKTRQSGCPSTSGAGDNNLAPLDLQTPTVFENNYKNLL 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGG+TD++V+ Y + TF +DF MIKMGDI+PLTGSNG+IRKNC

Sbjct: 265 SKKGLLHSDQELFNGGATDTLVQSYVGSQSTFFTFVTGMIKMGDITPLTGSNGQIRKNC 324

Query: 2167 RRIN 2178
RR+N

Sbjct: 325 RRVN 328

Score = 159 bits (401), Expect = 3e-36
Identities = 91/169 (53%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDT++F GEK A PN S RGFEVID +KSAVEKVCPGVVSCADILAI
Sbjct: 78 VQGCDASLLDDTATFQGEKMATPNNGSVRGFEVIDAVKSAVEKVCPGVVSCADILAI 137

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 138 RDSVVI-----LGGPSWDVKVG 154

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 155 RRDSTTASFSGANNIPPTSGLANLTS LFAAQGLSQKDMVALSGAHTI 203

Score = 77.4 bits (189), Expect = 1e-11
Identities = 38/70 (54%), Positives = 52/70 (74%), Gaps = 1/70 (1%)
Frame = +1

Query: 574 ASFC SRLTICLALFVL-IWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
AS S + L L L + G+++AQLST FY +SCP ++ +VKS ++SAI+ E RMGAS+
Sbjct: 9 ASSSSAAALLLLLLALAVAGTSSAQLSTGFYSYSCPGVYGAVKSVMSAIANEKRMGASI 68

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 69 VRLFFHDCFV 78

>gb|ABV24960.2| putative secretory peroxidase [Catharanthus roseus]
Length = 330

Score = 196 bits (498), Expect = 2e-47
Identities = 92/124 (74%), Positives = 108/124 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FRARIYNE+NIET+FARTRQ +CP +G+GDN+LAPLDLQ+P FD Y+KNL+
Sbjct: 207 QARCTVFRARIYNESNIETSFARTRQGNCLPTGNGDNSLAPLDLQSPNGFDINYYKNLI 266

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+L+NGGST+S+V YS + F SDFAAAMIKMGDISPLTGSNGE+RKNC
Sbjct: 267 NKKGLLHSDQELYNGGSTNSLVEAYSKDTKAFYSDFAAAMIKMGDISPLTGSNGEVRKNC 326

Query: 2167 RRIN 2178
RR+N
Sbjct: 327 RRVN 330

Score = 164 bits (414), Expect = 1e-37
Identities = 92/169 (54%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLDDTSS GEK A PN S RGF+V+DNIKS VEKVCPGVVSCADILAI
Sbjct: 80 VQGCDGSILLDDTSSLRGEKTAGPNVGSVRGFDVVDNIKSDVEKVCPGVVSCADILAI 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W VK+G
Sbjct: 140 RDSV-----VALGGPSWKVKVG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD++TAS S AN+ IP PTSNL LIS F A+GLS KD+V LSG+ I
Sbjct: 157 RRDSKTASLSGANSRIPPPTSNLRLISSFQAVGLSAKDMVVLSGSHTI 205

Score = 72.4 bits (176), Expect = 4e-10
Identities = 37/77 (48%), Positives = 52/77 (67%), Gaps = 3/77 (3%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVL---IWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKE 729
S + +SF S I + + VL + S + QLS+ FY +CP ++++V+ V+SA+SKE
Sbjct: 4 SSSSSSSFSNFGIVIMVIVLSIIMRSCSGQLSSEFYSKTCPQVYNTVRKGVESAVSKE 63

Query: 730 TRMGASLLRLFFHDCFV 780
RMGASLLRL FHDCFV
Sbjct: 64 KRMGASLLRLHFHDCFV 80

>sp|P00434.3|PERP7_BRARA RecName: Full=Peroxidase P7; AltName: Full=TP7
Length = 296

Score = 196 bits (498), Expect = 2e-47
Identities = 93/124 (75%), Positives = 107/124 (86%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC NFRAR+YNETNI AFA RQ+SCPR +GSGD NLAPLD+ + TSFDN YFKNL+
Sbjct: 173 QSRCVNFRARVYNETNINAAAFATLRQRCSPRAAGSGDANLAPLDINSATSFDNSYFKNLM 232

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ LFNGGSTDSIVRGYS +P +F+SDFAAAMIKMGDISPLTGS+GEIRK C
Sbjct: 233 AQRGLLHSDQVLFNGGSTDSIVRGYSNSPSSFNSDFAAAMIKMGDISPLTGSSGEIRKVC 292

Query: 2167 RRIN 2178
+ N
Sbjct: 293 GKTN 296

Score = 179 bits (455), Expect = 2e-42
Identities = 99/169 (58%), Positives = 114/169 (67%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTSSFTGE+NA PNRNSARGF VI++IKSAVEK CPGVVSCADILAIAA
Sbjct: 46 VNGCDGSILLDDTSSFTGEQNAGPNRNSARGFTVINDIKSAVEKACPGVVSCADILAIAA 105

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 106 RDSV-----VQLGGPNWNVKVG 122

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA+TASQ+AAAN+ IPAP+ +L+QLIS FSA+GLST+D+VALSG I
Sbjct: 123 RRDARTASQAAANSNIPAPSMSLSQLISSFSAVGLSTRDMVALSGAHTI 171

Score = 76.6 bits (187), Expect = 2e-11
Identities = 35/47 (74%), Positives = 41/47 (87%)
Frame = +1

Query: 643 QLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHDCFVN 783
QL+TNFY SCPNL S+VKS V+SA+S + RMGAS+LRLFFHDCFVN
Sbjct: 1 QLSTNFYSTSCPILLSTVKSGVKS AVSSQPRMGASILRRLFHDCFVN 47

>gb|AAD37423.1|AF149281_1 peroxidase 6 [Phaseolus vulgaris]
Length = 128

Score = 195 bits (495), Expect = 4e-47
Identities = 106/165 (64%), Positives = 116/165 (70%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330

+ GCDGSILLDDTSSFTGEKNA PN+NSARGF+VID IKSARE+VCPGVVSCADILAI
 Sbjct: 7 VNGCDGSILLDDTSSFTGEKNARPNKNSARGFDVIDKIKSAVEEVCPGVVSCADILAI 66
 Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV I+ GGP+WNVKLG
 Sbjct: 67 RDSVHIL-----GGPSWNVKLG 83
 Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
 RRD+RTASQSAANNGIP PTSN+NQLISRF++LGLS KDLVALSG
 Sbjct: 84 RRDARTASQSAANNGIPPTSNVNLISRFSNLGLSPKDLVALSG 128

>ref|XP_002520835.1| Peroxidase 52 precursor, putative [Ricinus communis]
 gb|EEF41544.1| Peroxidase 52 precursor, putative [Ricinus communis]
 Length = 318

Score = 194 bits (494), Expect = 5e-47
 Identities = 109/169 (64%), Positives = 115/169 (68%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
 + GCDGSILLDDTSSFTGE+ A PNRNS RGFEVID+IKSAVEK CPGVVSCADILAI
 Sbjct: 70 VNGCDGSILLDDTSSFTGEQTAVPNRNSVRGFEVIDSIKSAVEKACPGVVSCADILAI 129
 Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDS I+ GGP+WNVKLG
 Sbjct: 130 RDSTAIL-----GGPSWNVKLG 146
 Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 RRDARTAS SAANNGIPAPTSNLNQLISRFSALGLST+DLVALSG I
 Sbjct: 147 RRDARTASLSAANNGIPAPTSNLNQLISRFSALGLSTRDLVALSGAHTI 195

Score = 193 bits (490), Expect = 2e-46
 Identities = 93/124 (75%), Positives = 105/124 (84%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSFGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QARCTNFR RIYN+TNI+++FA+TR+ +CP T G DNNLAPLDLQTPTSFDN YFKNL+
 Sbjct: 197 QARCTNFRTRIYNDTNIDSSFAQTRRSNCPSTGG--DNNLAPLDLQTPTSFDNYYFKNLL 254
 Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 +KGLLHSDQ+LFN GSTDSIVR YS TF SDF A MIKMGDISPLTGS GEIRKNC
 Sbjct: 255 VQKGLLHSDQQLFNGGSTDSIVRTYSNGQSTFFSDFVAGMIKMGDISPLTGSQGEIRKNC 314
 Query: 2167 RRIN 2178
 ++N
 Sbjct: 315 GKV 318

Score = 88.2 bits (217), Expect = 7e-15
Identities = 43/63 (68%), Positives = 50/63 (79%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
TI +L+ +NAQLSTNFY SCPNLFS+VK VQSAI++E RMGASL+RLFFHDC
Sbjct: 9 TIVTLSELLVVSISNAQLSTNFYSKSCPRLFSTVKPVVQSAINQEKRMGASLVRLFFHDC 68

Query: 775 FVN 783
FVN
Sbjct: 69 FVN 71

>ref|XP_002319968.1| predicted protein [Populus trichocarpa]
gb|EEE95891.1| predicted protein [Populus trichocarpa]
Length = 325

Score = 193 bits (491), Expect = 1e-46
Identities = 92/124 (74%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI+++FA TRQ++CP GDN LAPLD+QTPTSFDN Y+KNL+
Sbjct: 202 QARCTSFARIYNETNIDSSFATTRQKNCPPGPKGDNKLAPLDVQTPTSFDNKYYKNLI 261

Query: 1987 QKGGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ LFNGGSTDS+VR YS+NP TFSSDF AMIKMGDI PLTGS GEIRK C
Sbjct: 262 SQKGLLHSDQVLFNGGSTDSLVRTYSSNPKTFFSSDFVTAMIKMGDIDPLTGSQGEIRKIC 321

Query: 2167 RRIN 2178
+ N
Sbjct: 322 SKRN 325

Score = 160 bits (406), Expect = 9e-37
Identities = 91/170 (53%), Positives = 107/170 (62%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
++GCDGSILL+DTSSFTGE+ A PN NS RGF V+ IKS VEKVC PG+VSCADI+AIAA
Sbjct: 74 VKGCDGSILLEDTSSFTGEQTAGPNNSVRGFNVVAKIKSQVEKVC PGIVSCADIVAIAA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP WNVKLG
Sbjct: 134 RDSTVI-----LGGPFWNVKLG 150

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS SAAN+G IP PTS L+ LI+RF++ GLS KD+VALSG+ I
Sbjct: 151 RRDSKTASLSAANSVIPPTSTLSNLINRFNSKGLSVKDMVALSGSHTI 200

Score = 86.7 bits (213), Expect = 2e-14
Identities = 44/70 (62%), Positives = 55/70 (78%), Gaps = 1/70 (1%)
Frame = +1

Query: 574 ASFC SRLTICLALFVLIWGS-ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
+SF S + I F++I+ S ++AQLSTNFY SCP +F +VKS VQSA+SKE RMGASL
Sbjct: 5 SSFSSYMAIFTLAFLVIFTSHSSAQLSTNFYKSCPKVFGAVKSVVQSAVSKERRMGASL 64

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 65 VRLFFHDCFV 74

>ref|NP_001151940.1| peroxidase 52 [Zea mays]
gb|ACG45093.1| peroxidase 52 precursor [Zea mays]
Length = 334

Score = 191 bits (486), Expect = 5e-46
Identities = 89/126 (70%), Positives = 106/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG--SGDNNLAPLDLQTPTSFDNYYFKN 1980
QARCTNFRA +YN+TNI+ +FARTRQ CPR+S SGDNNLAPLDLQTPT FDN Y+KN
Sbjct: 209 QARCTNFRAHVYNDTNIDGSFARTRQSGCPRSSSGSSGDNNLAPLDLQTPTVFDNYYKN 268

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
LV KKGLLHSDQ+LFNGG+TD++V+ Y++ F SDF M+KMGDI+PLTGS G+IRK
Sbjct: 269 LVCKKGLLHSDQELFNGGATDALVQSYASGQSEFFSDFVTGMVKMGDITPLTGS GGQIRK 328

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 329 NCRRVN 334

Score = 162 bits (409), Expect = 4e-37
Identities = 93/169 (55%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEKVC PGVVSCADILAIAA
Sbjct: 82 VQGCDASLLDDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKVC PGVVSCADILAIAA 141

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G
Sbjct: 142 RDSVVIL-----GGPTWDVKVG 158

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 159 RRDSTTASFSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 207

Score = 79.0 bits (193), Expect = 4e-12
Identities = 36/59 (61%), Positives = 47/59 (79%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
LAL + G+++AQLST FY SCP ++ +VKS VQSA++ E RMGAS++RLFFHDCFV
Sbjct: 24 LALLMAAAGTSSAQLSTGFYSSSCPGVYDAVKSVVQSAVASEQRMGASIVRLFFHDCFV 82

>ref|XP_002489046.1| hypothetical protein SORBIDRAFT_0246s002010 [Sorghum bicolor]
gb|EES20431.1| hypothetical protein SORBIDRAFT_0246s002010 [Sorghum bicolor]
Length = 320

Score = 190 bits (483), Expect = 1e-45
Identities = 88/124 (70%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR IYN+TN++ AFARTRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 197 QARCTNFRDHIYNDTNVDGAFARTRQSGCPSTSGTGDNNLAPLDLQTPTVFENDYYKNLV 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFNGG+TD++V+ Y ++ F +DF MIKMGDI+PLTGS GEIRKNC
Sbjct: 257 SNMGLLHSDQELFNGGATDALVQSYVSSQSAFFADFVTGMIKMGDITPLTGSAGEIRKNC 316

Query: 2167 RRIN 2178
RRIN
Sbjct: 317 RRIN 320

Score = 155 bits (392), Expect = 4e-35
Identities = 90/169 (53%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT++F GEK A PN S RGFEVID KSAVE VCPGVVSCADILAIAA
Sbjct: 70 VQGCDASLLDDTATFQGEKMATPNNGSVRGFEVIDAAKSAVENVCPGVVSCADILAIAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP+W+VK+G
Sbjct: 130 RDSVVI-----LGGPSWDVKVG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 147 RRDSTTASFSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 195

Score = 73.9 bits (180), Expect = 1e-10
Identities = 38/70 (54%), Positives = 47/70 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ L + L G++ AQLST FY SCP L+S+VK VQSAI E R+GAS+
Sbjct: 1 MAAQSIALWLLTTTLMALQAGTSAQLSTGFYSSSCPGLYSAVKPVVQSAIDSEKRVGASI 60

Query: 751 LRLFFHDCFV 780
+RLFFHDCFV
Sbjct: 61 VRLFFHDCFV 70

>ref|XP_002441702.1| hypothetical protein SORBIDRAFT_08g000980 [Sorghum bicolor]
gb|EES15540.1| hypothetical protein SORBIDRAFT_08g000980 [Sorghum bicolor]
Length = 131

Score = 190 bits (483), Expect = 1e-45
Identities = 88/124 (70%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR IYN+TN++ AFARTRQ CP TSG+GDNNLAPLDLQTPT F+N Y+KNLV
Sbjct: 8 QARCTNFRDHIYNDTNVDGAFARTRQSGCPSTSGTGDNNLAPLDLQTPTVFENDYYKNLV 67

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFNGG+TD++V+ Y ++ F +DF MIKMGDI+PLTGS GEIRKNC
Sbjct: 68 SNMGLLHSDQELFNGGATDALVQSYVSSQSAFFADFVTGMIKMGDITPLTGSAGEIRKNC 127

Query: 2167 RRIN 2178
RRIN
Sbjct: 128 RRIN 131

>gb|AAA96137.1| peroxidase [Stylosanthes humilis]
Length = 136

Score = 190 bits (483), Expect = 1e-45

Identities = 87/124 (70%), Positives = 106/124 (85%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FR IYN+T+I+ +FA+ RQ++CPR SG+GD+NLAPLDLQTPT F+N Y+KNL+

Sbjct: 13 QARCTSFGRHIYNDTIDPSFAKLRRQKNCPRQSGTGDSNLAPLDLQTPHFENNYKNLI 72

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS+V+ YS N F+SDF MIKMGD+ PLTGS GEIRKNC

Sbjct: 73 NKKGLLHSDQELFNGGSTDSLVTYSKNNKAFTSDFVPGMIKMGDLLPLTGSKEIRKNC 132

Query: 2167 RRIN 2178

RR+N

Sbjct: 133 RRMN 136

>gb|AAL93151.1|AF485265_1 class III peroxidase [Gossypium hirsutum]
Length = 320

Score = 189 bits (480), Expect = 2e-45
Identities = 91/124 (73%), Positives = 105/124 (84%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
+ARC FR RIYN+T I+T+FA+TR+ SCPRT GSGDNNLAPLDL TP SFD+ YF+NL+

Sbjct: 197 KARCLVFRNRIYNDTIIDTSFAKTRRSSCPRTSGSGDNNLAPLDLATPNSFDSKYFENLL 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS+V+ YS+N F SDF AAMIKMGDI PLTGSNGEIRKNC

Sbjct: 257 NKKGLLHSDQELFNGGSTDSLVTYSSNVKKFYSDFAAAMIKMGDIKPLTGSNGEIRKNC 316

Query: 2167 RRIN 2178

+ N

Sbjct: 317 GKPN 320

Score = 160 bits (404), Expect = 1e-36
Identities = 92/170 (54%), Positives = 106/170 (62%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSFTGE+ A PN S RGFEV+D IK+ VEKVCPGVVSCADILAIAA

Sbjct: 69 VNGCDGSVLLDDTSSFTGEQTATPNNGSLRGFEVVDEIKAKVEKVCPGVVSCADILAIAA 128

Query: 1331 RDSVQIVSGQTTNKNLTN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP TWNVKLG 1510
RDSV I LGGP W+VKLG

Sbjct: 129 RDSVVI-----LGGPDWDVKLG 145

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS S AN+G+ P ++NL+QLIS F A GLSTKD+VALSG I
Sbjct: 146 RRDSKTASFSDANSGVPLPGSANLSQLISLFQAQGLSTKDMVALSGAHTI 195

Score = 76.6 bits (187), Expect = 2e-11
Identities = 34/60 (56%), Positives = 48/60 (80%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+ +++++ + AQLSTNFY SCP + S+V+ V++A+SKE R+GASLLRLFFHDCFVN
Sbjct: 11 VGVWMMMGSGSYAQLSTNFYSKCPKVLSTVELVVETAVSKEQRLGASLLRLFFHDCFVN 70

>emb|CAD67478.1| peroxidase [Asparagus officinalis]
Length = 301

Score = 188 bits (478), Expect = 4e-45
Identities = 87/124 (70%), Positives = 104/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT+FR IYN+ +I+ +FA RQ+ CPR SGSGD NLAPLDLQTPT+FDN Y+KNL+
Sbjct: 178 QARCTSFGRHIIYNDADIDASFASLRQKICPRKSGSGDTNLAPLDLQTPTAFDNYYKNLI 237

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFN G+TDS+V+ YS + G+F+SDF AMIKMGDISPLTGS GEIRK C
Sbjct: 238 NKKGLLHSDQELFNGGATDSLVSYSNSEGSFNSDFVKAMIKMGDISPLTGSKEIRKIC 297

Query: 2167 RRIN 2178
+IN
Sbjct: 298 SKIN 301

Score = 161 bits (407), Expect = 7e-37
Identities = 90/169 (53%), Positives = 104/169 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILL DT++F GE++A PN S RGF+VID IK+AVE CPGVVSCADILA+AA
Sbjct: 51 VNGCDGSILLADTANFRGEQHGAPNNGSVRGFKVIDKIKTAVENACPGVVSCADILAVAA 110

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W VKLG
Sbjct: 111 RDSVVI-----LGGPDWKVKLG 127

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTAS + ANN IP PTS+L+ LIS+F+A GLSTKD+VALSG I
Sbjct: 128 RRDARTASATLANNIPPTSSLSNLISKFAAQLSTKDMVALSGAHTI 176

Score = 82.4 bits (202), Expect = 4e-13
Identities = 37/52 (71%), Positives = 45/52 (86%)
Frame = +1

Query: 628 GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
GS++A LSTNFY SCP +FS++K +QSAI+KE RMGAS+LRLFFHDCFVN
Sbjct: 1 GSSSAHLSTNFYSSSCP KVFSTIKPVLQSAIAKEKRMGASILRLFFHDCFVN 52

>gb|AAR31108.1| peroxidase precursor [Quercus suber]
Length = 330

Score = 188 bits (477), Expect = 5e-45
Identities = 88/125 (70%), Positives = 107/125 (85%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSG-SGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR RIY + NI+++FA+TRQ CP+T+G GDN +APLDLQTPT+FDNYY+KNL
Sbjct: 205 QARCTVFRDRIYKDKNIDSSFAKTRQNKCPKTTGLPGDNKIAPLDLQTPTAFDNYYKLN 264

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQQLFNGGSTDS+V+ YS + TF SDF AMIKMGDI PLTGS+GEIRKN
Sbjct: 265 IKEKGLLRSDQQLFNGGSTDSLVKKYSQDTKTFYSDFVNAMIKMGDIQPLTGSSGEIRKN 324

Query: 2164 CRRIN 2178
CR++N
Sbjct: 325 CRKVN 329

Score = 162 bits (409), Expect = 4e-37
Identities = 93/166 (56%), Positives = 103/166 (62%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDT +FTGEK A PN S R FEV+D IKS VEK CPGVVSCADILAIAA
Sbjct: 77 VNGCDGSILLDDTPTFTGEKTARPNGSIRAFEVVDEIKSKVEKECPGVVSCADILAIAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W+VKLG
Sbjct: 137 RDSVKI-----LGGPKWDVKLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD++TAS SAAN+G IP PTS L LI+RF A GLSTKD+VALSG

Sbjct: 154 RRDSKTASFSAANSVIPPTSTLGNLINRFKAKGLSTKDMVALSG 199

Score = 84.3 bits (207), Expect = 1e-13
Identities = 39/64 (60%), Positives = 51/64 (79%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHD 771
L + LA+ V+ G+++A+LSTNFY SCP +FS+V+S V SA+SK+ R GASLLRL FHD
Sbjct: 15 LIVSLAVLVIFTGNSSAKLSTNFYSKCPKVFSTVQSVVHSAVSKQPRQGASLLRLHFHD 74

Query: 772 CFVN 783
CFVN
Sbjct: 75 CFVN 78

>gb|AAR31106.1| peroxidase precursor [Quercus suber]
Length = 330

Score = 187 bits (474), Expect = 1e-44
Identities = 87/125 (69%), Positives = 108/125 (86%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSQ-SGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARCT FR RIY + NI+++FA+TRQ +CP+T+G GDN +APLDLQTPT+FDNYY+KNL
Sbjct: 205 QARCTVFRDRIYKDKNIDSSFAKTRQNTCPKTTGLPGDNKIAPLDLQTPTAFDNYYKKNL 264

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIRKN 2163
+++KGLL SDQQLFNGGSTDS+V+ YS + +F SDF AMIKMGDI PLTGS+GEIRKN
Sbjct: 265 IKQKGLLRSDQQLFNGGSTDSLVKKYSQDTKSFYSDFVNAMIKMGDIQPLTGSSGEIRKN 324

Query: 2164 CRRIN 2178
CR++N
Sbjct: 325 CRKVN 329

Score = 162 bits (410), Expect = 3e-37
Identities = 92/170 (54%), Positives = 105/170 (61%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDT +FTGEK A PN+ S RGFE +D IKS VEK CPGVVSCADILAIAA
Sbjct: 77 VNGCDGSVLLDDTPTFTGEKTAGPNKGSIRGFEFVDEIKSKVEKECPGVVSCADILAIAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV+I LGGP W+VKLG
Sbjct: 137 RDSVKI-----LGGPKWDVKLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS AAN+G IP PTS L+ LI+RF A GLSTKD+VALSG I
Sbjct: 154 RRDSKTASLKAANSVIPPTSTLSNLINRFKAKGLSTKDMVALSGAHTI 203

Score = 87.8 bits (216), Expect = 9e-15
Identities = 41/64 (64%), Positives = 52/64 (81%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L + LA+ V+ G+++A+LSTNFYY SCP +FS+V+S V SAISK+ R GASLLRL FHD
Sbjct: 15 LIVSLAVLVIFSGNSSAKLSTNFYYKSCP KVFSTVQSVVHSAISKQPRQGASLLRLHFHD 74

Query: 772 CFVN 783
CFVN
Sbjct: 75 CFVN 78

>ref|NP_001131000.1| hypothetical protein LOC100192105 [Zea mays]
gb|ACF79421.1| unknown [Zea mays]
gb|ACL53914.1| unknown [Zea mays]
Length = 320

Score = 186 bits (473), Expect = 1e-44
Identities = 89/126 (70%), Positives = 107/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRA IYN+T+I+ AFARTRQ CP TSG+G DNNLAPLDLQTPT F+N Y++NL
Sbjct: 195 QARCTNFRAHIYNDTDIDAAFARTRQSGCPSTSGAGGDNNLAPLDLQTPTVFENNYRNL 254

Query: 1984 VQKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS-NGEIRK 2160
+ KKGLLHSDQ+LFNGG+TD++V+ Y + F +DF A MIKMGDI+PLTGS NG+IRK
Sbjct: 255 LAKKGLLHSDQELFNNGGATDALVQSYVGSQS AFFADFVAGMIKMGDITPLTGSNNGQIRK 314

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 315 NCRRVN 320

Score = 160 bits (406), Expect = 9e-37
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEK+CPGVVSCADILAIAA

Sbjct: 68 VQGCASLLDDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKLCPGVVSCADILAI 127

Query: 1331 RDSVQIVSGGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G

Sbjct: 128 RDSVVIL-----GGPTWDVKVG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 145 RRDSTTASFGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 193

Score = 81.6 bits (200), Expect = 7e-13
Identities = 37/65 (56%), Positives = 51/65 (78%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
+R L L + + G+++AQLST FY +SCP ++ +VKS +QSAI++E RMGAS+LRLFF

Sbjct: 4 TRAAATLLLLLALAGTSSAQLSTGFYSYSCPGVYGAVKSVMQSAIAREKRMGASILRLFF 63

Query: 766 HDCFV 780
HDCFV

Sbjct: 64 HDCFV 68

>gb|AAD43561.1|AF155124_1 bacterial-induced peroxidase precursor [Gossypium hirsutum]
Length = 316

Score = 185 bits (470), Expect = 3e-44
Identities = 86/123 (69%), Positives = 104/123 (84%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
ARCT FR RIYN+TNI+ FA TR+ +CP + GDNNLAPLD+QTPT FDN YF+NLV

Sbjct: 196 ARCTTFRGRIYNDTNIDANFAATRRANCP--ASGGDNNLAPLDIQTPTFRFDNDYFRNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YS NP TFS+DFAAAM+KMG+ISPLTG+ GEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSNNPATFSADFAAAMVKMGNISPLTGTQGEIRRNCR 313

Query: 2170 RIN 2178
+N

Sbjct: 314 VVN 316

Score = 159 bits (403), Expect = 2e-36
Identities = 90/165 (54%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCDGSILLDDT++FTGEKNA PNRNSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 68 VNGCDGSILLDDTATFTGEKNAVPNRNSARGFEVIDTIKTNVEAACSATVSCADILALAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW V LG
Sbjct: 128 RDGVALL-----GGPTWQVPLG 144

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDARTASQSAANN IP+P +NL L S F+A GLST+DL ALSG
Sbjct: 145 RRDARTASQSAANNQIPSPFANLATLTSSFAAKGLSTRDLTALSG 189

Score = 76.6 bits (187), Expect = 2e-11
Identities = 35/62 (56%), Positives = 48/62 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCF 777
+ L + +L +ANAQLS NFY SCPNL + V++ + A+++ETR+GAS+LRLFFHDCF
Sbjct: 8 VTLIVMLSCHAANAQLSPNFYASSCPNLQTIVRNAMSRAVNRETRIGASILRLFFHDCF 67

Query: 778 VN 783
VN
Sbjct: 68 VN 69

>gb|ACN33662.1| unknown [Zea mays]
Length = 320

Score = 184 bits (468), Expect = 6e-44
Identities = 88/126 (69%), Positives = 107/126 (84%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNL 1983
QARCTNFRA IYN+T+I+ AFARTRQ CP TSG+G D+NLAPLDLQTPT F+N Y++NL
Sbjct: 195 QARCTNFRAHIYNDTDIDAAFARTRQSGCPSTSGAGGDSNLAPLDLQTPTVFENNYRNL 254

Query: 1984 VQKKGLLHSDQQLFNCGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS-NGEIRK 2160
+ KKGLLHSDQ+LFNCGG+TD++V+ Y + F +DF A MIKMGDI+PLTGS NG+IRK
Sbjct: 255 LAKKGLLHSDQELFNCGGATDALVQSYVGSQSAFFADFVAGMIKMGDITPLTGSNNGQIRK 314

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 315 NCRRVN 320

Score = 160 bits (406), Expect = 9e-37
Identities = 92/169 (54%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK ANPN S RGFEVID +KSAVEK+CPGVVSCADILAIAA
Sbjct: 68 VQGCDAASLLDDTPSFQGEKMANPNNGSVRGFEVIDAVKSAVEKLCPGVVSCADILAIAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGPTW+VK+G
Sbjct: 128 RDSVVIL-----GGPTWDVKVG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 145 RRDSTTASFSGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 193

Score = 81.6 bits (200), Expect = 7e-13
Identities = 37/65 (56%), Positives = 51/65 (78%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPFLSSVKSTVQSAISKETRMGASLLRLFF 765
+R L L + + G+++AQLST FY +SCP ++ +VKS +QSAI++E RMGAS+LRLFF
Sbjct: 4 TRAAATLLLLALAGTSSAQLSTGFYSYSCPGVYGAVKSVMQSAIAREKRMGASILRLFF 63

Query: 766 HDCFV 780
HDCFV
Sbjct: 64 HDCFV 68

>emb|CBI25393.1| unnamed protein product [Vitis vinifera]
Length = 179

Score = 184 bits (466), Expect = 1e-43
Identities = 100/169 (59%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTSSF GEKNA PN NS RGF+V+D+IKS VE CPGVVSCAD+LAIAA
Sbjct: 15 VNGCDGSVLLDDTSSFIGEKNAAPNANSVRGFDVDDIKSVETACPGVVSCADVLAIAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I+ GGP+WNVKLG
Sbjct: 75 RDSVVIL-----GGPSWNVKLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQ+AANN IP PTSNLNQLISRF ALGLST+DLVAL+G+ I
Sbjct: 92 RRDARTASQAAANNSIPPPTSNLNQLISRFQALGLSTRDLVALAGSHTI 140

Score = 57.8 bits (138), Expect = 1e-05
Identities = 24/31 (77%), Positives = 29/31 (93%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR 1899
QARCT+FRARIYNETNI+ +FA+TRQ +CPR
Sbjct: 142 QARCTSFARIYNETNIDNSFAKTRQSNCP 172

Score = 38.1 bits (87), Expect = 8.5
Identities = 16/16 (100%), Positives = 16/16 (100%)
Frame = +1

Query: 736 MGASLLRLFFHDCFVN 783
MGASLLRLFFHDCFVN
Sbjct: 1 MGASLLRLFFHDCFVN 16

>gb|ACU23223.1| unknown [Glycine max]
Length = 328

Score = 182 bits (462), Expect = 3e-43
Identities = 86/124 (69%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR RIYN+TNI+ FA RQ+ CPRT+G+GDNNLA LD +TP FDN YFKNL+
Sbjct: 205 KARCTSFDRINQTNIDRTFALARQRRCPRTNGTGDNNLANLDFRTPNHFDNYYFKNLL 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLL+SDQ LFNNGGSTDS+VR YS N F +DF AMI+MGDI PLTGS GEIRKNC
Sbjct: 265 IKRGLLNSDQVLFNNGGSTDSLVRTYSQNNKAFDTDFVKAMIRMGDIKPLTGSQGEIRKNC 324

Query: 2167 RRIN 2178
RR+N
Sbjct: 325 RRVN 328

Score = 152 bits (383), Expect = 4e-34
Identities = 88/166 (53%), Positives = 100/166 (60%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADIL AIAA 1330
+QGCDGSILLDDT +F GEK A N NS RGFEVID IKS VEK+CPGVVSCADIL IA+

Sbjct: 77 VQCGDGSILLDDTPTFQGEKTAAANNNSVRGFEVIDAIKSEVEKICPGVVSCADILDIAS 136

Query: 1331 RDSVQIVSGGTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W V+LG

Sbjct: 137 RDSVVL-----LGGPFWKVRLG 153

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+RTA+ +AAN G IP PTSNL LI+RF GLS +D+VALSG

Sbjct: 154 RRDSRTANFTAANTGVIPPTSNTLNLTRFRDQGLSARDMVALSG 199

Score = 87.0 bits (214), Expect = 2e-14
Identities = 39/77 (50%), Positives = 59/77 (76%)
Frame = +1

Query: 550 VCLSKLTMAFSCRLTICLALFVLIWGSANAQLSTNFYYHSCPNTLFSSVKSTVQSAISKE 729
+ LS + +SF S + LA+ +L+ G+++A LS NFY +CPN+F++VKS V+SA+ +E

Sbjct: 1 MALSPIRSSSFSSSAIVALAVLLLLTGTSSANLSKNFYSKTCPNVFNTVKS VVKS AVVRE 60

Query: 730 TRMGASLLRLFFHDCFV 780
R+GAS++RLFFHDCFV

Sbjct: 61 PRIGASIVRLFFHDCFV 77

>emb|CAA71491.1| peroxidase [Spinacia oleracea]
Length = 323

Score = 182 bits (462), Expect = 3e-43
Identities = 84/123 (68%), Positives = 102/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFR IYN++NI+ FA TR+ SCPR +G+GD NLAP+D+QTP +FDN Y+KNLV

Sbjct: 201 ARCTNFRDHIYNDNIDPNFAATRKASCPRPRTGTGDFNLAPMDIQTPTNTFDNDYYKNLVA 260

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+L+NGGS DS+V+ YSTN F DFAAAMI+MGD+ PLTG+NGEIR NCR

Sbjct: 261 KRGLLHSDQELYNGGSQDSL VKMYSTNQALFFQDFAAAMIRMGDLKPLTGTNGEIRNNCR 320

Query: 2170 RIN 2178
IN

Sbjct: 321 VIN 323

Score = 123 bits (308), Expect = 2e-25
Identities = 74/166 (44%), Positives = 89/166 (53%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+ GCDGS+LLDDT + GEK A PNRN S RGFEVID IKS VE C G VSCADILA+A
Sbjct: 72 VNGCDGSVLLDDTPTSQGEKMAFPNRNNSIRGFEVIDAIKSNVEAACSGTVSCADILALA 131

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD VQ++ G PTWNVKL
Sbjct: 132 ARDGVQLLGG-----PTWNVKL 148

Query: 1508 GRRDARTASQSAANGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
GRRDARTA+ + AN +P + L L F+ L+ +++ ALSG
Sbjct: 149 GRRDARTANMTLANLNLPPGNAPLANLTELFAHQNLNIREMTALSG 194

Score = 66.6 bits (161), Expect = 2e-08
Identities = 32/60 (53%), Positives = 46/60 (76%), Gaps = 1/60 (1%)
Frame = +1

Query: 607 ALFVLIWGSANAQL-STNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
++ +L+ G+++A L +FY SCPN+ V +T++ A+SKE RMGAS+LRLFFHDCFVN
Sbjct: 14 SIILLLAGTSDAWLRKPHFYASSCPNVEQIVFNTMKQAVSKEPRMGASILRLFFHDCFVN 73

>gb|ABK21858.1| unknown [Picea sitchensis]
Length = 326

Score = 180 bits (457), Expect = 1e-42
Identities = 86/124 (69%), Positives = 104/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR RI++E+NI+ +FAR RQ +CP T G D+NLAPLDL TPT+FDN Y+KNL
Sbjct: 205 QARCTNFRNRIHSESNIIDLSFARARQANCPSTGG--DDNLAPLDLLTPTTFDNYYKNLE 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+++GLLHSDQQLFNGGSTD++V Y+T P FS DFA AM+KMG I PLTG+NGEIRKNC
Sbjct: 263 RRRGLLHSDQQLFNGGSTDNLVSFYTTYPIAFSIDFAVAMVKMGIEPLTGNGEIRKNC 322

Query: 2167 RRIN 2178
R+IN
Sbjct: 323 RKIN 326

Score = 153 bits (386), Expect = 2e-34
Identities = 88/169 (52%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILLDDTS+F GEK A PN+NS RGFEVID IK+ VE CPGVVSCADI+AIAA
Sbjct: 78 VNGCDGSILLDDTSTFQGEKTAVPNKNSVRGFEVIDAIKTQVEAACPGVVSCADIVAIA 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LGGPTW V LG
Sbjct: 138 RDAV-----VQLGGPTWLVLLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ +P P SNL+ LIS F + GLS +DLVALSG+ I
Sbjct: 155 RRDSTTASLSAANSNLPPASNLSALISSFQSHGLSIRDLVALSGSHTI 203

Score = 67.8 bits (164), Expect = 1e-08
Identities = 35/65 (53%), Positives = 42/65 (64%)
Frame = +1

Query: 589 RLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFH 768
R +CL+ V + + QL FY SCP+ FS V S V A++KE RMGASLLRL FH
Sbjct: 16 RSLCLLLILVRL-SAVYGQLCPRFYDISCP SAFSIVNSVVTQAVAKEKRMGASLLRLHFH 74

Query: 769 DCFVN 783
DCFVN
Sbjct: 75 DCFVN 79

>emb|CAD67477.1| peroxidase [Asparagus officinalis]
Length = 315

Score = 179 bits (455), Expect = 2e-42
Identities = 82/124 (66%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARCT+FR+ IYN+++I+ +FA R+ +CP+ SGSGD NLAPLDLQTPT+FDN Y++NLV
Sbjct: 192 QARCTSF RSHIYNDSDIDPSFATLRKSNCPKQSGSGDMNLAPLDLQTPTTFDNNYYRNLV 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGL+HSDQ+LFNGGSTDS+V+ YS G F S F MIKMGD+SPL GSNGEIRK C
Sbjct: 252 VKKGLMHSDQELFNGGSTDSLVSYS DGTGKFYSAFVEGMIKMGDV SPLVGSNGEIRKIC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 162 bits (409), Expect = 4e-37

Identities = 92/169 (54%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILL DT F GE++ANPN SARGF+VID IK+AVEK CPGVVSCADILAIAA

Sbjct: 65 VNGCDGSILLADTPHFVGEQHANPNRNSARGFKVIDRIKTAVEKACPGVVSCADILAIAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W+VKLG

Sbjct: 125 RDSVVI-----LGGPNWDVKLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+RTA+++AANN IP PTS+L L S F+A GLSTKD+VALSG I

Sbjct: 142 RRDSRTANKTAANNEIPPPTSSLANLTSLFAAKGLSTKDMVALSGAHTI 190

Score = 82.8 bits (203), Expect = 3e-13
Identities = 40/64 (62%), Positives = 51/64 (79%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRRLFHD 771

L I L+L ++ S+NAQLST FY +SCPN+F+++K +Q AI KE RMGAS+LRLFHD

Sbjct: 6 LAIILSLCIV---SSNAQLSTTFYSNSCPNVFTTIKPVLQHAIEKEKRMGASILRRLFHD 62

Query: 772 CFVN 783

CFVN

Sbjct: 63 CFVN 66

>emb|CAA62597.1| korean-radish isoperoxidase [Raphanus sativus]
Length = 315

Score = 179 bits (455), Expect = 2e-42
Identities = 89/124 (71%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

Q+RCTNFR RIYNETNI AFA RQ+SCPR + PLD+ +PTSFDN YFKNL+

Sbjct: 193 QSRCTNFRTRIYNETNINAAFATLRQKSCPRAAFRR-RKPQLDINSPTSFDNSYFKNLM 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

++GLLHSDQ LFNGGSTDSIVRGYS +P +F+SDFAAAMIKMGDISPLTGS+GEIRK C

Sbjct: 252 AQRGLLHSDQVLFNGGSTDSIVRGYSNSPSSFNDFAAAMIKMGDISPLTGSSGEIRKVC 311

Query: 2167 RRIN 2178

R N

Sbjct: 312 GRTN 315

Score = 176 bits (445), Expect = 3e-41
Identities = 99/169 (58%), Positives = 112/169 (66%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGSILLDDTS FTGE+NA PNRNSARGF VIDNIKSAVEK CPGVVSCADILAI AA
Sbjct: 67 VNGCDGSILLDDTS-FTGEQNAGPNRNSARGFNVIDNIKSAVEKACPGVVSCADILAI AA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNVK+G
Sbjct: 126 RDSV-----VQLGGPNWNVKVG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSA LGLSTKDLVALSGTKHI 1657
RRDA+TASQ+AA N+ IPAP+ +L+QLIS F A+GLST+D+VALSG I
Sbjct: 143 RRDARTASQSAANNSIPAPSM SLSQLISSFRAVGLSTRDMVALSGAHTI 191

Score = 82.8 bits (203), Expect = 3e-13
Identities = 39/66 (59%), Positives = 49/66 (74%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S + I + + L+ AQL+TNFY SCPNL S+VKS V+SA+S + RMGAS+LRLFF
Sbjct: 3 SNIAILVIVITLLLQGGEAQLTTFYSTSCPNNLSTVKSGVKS AVSSQPRMGASILRLFF 62

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 63 HDCFVN 68

>gb|AC090366.1| peroxidase precursor [Triticum aestivum]
Length = 180

Score = 179 bits (454), Expect = 2e-42
Identities = 83/123 (67%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCTNFR IYN+TNI+ FAR+RQ CP +GS DNNLAPLDLQT T F+N+Y+KNLVQ
Sbjct: 58 ARCTNFRDHIYNDTNIDAGFARSRQSGCPHATGSRDNNLAPLDLQTLTVFENHYK NLVQ 117

Query: 1990 KKGLLHSDQQLFN GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+LFNGG+ D++VR Y + F DF MI MGDI+PLTGSNG+IR NCR
Sbjct: 118 KRGLLHSDQELFN GGAADALVREYVGSQS AFFQDFVEGMIMMGDITPLTGSNGQIRMNCR 177

Query: 2170 RIN 2178

RIN
Sbjct: 178 RIN 180

Score = 64.7 bits (156), Expect = 8e-08
Identities = 33/55 (60%), Positives = 38/55 (69%)
Frame = +2

Query: 1493 WNVKLGRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
W VK+GRRD+ TAS + A N IP PTS L L S F+A GLS KD+VALSG I
Sbjct: 1 WEVKMGRRDSTTASFNGAENNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 55

>gb|ACN34270.1| unknown [Zea mays]
Length = 332

Score = 179 bits (453), Expect = 3e-42
Identities = 85/127 (66%), Positives = 103/127 (81%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG---DNNLAPLDLQTPTSFDNYYFK 1977
QARCTNFRA +YN+TNI+ AFAR R+ CP + SG DNNLAPLDLQTPT F+N Y++
Sbjct: 206 QARCTNFRAHVYNDTNIDGAFARARRSVCPAASSGSGGDNNLAPLDLQTPTVFENDYYR 265

Query: 1978 NLVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIR 2157
NLV +KGLLHSDQ+LFNG +TD+ V+ Y ++ F +DF A M+KMGDISPLTGSGEIR
Sbjct: 266 NLVCRKGLLHSDQELFNGAATDAQVQAYVSSQSAFFADVFAGMVKMGDISPLTGSSGEIR 325

Query: 2158 KNCRRIN 2178
KNCRRIN
Sbjct: 326 KNCRRIN 332

Score = 159 bits (401), Expect = 3e-36
Identities = 92/169 (54%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LLDDT SF GEK A PN S RGFEVID IKS AV+K CPGVVSCADILAIAA
Sbjct: 79 VQGCDASLLDDTPSFQGEKMAKPNGSVRGFEVIDAIKS AVDKACPGVVSCADILAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 139 RDSV-----VTLGGPNWDVKLG 155

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+RTAS S ANN IP PTS L L S F+A GLS KD+VALSG I

Sbjct: 156 RRDSRTASFGANNIPPTSGLANLTSLFAAQGLSQKDMVALSGAHTI 204

Score = 76.6 bits (187), Expect = 2e-11
Identities = 35/61 (57%), Positives = 47/61 (77%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRRLFHDCF 777
+ LAL +++AQLST FY HSCP + +V+S +Q+AI++E RMGAS+LRLFHDCF
Sbjct: 19 LLLALLAAGTSTSSAQLSTGFYSHSCPGVHDAVRSVLQAAIAREQRMGASILRRLFHDCF 78

Query: 778 V 780
V
Sbjct: 79 V 79

>gb|ACU24215.1| unknown [Glycine max]
Length = 329

Score = 178 bits (451), Expect = 5e-42
Identities = 85/124 (68%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR RIYN+TNI+ FA RQ+ CPRT+G+GDNNLA LD +TP FDN YFKNL
Sbjct: 206 KARCTSFDRRIYNQTNIDRTFALARQRRCPRTNGTGDNNLANLDFRTPNHFDNYYFKNLF 265

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GLL+ DQ LFNGGSTDS+VR YS N F DF AMI+MGDI PLTGS GEIRKNC
Sbjct: 266 IKRGLLNFDQVLFNGGSTDSLVRTYSQNNKAFDFDFVKAMIRMGDIKPLTGSQGEIRKNC 325

Query: 2167 RRIN 2178
RR+N
Sbjct: 326 RRVN 329

Score = 152 bits (383), Expect = 4e-34
Identities = 86/166 (51%), Positives = 102/166 (61%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCDGSILLDDT +F GEK A N NS RG+E+ID+IKS VEK+CPGVVSCADIL IA+
Sbjct: 78 VQGCDGSILLDDTPTFQGEKTAANNNSVRGYELIDDIKSKVEKICPGVVSCADILDIAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP WNV+LG
Sbjct: 138 RDSVVL-----LGGPFWNVRLG 154

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+R+A+ +AAN G IP PTSNL LI+RF GLS +D+VALSG
Sbjct: 155 RRDSRSANFTAANTGVIPPTSNLTNLITRFQDQGLSARDMVALSG 200

Score = 80.1 bits (196), Expect = 2e-12
Identities = 39/78 (50%), Positives = 59/78 (75%), Gaps = 1/78 (1%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTIC-LALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISK 726
+ LS + ++F S I LA+ +L+ +++A LS NFY +CPN+F++VKS V+SA++K
Sbjct: 1 MALSPIRSSTFSSSSAIVTLAVLLLLTRTSSATLSKNFYSKTCPNVFNTVKS VVKS AVAK 60

Query: 727 ETRMGASLLRLFFHDCFV 780
E R+GAS++RLFFHDCFV
Sbjct: 61 EPRIGASIVRLFFHDCFV 78

>gb|AAB48184.1| peroxidase precursor [Linum usitatissimum]
Length = 323

Score = 178 bits (451), Expect = 5e-42
Identities = 83/123 (67%), Positives = 100/123 (81%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC +FR RIYNETNI+ +FA +++CP SGD+NLAPLDL+TPTSFDN Y+ NL++
Sbjct: 201 ARCVSFRDRIYNETNIDPSFASQSEENCPLAPNSGDDNLAPLDLKTPTSFDNNYYNNLIE 260

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+KGLLHSDQ LFNGGSTDS+VR YS +P F++DFAAAM+KMGDI PLTGS GEIR C
Sbjct: 261 QKGLLHSDQVLFNGGSTDSLRSYSQSPKRFAADFAAAMVKMGDIKPLTGSQGEIRNVCS 320

Query: 2170 RIN 2178
R N
Sbjct: 321 RPN 323

Score = 143 bits (361), Expect = 1e-31
Identities = 82/170 (48%), Positives = 101/170 (59%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGSILL+DT SFTGE+ A PN S RG+ VI++IKS VE+VCPGVVSCADI+AIAA
Sbjct: 72 VNGCDGSILLEDTDSFTGEQTAAPNNGSVRGYYVIEDIKSKVEQVCPGVVSCADIVAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I GQ +W VK+G
Sbjct: 132 RDSTVIAGGQ-----SWEVKVG 148

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS +AAN+G+ PAPTS+LN+LI F GLS D+V LSG+ I
Sbjct: 149 RRDSKTASFNAANSGLVPAPTSSLNELIKSFGDQGLSANDMVVLSGSHTI 198

Score = 73.9 bits (180), Expect = 1e-10
Identities = 37/66 (56%), Positives = 45/66 (68%), Gaps = 2/66 (3%)
Frame = +1

Query: 592 LTICLALFVLIWGSANA--QLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
L CL L V + G+ QLST+FY SCP L +V+ V+SA+ KETR+ ASLLRL F
Sbjct: 8 LRSCLVLLVAVCGAGKCWGLSTDFYSESCPMLMDTVRCEVESAVDKETRIAASLLRLHF 67

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 68 HDCFVN 73

>emb|CBI27506.1| unnamed protein product [Vitis vinifera]
Length = 266

Score = 177 bits (450), Expect = 7e-42
Identities = 89/125 (71%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RI+ N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 142 QARCVTFRDRIHDNGTNIDAGFASTRRRRCVPDNGNGDDNLAPLDLVTGPSFDNYYFKNL 201

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS + TFSSDFAAAM+KMGGDI PLTGSNGEIRK
Sbjct: 202 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSRSTFSSDFAAAMVKMGDIDPLTGSNGEIRKL 261

Query: 2164 CRRIN 2178
C IN
Sbjct: 262 CNAIN 266

Score = 138 bits (347), Expect = 6e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+QGCD SILLDD+++ EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
 Sbjct: 15 VQGCDASILLDDSATIQSEKNAPNNNSVRGFEVIDNVKSQVESICPGVVSCADILAVAA 74

 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDS S+ +GGPTW VKLG
 Sbjct: 75 RDS-----SVAVGGPTWTWVKLG 91

 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ T+ S A +P+ L++L+S FS+ GL+T+++VALSG+ I
 Sbjct: 92 RRDSTTSGLSQAAANLPSFRDGLDKLVSLFSSKGLNTREMAVALSGSHTI 140

>ref|XP_002274550.1| PREDICTED: hypothetical protein [Vitis vinifera]
 Length = 320

Score = 177 bits (450), Expect = 7e-42
 Identities = 89/125 (71%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
 Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
 QARC FR RI+ N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
 Sbjct: 196 QARCVTFRDRIHDNGTNIDAGFASTRRRRCVPDNGNGDDNLAPLDLVTNSFDNYYFKNL 255

 Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
 +Q+KGLL SDQ LFNGGSTDSIV YS + TFSSDFAAAM+KMGGI PLTGSNGEIRK
 Sbjct: 256 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSRSTFSSDFAAAMVKMGDIDPLTGSNGEIRKL 315

 Query: 2164 CRRIN 2178
 C IN
 Sbjct: 316 CNAIN 320

Score = 138 bits (347), Expect = 6e-30
 Identities = 77/169 (45%), Positives = 99/169 (58%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
 +QGCD SILLDD+++ EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
 Sbjct: 69 VQGCDASILLDDSATIQSEKNAPNNNSVRGFEVIDNVKSQVESICPGVVSCADILAVAA 128

 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDS S+ +GGPTW VKLG
 Sbjct: 129 RDS-----SVAVGGPTWTWVKLG 145

 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ T+ S A +P+ L++L+S FS+ GL+T+++VALSG+ I
 Sbjct: 146 RRDSTTSGLSQAAANLPSFRDGLDKLVSLFSSKGLNTREMAVALSGSHTI 194

Score = 62.0 bits (149), Expect = 5e-07
Identities = 25/47 (53%), Positives = 38/47 (80%)
Frame = +1

Query: 640 AQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
AQLS+ FY ++CP S++++ +++A+S+E RM ASL+RL FHDCFV
Sbjct: 23 AQLSSKFYDNTCPKALSTIRTAIRTAVSRERRMAASLIRLHFHDCFV 69

>gb|ACN42168.1| peroxidase 1 [Sesuvium portulacastrum]
Length = 318

Score = 177 bits (449), Expect = 9e-42
Identities = 83/124 (66%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFRA IYN+++I +FA++ + +CP +G+GDNNLAPLD QTP FD+ YF+ LV
Sbjct: 195 QARCTNFRAHIYNDSDINASFAKSLKANCPPKNGTGDNNLAPLDPQTPNKFHDHIYFQGLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNP GTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KK LHSDQ+L NG ST S ++ YSTNP FSSDF +MIKMGDI PLTGSNGEIRKNC
Sbjct: 255 NKKAPLHSDQELTNGASTSSWIQKYSTNP SLFSSDFGTSMIKMGDIKPLTGSNGEIRKNC 314

Query: 2167 RRIN 2178
RRIN
Sbjct: 315 RRIN 318

Score = 157 bits (398), Expect = 7e-36
Identities = 89/165 (53%), Positives = 105/165 (63%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS LLDDTSSF GEK+A+PN SARGFEVID IK+AVE+VCPGVVSCADILA+ A
Sbjct: 68 VNGCDGSNLLDDTSSFKGEKSASP NFQSARGFEVIDQIKAAVERVCPGVVSCADILAVTA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW+VKLG
Sbjct: 128 RDSV-----VGLGGPTWDVKLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRF SALGLSTKDLVALSG 1645
RRDARTA+Q+AA N+ IP +S+L++LIS F GL+ KDLVAL G
Sbjct: 145 RRDARTANQAAANSSIPPASSSLRLISSFQNNQGLTIKDLVALYG 189

Score = 86.3 bits (212), Expect = 3e-14
Identities = 46/68 (67%), Positives = 55/68 (80%), Gaps = 2/68 (2%)
Frame = +1

Query: 586 SRLTICLAL-FVLIW-GSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRL 759
+RLT LAL FV+++ GS++AQL+TNFY SCP+LF V+ VQSAI KE RMGASLLRL
Sbjct: 2 ARLTCFLALAFVIVFVGSSSAQLTTNFYEKSCPHLFPVVRDVVQSAIRKEARMGASLLRL 61

Query: 760 FFHDCFVN 783
FHDCFVN
Sbjct: 62 HFHDCFVN 69

>ref|XP_002269058.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 319

Score = 177 bits (448), Expect = 1e-41
Identities = 88/125 (70%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP TSG GD+N+A LDL TP SFDN YFKNL
Sbjct: 195 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPATSGDGDNNIAALDLVTPNSFDNYYFKNL 254

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV GYS +P TFSSDFA+AM+KMG+I PLTGS GEIRK
Sbjct: 255 IQKKGLLQSDQVLFSGGSTDSIVTGYSKSPSTFSSDFASAMVKMGNIEPLTGSAGEIRKL 314

Query: 2164 CRRIN 2178
C IN
Sbjct: 315 CSAIN 319

Score = 127 bits (318), Expect = 1e-26
Identities = 73/169 (43%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILL+D+SS EKNA N NS RG++VID++KS VE +CPG+VSCADILA+AA
Sbjct: 68 VQGCDASILLNDSSSIQSEKNAPNNLSVRGYDVIDDVKEVESICPGIVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VSG PTW V LG
Sbjct: 128 RDASVAVSG-----PTWTVNLG 144

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P + L++LIS F + GLS +D+VALSG+ I

Sbjct: 145 RRDSTTSGLSQAATNLPNFSDDLRLISLFGSKGLSERDMVALSGSHTI 193

Score = 63.9 bits (154), Expect = 1e-07
Identities = 28/57 (49%), Positives = 42/57 (73%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
LF+ AQLS++FY ++CP S++++ V++A+S+E RM ASL+RL FHDCFV
Sbjct: 12 LFIFSNMPCEAQLSSSFYDNTCPKALSTIRTAVRTAVSRERRMAASLIRLHFHDCFV 68

>emb|CBI27505.1| unnamed protein product [Vitis vinifera]
Length = 302

Score = 177 bits (448), Expect = 1e-41
Identities = 88/125 (70%), Positives = 100/125 (80%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP TSG GD+N+A LDL TP SFDN YFKNL
Sbjct: 178 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPATSGDGDNNIAALDLVTPNSFDNYYFKNL 237

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV GYS +P TFSSDFA+AM+KMG+I PLTGS GEIRK
Sbjct: 238 IQKKGLLQSDQVLFSGGSTDSIVTGYSKSPSTFSSDFASAMVKGNIPLTGSAGEIRKL 297

Query: 2164 CRRIN 2178
C IN
Sbjct: 298 CSAIN 302

Score = 127 bits (318), Expect = 1e-26
Identities = 73/169 (43%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+QGCD SILL+D+SS EKNA N NS RG++VID++KS VE +CPG+VSCADILA+AA
Sbjct: 51 VQGCDASILLNDSSSIQSEKNAPNNLSVRGYDVIDDVKSEVESICPGIVSCADILAVAA 110

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VSG PTW V LG
Sbjct: 111 RDASVAVSG-----PTWTVNLG 127

Query: 1511 RRDARTASQSAANNIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P + L++LIS F + GLS +D+VALSG+ I
Sbjct: 128 RRDSTTSGLSQAATNLPNFSDDLRLISLFGSKGLSERDMVALSGSHTI 176

Score = 62.8 bits (151), Expect = 3e-07
Identities = 26/47 (55%), Positives = 39/47 (82%)
Frame = +1

Query: 640 AQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
AQLS++FY ++CP S++++ V++A+S+E RM ASL+RL FHDCFV
Sbjct: 5 AQLSSSFYDNTCPKALSTIRTAVRTAVSRERRMAASLIRLHFHDCFV 51

>emb|CAL25300.1| properoxidase [Picea abies]
Length = 310

Score = 176 bits (447), Expect = 2e-41
Identities = 81/124 (65%), Positives = 101/124 (81%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFRA IYNETNI++ ++ + Q CP T+GSGD+NL+PLD TPT+FD Y+ NL
Sbjct: 187 QARCVNFRAHIYNETNIDSTYSTSLQSKCPSTAGSGDSNLSPLDYVTPTAFDKNYYSNLK 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ+LFNGGSTDS V Y++N +F SDFAAAM+KMG+I PLTG++G+IRKNC
Sbjct: 247 SKKGLLHSDQELFNGGSTDSQVTTYASNQNSFFSDFAAAMVKMGNIKPLTGTSGQIRKNC 306

Query: 2167 RRIN 2178
R+ N
Sbjct: 307 RKPN 310

Score = 159 bits (401), Expect = 3e-36
Identities = 88/165 (53%), Positives = 103/165 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDD+S+ TGEK ANPN NSARGF+VID IKS VEK C GVVSCADILAI+A
Sbjct: 60 VNGCDGSVLLDDSSITITGEKTANPNANSARGFDVIDTIKSNEKACSGVVSCADILAI 119

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 120 RDSV-----VELGGPSWTVM LG 136

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RRD+ TAS++ ANN IP PTS+L+ LIS F A GLSTK++VALSG
Sbjct: 137 RRDSTTASKNGANNIPPTSSLSNLISLFFQAQGLSTKEMVALSG 181

Score = 69.7 bits (169), Expect = 3e-09
Identities = 32/51 (62%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+AN QLS+ FY SCP S VK+ V+ A++ E RMGASLLRL FHDCFVN
Sbjct: 11 TANGQLSSTFYAQSCPTALSVVKA AVRQAVANEKRMGASLLRLHFHDCFVN 61

>ref|XP_002269145.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 175 bits (444), Expect = 3e-41
Identities = 87/125 (69%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGGTNIDAGFASTRRRRC PADNGNGDDNLAPLDLVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS GEIRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGEIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGC DASILLDDSP TIQSEKNAPNNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQT TNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 2e-07
Identities = 32/72 (44%), Positives = 49/72 (68%), Gaps = 1/72 (1%)
Frame = +1

Query: 568 TMAFCSRLTICLA-LFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGA 744
T S S I +A L +L AQLS++FY ++CP+ S++++ +++A+S+E RM A
Sbjct: 9 TWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNTCPSALSTIRTAIRTAVSRERRMAA 68

Query: 745 SLLRLFFHDCFV 780
SL+RL FHDCFV
Sbjct: 69 SLIRLHFHDCFV 80

>gb|ACJ85500.1| unknown [Medicago truncatula]
Length = 229

Score = 174 bits (441), Expect = 8e-41
Identities = 99/169 (58%), Positives = 106/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEKNA PN+NS RGF+VIDNIK+AVE VCPGVVSCADILAIAA
Sbjct: 72 VNGCDGSILLDDTSNFTGEKNALPNKNSVRGFDVIDNIKTAVENVCPGVVSCADILAIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
DSV I+ G PTWNVKLG
Sbjct: 132 TDSVAILGG-----PTWNVKLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRDA TASQS AN IP PTSNLN L S F +GLSTKDLVALSG I
Sbjct: 149 RRDATTASQSDANTAIPRPTSNLNILTSMFKNVGLSTKDLVALSGAHTI 197

Score = 95.1 bits (235), Expect = 6e-17
Identities = 49/68 (72%), Positives = 55/68 (80%), Gaps = 1/68 (1%)
Frame = +1

Query: 583 CSRLTI-CLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRL 759
CSR+T+ L LFVLI GS NAQLSTNFY +CP L S V+ VQSAISKE R+GAS+LRL
Sbjct: 6 CSRITMFSLVLFVLIIGSVNAQLSTNFYSKTCPKLSSIVQRQVQSAISKEARIGASILRL 65

Query: 760 FFHDCFVN 783
FFHDCFVN
Sbjct: 66 FFHDCFVN 73

Score = 43.1 bits (100), Expect = 0.26
Identities = 18/24 (75%), Positives = 21/24 (87%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFART 1878
QA+CT FR RIYNETNI+T+FA T
Sbjct: 199 QAKCTTFRVRIYNETNIDTSFAST 222

>emb|CAN80097.1| hypothetical protein [Vitis vinifera]
Length = 331

Score = 173 bits (438), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGGTNIDAGFASTRRRRCPADNGNGDDNLAPLDLVTNPSFDNNYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGXIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDA SILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.9 bits (154), Expect = 1e-07

Identities = 32/78 (41%), Positives = 52/78 (66%), Gaps = 8/78 (10%)
Frame = +1

Query: 571 MASFCSRLTICLA-LFVLIWG-----SANAQLSTNFYYHSCPRLFSSVKSTVQSAISK 726
+A+ SR C++ F+L+ G AQLS++FY + CP+ S++++ +++A+S+
Sbjct: 3 LAAGSSRWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNXCPSALSTIRTAIRTAIVSR 62

Query: 727 ETRMGASLLRLFFHDCFV 780
E RM ASL+RL FHDCFV
Sbjct: 63 ERRMAASLIRLHFHDCFV 80

>emb|CBI27503.1| unnamed protein product [Vitis vinifera]
Length = 357

Score = 172 bits (437), Expect = 2e-40
Identities = 85/121 (70%), Positives = 97/121 (80%), Gaps = 1/121 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSFGSDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYGNGTNI DAGFASTRRRRC PADNGNGDDNLAPLDLVTNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMEDI PL GS GEIRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGEIRKF 326

Query: 2164 C 2166
C
Sbjct: 327 C 327

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDASILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 2e-07
Identities = 32/72 (44%), Positives = 49/72 (68%), Gaps = 1/72 (1%)
Frame = +1

Query: 568 TMAFCSRLTICLA-LFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGA 744
T S S I +A L +L AQLS++FY ++CP+ S++++ +++A+S+E RM A
Sbjct: 9 TWPSCVSHAFILVAGLLILSNMPCEAQLSSSFYDNTCPSALSTIRTAIRTAIVSRERRMAA 68

Query: 745 SLLRLFFHDCFV 780
SL+RL FHDCFV
Sbjct: 69 SLIRLHFHDCFV 80

>emb|CBI27502.1| unnamed protein product [Vitis vinifera]
Length = 266

Score = 172 bits (437), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 142 QARCVTFRDRIYGNGTNIDAGFASTRRRRCPADNGNGDDNLAPLDLVTNPSFDNYYFKNL 201

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGDI PL GS G IRK
Sbjct: 202 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFSSAMVKMGDIEPLIGSAGVIRKF 261

Query: 2164 CRRIN 2178
C IN
Sbjct: 262 CNVIN 266

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 15 VQGCDASILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 75 RDA-----SVAVGGPTWTLKLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 92 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 140

>ref|XP_002269169.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 172 bits (437), Expect = 2e-40
Identities = 86/125 (68%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N TNI+ FA TR++ CP +G+GD+NLAPLDL TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYNGGTNIDAGFASTRRRRCPADNGGDDNLAPLDLVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSSDF++AM+KMGGDI PL GS G IRK
Sbjct: 267 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSDFAAMVKGMDIEPLIGSAGVIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 136 bits (343), Expect = 2e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+ + EKNA N NS RGFEVIDN+KS VE +CPGVVSCADILA+AA
Sbjct: 80 VQGCDA SILLDDSPTIQSEKNAPNNNSVRGFEVIDNVKSQVENICPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW +KLG
Sbjct: 140 RDA-----SVAVGGPTWTLKLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P L++L S FS+ GLST+D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPTFRDGLDRLTSLFSSKGLSTRDMVALSGSHTI 205

Score = 64.7 bits (156), Expect = 8e-08
Identities = 32/78 (41%), Positives = 53/78 (67%), Gaps = 8/78 (10%)
Frame = +1

Query: 571 MASFCSRLTICLA-LFVLIWG-----SANAQLSTNFYHSCPNIHFSSVKSTVQSAISK 726
+A+ SR C++ F+L+ G AQLS++FY ++CP+ S++++ +++A+S+

Sbjct: 3 LAAGSSRWPCVSHAFILVAGLLILSNMPCEAQLSSSFYDNACPSALSTIRTAIRTAISR 62

Query: 727 ETRMGASLLRLFFHDCFV 780
E RM ASL+RL FHDCFV

Sbjct: 63 ERRMAASLIRLHFHDCFV 80

>gb|AA013838.1|AF405326_1 peroxidase 2 [Lupinus albus]
Length = 260

Score = 172 bits (437), Expect = 2e-40
Identities = 81/126 (64%), Positives = 102/126 (80%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSG--DNNLAPLDLQTPTSFDNYYFKN 1980
+ARC+++R RIY++TNI+ FA++RQ++CPR S DNN+A LD +TPT FDN Y+KN
Sbjct: 135 KARCSSYRDRIYDDTNIDKLFAKSRQRNCPRKSSGTVKDNNVAVLDFKTPTHFDNLYYKN 194

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ KKGLLHSDQ+LFNGGSTDS+V YS N F+SDF AMIKMG+I PLTGSNG+IRK
Sbjct: 195 LINKKGLLHSDQELFNGGSTDSLVTYTSNNEKAFNSDFVTAMIKMGNIKPLTGSNGQIRK 254

Query: 2161 NCRRIN 2178
+CRR N
Sbjct: 255 HCRRAN 260

Score = 155 bits (392), Expect = 4e-35
Identities = 92/170 (54%), Positives = 102/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILLDDTSSF GEK A PN NS RGFEVID IKS VE+ CPGVVSCADI+AIAA
Sbjct: 7 VNGCDGSILLDDTSSFRGEKTAPPNNNSVRGFEVIDAIKSKVEEACPGVVSCADIVAIAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS I LGGP WNVK+G
Sbjct: 67 RDSTAI-----LGGPYWNVKVG 83

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD++TAS S A++G IP P S L+ LISRF A GLS KD+VALSG I
Sbjct: 84 RRDSKTASFS DASSGVIPPPFSTLSNLISRFQAQGLSIKDMVALSGAHTI 133

>gb|ABA96220.1| Cationic peroxidase 1 precursor, putative, expressed [Oryza sativa
(japonica cultivar-group)]
gb|EAY79691.1| hypothetical protein OsI_34838 [Oryza sativa Indica Group]
gb|EAY19422.1| hypothetical protein OsJ_34979 [Oryza sativa Japonica Group]

Length = 291

Score = 172 bits (437), Expect = 2e-40
Identities = 78/124 (62%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 170 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYAFDNFYKLL 227

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AAM+KMG+I+P+TGS+G+IRKNC
Sbjct: 228 NKKGVLSHSDQQLFNGGSADSQTTTYSNMATFFTFSAAMVKMGNNINPITGSSGQIRKNC 287

Query: 2167 RRIN 2178
R++N
Sbjct: 288 RKNV 291

Score = 146 bits (369), Expect = 2e-32
Identities = 82/170 (48%), Positives = 98/170 (57%)
Frame = +2

Query: 1148 QMQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
++ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ +E +CP VVSCADILA+A
Sbjct: 42 RIAGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAHIEGICPQVVSCADILAVA 101

Query: 1328 ARDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
AR+SV + LGGPTW V+L
Sbjct: 102 ARESV-----VALGGPTWVVQL 118

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 119 GRRDSTTASLDTANNDIPAPTFDLGDLTKSFSNKGLSATDMIALSGAHTI 168

>tpe|CAH69378.1| TPA: class III peroxidase 136 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 317

Score = 172 bits (437), Expect = 2e-40
Identities = 78/124 (62%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 196 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYAFDNFYKLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AAM+KMG+I+P+TGS+G+IRKNC
Sbjct: 254 NKKGVLHSDQQLFNGGSADSQTTTYSSNMATFFTFDSAAMVKMGINPITGSSGQIRKNC 313

Query: 2167 RRIN 2178
R++N
Sbjct: 314 RKNV 317

Score = 146 bits (369), Expect = 2e-32
Identities = 82/169 (48%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ +E +CP VVSCADILA+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAHIEGICPQVVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R+SV + LGGPTW V+LG
Sbjct: 129 RESV-----VALGGPTWVWQLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 146 RRDSTTASLDTANNDIPAPTFDLGDLTKSFSNKGLSATDMIALSGAHTI 194

Score = 71.2 bits (173), Expect = 9e-10
Identities = 35/62 (56%), Positives = 45/62 (72%), Gaps = 1/62 (1%)
Frame = +1

Query: 601 CLALFVLIWGS-ANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
C A+ +L + +AQLS NFY SCPN +++ V+SAI++E RMGASLLRL FHDCF
Sbjct: 9 CSAIALLFAANLVSAQLSANFYDKSCPINALPTIRIAVRSIAIARENRMGASLLRLHFHDCF 68

Query: 778 VN 783
VN
Sbjct: 69 VN 70

>ref|XP_002269216.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 199

Score = 172 bits (436), Expect = 3e-40
Identities = 86/125 (68%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983

QARC R RIY N TNI+T FA TR++ CP +G+GD+NLAPLD+ TP SFDN YFKNL
Sbjct: 75 QARCVTVRDRIYDNGTNIDTGFSTRRRRCVPDNGNGDDNLAPLDVVTTPNSFDNNYFKNL 134

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGSTDSIV YS +P TFSS+FA+AM+KMGGDI PL GS GEIRK

Sbjct: 135 IQRKGLLQSDQVLFNGGSTDSIVTEYSKSPSTFSSEFASAMVKMGDIEPLLGSAGEIRKI 194

Query: 2164 CRRIN 2178

C IN

Sbjct: 195 CNVIN 199

Score = 38.9 bits (89), Expect = 5.0
Identities = 22/42 (52%), Positives = 31/42 (73%)
Frame = +2

Query: 1532 SQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

SQ+AAAN +P+ L++LI FS+ GLST+D+VALSG+ I

Sbjct: 34 SQAAAN--LPSFRDGLDRLIPLFSSKGLSTRDMVALSGSHTI 73

>emb|CAH10839.1| peroxidase [Picea abies]
Length = 317

Score = 172 bits (436), Expect = 3e-40
Identities = 83/124 (66%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FRARIYNE+NI+T+FA + + SCP S GDN L+PLDL TPT+FDN Y+ +L

Sbjct: 196 QARCTTFRARIYNESNIDTSFATSVKSSCP--SAGGDNTLSPLDLATPTTFDNKYITDLG 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

+KGLLHSDQQLF+GGST+S V YS N TF +DFAAAM+KMG+ISPLTG++G+IRKNC

Sbjct: 254 NRKGLLHSDQQLFSGGSTNSQVTTYSANQNTFFTFDFAAAMVKMGNISPLTGTSGQIRKNC 313

Query: 2167 RRIN 2178

R+ N

Sbjct: 314 RKAN 317

Score = 158 bits (400), Expect = 4e-36
Identities = 91/165 (55%), Positives = 100/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI 1330

+ GCDGSILLDD S+FTGEK A PN NS RGF+VID IK+ VE C GVVSCADILAI A

Sbjct: 69 VNGCDGSILLDDNSTFTGEKTALPNANSVRGFDVIDTIKTQVEAACSGVSCADILAIVA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 129 RDSV-----VQLGGPTWTVLLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSAALGLSTKDLVALSG 1645
RRD+ TAS SAANN IP+P SNL+ LIS F+A GLSTKDLVALSG

Sbjct: 146 RRDSTTASLSAANNIPSPASNLSALISSFTAHLSTKDLVALSG 190

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/64 (48%), Positives = 41/64 (64%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
+ +C+ I +A+ QL++ FY CP S VK+ V A++ E RMGASLLRL FHD

Sbjct: 7 IVLCVLCISSINNAHGLTSTFYNKLCPALSIVKAAVNKAVNNEKRMGASLLRLHFHD 66

Query: 772 CFVN 783
CFVN

Sbjct: 67 CFVN 70

>ref|XP_002266365.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 328

Score = 172 bits (435), Expect = 4e-40
Identities = 81/124 (65%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYNE NI+ +F + Q +CP S GDN L+PLD QTPT+FDN Y+ NLV

Sbjct: 207 QARCTTFRTRIYNEANIDASFKTSLQANCP--SSGGDNTLSPLDTQTPTTFDNAYYTNLV 264

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNGGSTD++V YST TF +DFA AM+KMG++SPLTG++G+IR NC

Sbjct: 265 NKKGLLHSDQQLFNGGSTDAVVNTYSTRSTTFFTDANAMVKMGNLSPLTGTSGQIRTNC 324

Query: 2167 RRIN 2178
R+ N

Sbjct: 325 RKTN 328

Score = 147 bits (372), Expect = 8e-33
Identities = 83/169 (49%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RG+EV+D IKS +E CPGVVSCADILA+AA
Sbjct: 80 VNGCDASILLDDTSNFTGEKTAGPNANSVRGYEVVDTIKSQLEASCPGVVSCADILAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GP+W V+LG
Sbjct: 140 RDSV-----VALRGPSWMVRLG 156

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LIS F+ G + +++VALSG+ I
Sbjct: 157 RRDSTTASLSAANSNIPAPTLNLSGLISAFTNKGFNAREMVALSGSHTI 205

Score = 76.3 bits (186), Expect = 3e-11
Identities = 35/52 (67%), Positives = 40/52 (76%)
Frame = +1

Query: 628 GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
G A+AQL+TNFY +CPN S +KS V SA+ E RMGASLLRL FHDCFVN
Sbjct: 30 GMSAQLTTFYAKTCPNALSIIKSAVNSAVKSEARMGASLLRLHFHDCFVN 81

>ref|NP_001106040.1| plasma membrane-bound peroxidase 2b precursor [Zea mays]
sp|A5H452.1|PER70_MAIZE RecName: Full=Peroxidase 70; AltName: Full=Plasma membrane-bound
peroxidase 2b; Short=pmPOX2b; Flags: Precursor
gb|ABN48843.1| plasma membrane-bound peroxidase 2b [Zea mays]
Length = 321

Score = 172 bits (435), Expect = 4e-40
Identities = 77/123 (62%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C NFRA IYN+TN+ AFA R+ +CP +G+GD NLAPLD TPT+FDN Y+ NL+
Sbjct: 199 AQCKNFRAHIYNDTNVNAAFATLRRANCPAAAGNGDGNLAPLDTATPTAFDNAYYTNLLA 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQQLFNGG+TD +VR Y++ P FS DFAAAMI+MG+ISPLTG+ G+IR+ C
Sbjct: 259 QRGLLHSDQQLFNGGATDGLVRTYASTPRRFSRDFAAAMIRMGNISPLTGTGQGIIRRACS 318

Query: 2170 RIN 2178
R+N
Sbjct: 319 RVN 321

Score = 140 bits (353), Expect = 1e-30

Identities = 80/169 (47%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGS+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE VCPGVVSCADILA+AA

Sbjct: 71 VQGCDGSVLLNDTATFTGEQTANPNVGSIRFGVVDNIKAQVEAVCPGVVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 131 RDSV-----VALGGPSWRVLLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS + AN+ +PAP+ +L L + F+ LS DLVALSG I

Sbjct: 148 RRDSTTASLALANSDLPAPSLDLANLTAAFAKKRLSRTDLVALSGAHTI 196

Score = 68.2 bits (165), Expect = 8e-09
Identities = 34/72 (47%), Positives = 49/72 (68%)
Frame = +1

Query: 565 LTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGA 744
+ +SF S L++ + L + A+AQLS FY SCP +++K+ V +A+++E RMGA

Sbjct: 1 MASSSFTS-LSVMVLLCLAAA AVASAQLSPTFYSRSCPRLATIKAAVTA AVAQEARMGA 59

Query: 745 SLLRLEFFHDCFV 780

SLLRL FHDCFV

Sbjct: 60 SLLRLHFHDCFV 71

>gb|EAY82023.1| hypothetical protein OsI_37207 [Oryza sativa Indica Group]
gb|EAZ17184.1| hypothetical protein OsJ_32691 [Oryza sativa Japonica Group]
Length = 291

Score = 171 bits (434), Expect = 5e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+

Sbjct: 170 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYTFDNFYKNNL 227

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC

Sbjct: 228 NKKGVLEHSDQQLFNGGSADSQTTTYSNMATFFTFDSAAIVKMGNIPLTGSSGQIRKNC 287

Query: 2167 RRIN 2178

R++N

Sbjct: 288 RKNV 291

Score = 146 bits (368), Expect = 2e-32
Identities = 83/167 (49%), Positives = 95/167 (56%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AARD
Sbjct: 45 GCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAARD 104

Query: 1337 SVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR R 1516
SV + GGPTW V+LGRR
Sbjct: 105 SVFAL-----GGPTWVVLGR R 121

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 122 DSTTASLDTANNDIPAPTLDLGLTKSFSNKGLSATDMIALSGAHTI 168

>gb|ABA91154.1| Cationic peroxidase 1 precursor, putative, expressed [Oryza sativa
(japonica cultivar-group)]
Length = 254

Score = 171 bits (434), Expect = 5e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 133 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYTFDNFYK NLL 190

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC
Sbjct: 191 NKKGV LHSDQQLFNGGSADSQTTTYSSNMATFFTFDSAAIVKMGNIDPLTGSSGQIRKNC 250

Query: 2167 RRIN 2178
R++N
Sbjct: 251 RKNV 254

Score = 148 bits (374), Expect = 4e-33
Identities = 84/169 (49%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
M+GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AA
Sbjct: 6 MKGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAA 65

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + GGPTW V+LG
Sbjct: 66 RDSVFAL-----GGPTWVVLG 82

Query: 1511 RRDARTASQAANNIPAPTSNLNLISRFSLGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 83 RRDSTTASLDTANNDIPAPTLDLGLTKSFSNKGLSATDMIALSGAHTI 131

>ref|NP_001065566.1| Os11g0112200 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69373.1| TPA: class III peroxidase 131 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF27411.1| Os11g0112200 [Oryza sativa Japonica Group]
Length = 317

Score = 171 bits (434), Expect = 5e-40
Identities = 78/124 (62%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
QARC NFR RIY+ETNI+T+ A + + +CP T+G DNN++PLD TP +FDN+Y+KNL+
Sbjct: 196 QARCVNFRNRIYSETNIDTSLATSLKSNCPNTTG--DNNISPLDASTPYTFDNFYKNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N TF +DF+AA++KMG+I PLTGS+G+IRKNC
Sbjct: 254 NKKGVHLHSDQQLFNGGSADSQTTTYSSNMATFFTFDSAAIVKMGNIDPLTGSSGQIRKNC 313

Query: 2167 RRIN 2178
R++N
Sbjct: 314 RKNV 317

Score = 146 bits (369), Expect = 2e-32
Identities = 83/169 (49%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VIDNIK+ VE +CP VVSCADILA+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAAPNNNSLRGFDVIDNIKAQVEGICPQVVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + GGPTW V+LG
Sbjct: 129 RDSVFAL-----GGPTWVVLG 145

Query: 1511 RRDARTASQAANNIPAPTSNLNLISRFSLGLSTKDLVALSGTKHI 1657
RRD+ TAS ANN IPAPT +L L FS GLS D++ALSG I
Sbjct: 146 RRDSTTASLDTANNDIPAPTLDLGLTKSFSNKGLSATDMIALSGAHTI 194

Score = 74.7 bits (182), Expect = 8e-11
Identities = 36/67 (53%), Positives = 48/67 (71%)
Frame = +1

Query: 583 CSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLF 762
CS + + A ++ +AQLS NFY SCPN S++++ V+SA++KE RMGASLLRL
Sbjct: 9 CSVIALLLFAAHLV-----SAQLSANFYDKSCPNALSTIRTAVRSAVAKENRMGASLLRLH 63

Query: 763 FHDCFVN 783
FHDCFVN
Sbjct: 64 FHDCFVN 70

>gb|EEE67815.1| hypothetical protein OsJ_25569 [Oryza sativa Japonica Group]
Length = 324

Score = 171 bits (433), Expect = 6e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
Sbjct: 200 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 260 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGQIRLSC 319

Query: 2167 RRIN 2178
++N
Sbjct: 320 SKVN 323

Score = 116 bits (290), Expect = 2e-23
Identities = 71/167 (42%), Positives = 86/167 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD
Sbjct: 80 GCDASVLLSQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 198

Score = 71.6 bits (174), Expect = 7e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNI FSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SSSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792
HDCFV +
Sbjct: 67 HDCFVQASF 75

>ref|NP_001060628.1| Os07g0677200 [Oryza sativa (japonica cultivar-group)]
dbj|BAC83103.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAF22542.1| Os07g0677200 [Oryza sativa Japonica Group]
dbj|BAG93342.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96895.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 317

Score = 171 bits (433), Expect = 6e-40
Identities = 78/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGQIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 5e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
 Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAA 125

 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV + LGGP+W V LG
 Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
 RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
 Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 9e-10
 Identities = 34/65 (52%), Positives = 45/65 (69%)
 Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYHHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
 S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
 Sbjct: 7 SSSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITAAVNSEARMGASLLRLHF 66

 Query: 766 HDCFV 780
 HDCFV
 Sbjct: 67 HDCFV 71

>tpe|CAH69353.1| TPA: class III peroxidase 111 precursor [Oryza sativa (japonica
 cultivar-group)]
 Length = 323

Score = 171 bits (433), Expect = 6e-40
 Identities = 78/124 (62%), Positives = 98/124 (79%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAPLD TP +FDN Y+ NL+
 Sbjct: 199 QAQCQNFDRDIYNETNIDSAFATQRQANCPRPTGSGDSNLAPLDTTTPNAFDNAYYSNLL 258

 Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
 Sbjct: 259 SNKGLLHSDQVLFNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTGQGIIRLSC 318

Query: 2167 RRIN 2178
 ++N
 Sbjct: 319 SKVN 322

Score = 113 bits (283), Expect = 2e-22

Identities = 69/162 (42%), Positives = 84/162 (51%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD

Sbjct: 80 GCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALS 1642

D+ TAS++ AN +PAP+S+L +LI FS GL D+VALS
Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALS 193

Score = 71.6 bits (174), Expect = 7e-10
Identities = 34/69 (49%), Positives = 46/69 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SSLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792

HDCFV +
Sbjct: 67 HDCFVQASF 75

>emb|CBI27501.1| unnamed protein product [Vitis vinifera]
Length = 265

Score = 170 bits (431), Expect = 1e-39
Identities = 82/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+

Sbjct: 142 QARCVTFRDRVYNGTDIDAGFASTRRRRC PADNGGDANLAPLELVTPNSFDNYYFKNLI 201

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNP GTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTD+IV YS +P TF SDFA+AM+KM GDI PLTGS G IRK C

Sbjct: 202 QRKGLLQSDQVLFGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEPLTGSAGVIRKFC 261

Query: 2167 RRIN 2178

IN
Sbjct: 262 NVIN 265

Score = 134 bits (337), Expect = 9e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 15 VQGCDASILLDDSSSIQSEKNAPNNLSVRGYEVIDNIKSKVESICPGVVSCADIVAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VS GPTW VKLG
Sbjct: 75 RDASVAVS-----GPTWTVKLG 91

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I
Sbjct: 92 RRDSTTSGLSLAATNLPSFRDSLDKLVSLFGSKGLSARDMVALSGSHTI 140

>ref|XP_002269266.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 326

Score = 170 bits (431), Expect = 1e-39
Identities = 82/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+
Sbjct: 203 QARCVTFRDRVYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 262

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTD+IV YS +P TF SDFA+AM+KMGGDI PLTGS G IRK C
Sbjct: 263 QRKGLLQSDQVLFGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEPLTGSAGVIRKFC 322

Query: 2167 RRIN 2178
IN
Sbjct: 323 NVIN 326

Score = 134 bits (337), Expect = 9e-29
Identities = 77/169 (45%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 76 VQGCDASILLDDSSSIQSEKNAPNNLSVRGYEVIDNIKSKVESICPGVVSCADIVAVAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD+ VS GPTW VKLG
Sbjct: 136 RDASVAVS-----GPTWTVKLG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I

Sbjct: 153 RRDSTTSGLSLAATNLPFRDSDLKLVSLFGSKGLSARDMVALSGSHTI 201

Score = 62.4 bits (150), Expect = 4e-07
Identities = 31/69 (44%), Positives = 46/69 (66%), Gaps = 1/69 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGS-ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753

S S I LA+F+++ AQLS FY +CP +++++ V++A+S+E RM ASL+

Sbjct: 8 SCISPACIFLAVFLILSNMPCEAQLSPTFYDDTCPTALTIRTAVRTAVSRERRMAASLI 67

Query: 754 RLFFHDCFV 780

RL FHDCFV

Sbjct: 68 RLHFHDCFV 76

>ref|XP_002509730.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]

gb|EEF51117.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]

Length = 323

Score = 170 bits (431), Expect = 1e-39
Identities = 82/125 (65%), Positives = 98/125 (78%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983

QARC FR RIYN ++I+ FA TR++ CP +G+GD NLA LDL TP SFDN YF+NL

Sbjct: 199 QARCLTFRGRIYNNASDIDAGFASTRRRQCPANNGNGDGNLAALDLVTPNSFDNYYFRNL 258

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163

+QKKGLL SDQ LF+GGSTD+IV YS +P TFSSDFA+AM+KMGDI PLTGS GEIR+

Sbjct: 259 IQKKGLLQSDQVLFSGGSTDNIVNEYSRSPSTFSSDFASAMVKMGDIEPLTGSQGEIRRL 318

Query: 2164 CRRIN 2178

C +N

Sbjct: 319 CNVVN 323

Score = 141 bits (355), Expect = 7e-31
Identities = 79/169 (46%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+QGCDGSILLDDTSS TGEK A N NS RGF+VIDN K+ VE +CPG+VSCADI+A+AA
Sbjct: 72 VQGCDGSILLDDTSSMTGEKFARNNNNSVRGFQVIDNAKAQVESICPGIVSCADIVAVAA 131

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W VKLG
Sbjct: 132 RDA-----SVAVGGPSWTVKLG 148

Query: 1511 RRDARTASQSAANNIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ +ASQ A+ +P T +L LIS F GLS +D+VALSG I
Sbjct: 149 RRDSTSASQRLADANLPGFTDSLESLSLFRKGLSARDMVALSGAHTI 197

Score = 74.7 bits (182), Expect = 8e-11
Identities = 33/67 (49%), Positives = 51/67 (76%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
F +R+ + + L VL ++AQLS+NFY ++CPN S++++ ++SA+S+E RM ASL+RL
Sbjct: 6 FFNRMLTIFLIVLSSMQSHAQLSSNFYDNTCPNALSTIRTAIRSAVSRERRMSASLRL 65

Query: 760 FFHDCFV 780
FHDCFV
Sbjct: 66 HFHDCFV 72

>emb|CBI18066.1| unnamed protein product [Vitis vinifera]
Length = 263

Score = 170 bits (430), Expect = 1e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETNI+ +F + Q +CP S GDNNL+PLD ++PT+FDN YF NLV
Sbjct: 142 QARCTNFRDRLYNETNIDASQSSLQANCP--SSGGDNNLSPLDTKSPTTFDNAYFTNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLFNGGSTDS V YST TF +DFA A++KMG++SPLTG++G+IR NC
Sbjct: 200 NNKGLLHSDQQLFNGGSTDSQVTTYSTKSTTFFTFANAIKMGNSPLTGTSGQIRTNC 259

Query: 2167 RRIN 2178
R+ N
Sbjct: 260 RKTN 263

Score = 150 bits (379), Expect = 1e-33
Identities = 86/169 (50%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RGF+VID IKS VE CPGVVSCADILA+ A
Sbjct: 15 VNGCDASILLDDTSNFTGEKTAVPNANSVRGFDVIDTIKSQVESSCPGVVSCADILAVVA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 75 RDSV-----VALGGPSWTVRLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ IPAPT NL+ LIS FS G S ++VALSG+ I
Sbjct: 92 RRDSTTASLSTANS DIPAPTLNLSGLISSFSNKGFSANEMVALSGSHTI 140

>ref|XP_002268259.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 298

Score = 170 bits (430), Expect = 1e-39
Identities = 81/124 (65%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETNI+ +F + Q +CP S GDNNL+PLD ++PT+FDN YF NLV
Sbjct: 177 QARCTNFRDRLYNETNIDASFQSSLQANCP--SSGGDNNLSPLDTKSPTTFDNAYFTNLV 234

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQQLFNGGSTDS V YST TF +DFA A++KMG++SPLTG++G+IR NC
Sbjct: 235 NNKGLLHSDQQLFNGGSTDSQVTTYSTKSTTFFTFANAIKMGNLSPLTGTSGQIRTNC 294

Query: 2167 RRIN 2178
R+ N
Sbjct: 295 RKTN 298

Score = 150 bits (380), Expect = 9e-34
Identities = 86/169 (50%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCD SILLDDTS+FTGEK A PN NS RGF+VID IKS VE CPGVVSCADILA+ A
Sbjct: 50 VKGCDASILLDDTSNFTGEKTAVPNANSVRGFDVIDTIKSQVESSCPGVVSCADILAVVA 109

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 110 RDSV-----VALGGPSWTVRLG 126

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ IPAPT NL+ LIS FS G S ++VALSG+ I
Sbjct: 127 RRDSTTASLSTANS DIPAPTLNLSGLISSFSNKGFSANEMVALSGSHTI 175

Score = 71.2 bits (173), Expect = 9e-10
Identities = 32/49 (65%), Positives = 39/49 (79%)
Frame = +1

Query: 634 ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFV 780
A+ AQL+TN+Y SCPN S +KS V +A++ E RMGASLLRL FHDCFV
Sbjct: 2 ASAQLTTNYSSCPNALSIKSAVNTAVNNEARMGASLLRLLFHDCFV 50

>ref|XP_002299006.1| predicted protein [Populus trichocarpa]
gb|EEE83811.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 170 bits (430), Expect = 1e-39
Identities = 82/125 (65%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N ++I+ FA TR+++CP SG+G+NNLAPLDL TP SFDN YF+NL
Sbjct: 198 QARCVTFRGRIYDNSSDIDAGFASTRRRNCPSASGNGNNLAPLDLVTSPN SFDNNYFRNL 257

Query: 1984 VQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q++GLL SDQ LF+G STDSIV YS NP FSSDFAAAM++MGDI PLTGS GEIR+
Sbjct: 258 IQRRGLLQSDQVLFSGQSTDSIVTEYSRNP SLFSSDFAAAMLRMGDIEPLTGSQGEIRRV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSVVN 322

Score = 126 bits (317), Expect = 2e-26
Identities = 72/169 (42%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SI+LD++ S EK + N NS RGFEVID+ K+ VE +CPGVVSCADI A+AA
Sbjct: 71 VQGCDASIMLDNSPSIDSEKFSFSNNNSIRGFEVIDDAKAQVESICPGVVSCADIAAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 131 RDA-----SVAVGGPSWTVRLG 147

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ IP T++L LI F+ GLS +D+VALSG+ I
Sbjct: 148 RRDSTTASRLADSDIPRATTSLVNLIGMFNGKGLSERDMVALSGSHTI 196

Score = 66.2 bits (160), Expect = 3e-08
Identities = 32/69 (46%), Positives = 47/69 (68%), Gaps = 4/69 (5%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSA----NAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
SRL++ +F L S+ AQLS+NFY +CPN +++++ ++ A+S E RM ASL+
Sbjct: 3 SRLSLACVVFS LFLISSCLPCQAQLSSNFYDSTCPNALT TIRTAIRRAVSSERRMAASLI 62

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 63 RLHFHDCFV 71

>ref|XP_002333334.1| predicted protein [Populus trichocarpa]
gb|EEE74658.1| predicted protein [Populus trichocarpa]
Length = 322

Score = 170 bits (430), Expect = 1e-39
Identities = 82/125 (65%), Positives = 99/125 (79%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSF DNYYFKNL 1983
QARC FR RIY N ++I+ FA TR+++CP SG+G+NNLAPLDL TP SFDN YF+NL
Sbjct: 198 QARCVTFRGRIYDNSSDIDAGFASTRRRNCPSASGNGNNLAPLDLVTPNSFDN NYFRNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q++GLL SDQ LF+G STDSIV YS NP FSSDFAAAM++MGDI PLTGS GEIR+
Sbjct: 258 IQRRGLLQSDQVLFSGQSTDSIVTEYSRNP SLFSSDFAAAMLRMGDIEPLTGSQGEIRRV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CSVVN 322

Score = 126 bits (316), Expect = 2e-26
Identities = 71/169 (42%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AA 1330
+QGCD SI+LD++ S EK + N NS RGFEV+D+ K+ VE +CPGVVSCADI A+AA
Sbjct: 71 VQGCDASIMLDNPSIDSEKFSFSNNNSIRGFEVVDDAKAQVESICPGVVSCADIAAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 131 RDA-----SVAVGGPSWTVRLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ IP T++L LI F+ GLS +D+VALSG+ I
Sbjct: 148 RRDSTTASRLADSDIPRATTSLVNLIGMFNGKGLSERDMVALSGSHTI 196

Score = 66.2 bits (160), Expect = 3e-08
Identities = 32/69 (46%), Positives = 47/69 (68%), Gaps = 4/69 (5%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSA----NAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
SRL++ +F L S+ AQLS+NFY +CPN +++++ ++ A+S E RM ASL+
Sbjct: 3 SRLSLACVVFSLFLISSCLPCQAQLSSNFYDSTCPNALTTIRTAIRRAVSSERRMAASLI 62

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 63 RLHFHDCFV 71

>ref|XP_002285723.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 170 bits (430), Expect = 1e-39
Identities = 84/124 (67%), Positives = 102/124 (82%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR+RIYNETNI+ AFA ++Q+ CP T G DNNL+ LD +T T FDN YF+NL
Sbjct: 195 KARCTSFRRSRIYNETNIDAAFATSKQKICPSTGG--DNNLSDLD-ETTTVFDNVYFRNLK 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQL+NGGSTDSIV YSTN TF +D A AMIKMG++SPLTG+NGEIR +C
Sbjct: 252 AKKGLLHSDQQLYNGGSTDSIVETYSTNSATFFTDVANAMIKMGNLSPLTGTNGEIRTDC 311

Query: 2167 RRIN 2178
++IN
Sbjct: 312 KKIN 315

Score = 155 bits (391), Expect = 5e-35
Identities = 85/167 (50%), Positives = 103/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLDDT+SFTGEK A PN++S RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTASFTGEKTAGPNKDSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW ++LGRR
Sbjct: 130 SV-----VALGGPTWTLQLGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +P P S+L+ LISRFS G +TK++VALSGT I
Sbjct: 147 DSTTASLSTANS DLP GPASDLSTLISRFSNKGFTTKEMVALSGTHTI 193

Score = 75.1 bits (183), Expect = 6e-11
Identities = 38/70 (54%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSLFCVFSFLL--GMAHAQLSSNFYASSCPKALSTIRAAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAA46916.1| peroxidase [Oryza sativa (japonica cultivar-group)]
prf||1909367A peroxidase
Length = 317

Score = 170 bits (430), Expect = 1e-39
Identities = 77/124 (62%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLAP+D TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTSGGDSNLAPVDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNNGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNNGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTQGQIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 5e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 9e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITAAVNSEARMGASLLRLHF 66

Query: 766 HDCFV 780
HDCFV
Sbjct: 67 HDCFV 71

>ref|XP_002319967.1| predicted protein [Populus trichocarpa]
gb|EEE95890.1| predicted protein [Populus trichocarpa]
Length = 312

Score = 169 bits (429), Expect = 2e-39
Identities = 82/120 (68%), Positives = 94/120 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
Q +C FRARIYNETNI+ +FA RQ+ CP T+G D+NLAPLD QTP FDN Y+KNL+
Sbjct: 191 QTKCKTFRARIYNETNIDKSFATMRQKMCPLTTG--DDNLAPLDFQTPNVFDNNYYKNLI 248

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ LF+G STDS+VR YS NP F SDFAAAM+KMGGDI P TG+ GEIRK C
Sbjct: 249 HKKGLLHSDQVLFSGESTDSLVRTYSNPNPDIFFSDFAAAMVKMGDIDPRTGTRGEIRKNC 308

Score = 140 bits (352), Expect = 2e-30
Identities = 75/169 (44%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCD SILL+DT++F GE+ A PN NS RG+ V+ IKS +EKVCPG+VSCADI+ IAA
Sbjct: 64 VKGCDASILLEDATATFKGEQGAGPNNSVRGYNVVAIKSKLEKVCPGIVSCADIVVIAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS ++ LGGP W VKLG
Sbjct: 124 RDS-----TVLLGGPYWKVKLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TA+ +AA+ +P+ TS ++QLI RF + GLS D+VALSG+ I
Sbjct: 141 RRDSKTANMNAASKSLPSDTSTVSQLIKRFKSKGLSATDMVALSGSHTI 189

Score = 84.3 bits (207), Expect = 1e-13
Identities = 40/63 (63%), Positives = 51/63 (80%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
+++ LAL ++ S++A LST+FY SCP LF +VKS VQSAI+KE RMGASL+RLFFHD
Sbjct: 2 VSVTLALLLIYTSSSSAHLSTDFYDKSCPQLFGTVKSVVQSAIAKERRMGASLVRLFFHD 61

Query: 772 CFV 780
CFV
Sbjct: 62 CFV 64

>gb|ABK24123.1| unknown [Picea sitchensis]
Length = 208

Score = 169 bits (427), Expect = 3e-39
Identities = 81/124 (65%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN++NI+TA+A++ Q CPR+ G DN L+PLD QTPT F+N Y+KNLV
Sbjct: 87 KARCTSRDHIYNSNIDTAYAKSLQAKCPRSGG--DNRLSPLDYQTPTKFENYYKNLV 144

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNG STDS+V YS N F +DFAAAMIKMG+I PLTGS G+IRKNC
Sbjct: 145 ARKGLLHSDQELFNGVSTDSLVTKYSKNLKLFENDFAAAMIKMGNIMPLTGSQGGIRKNC 204

Query: 2167 RRIN 2178
R+ N
Sbjct: 205 RKRN 208

Score = 91.7 bits (226), Expect = 6e-16
Identities = 54/124 (43%), Positives = 66/124 (53%)
Frame = +2

Query: 1274 VEKVC PGV VSCADILAI AARDSVQIVSGQTTNKNTLN*IIKLYISK LITNLVPHMQLKRT 1453
+EK C GVVSCADILA+AARDSV
Sbjct: 1 MEKACSGV VSCADILAVAARDSV----- 23

Query: 1454 FC*F*SI*LGGPTWNVKLGRRDARTASQSAANN GIPAPTSNLNLISRFSALGLSTKDLV 1633
+ LGGPTW V LGRRD+ TA+++AAN IPAPT+NL L S+F A GLS +++V
Sbjct: 24 -----VTLGGPTWTVMLGRRDSGTANRTAANTNIPAPTANLANLTSKFGAQGLSKREMV 77

Query: 1634 ALSG 1645
LSG
Sbjct: 78 VLSG 81

>gb|AAA20473.1| peroxidase [Cenchrus ciliaris]
Length = 313

Score = 169 bits (427), Expect = 3e-39
Identities = 78/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR IYN+TNI T FA + + +CPR +GSGD NLA LD TP +FDN YFKNL+
Sbjct: 190 QAQCLNFRDHIYNDTNINTGFASSLKANCPRPTGSGDGNLASLDTSTPYTFDNAYFKNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI KMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++NP FSS FAAAM+KM +SPLTGS G+IR C
Sbjct: 250 SQKGLLHSDQQLFNGGSTDNTVRNFASNPFAFSSAFAAAMVKMASLSPLTGSQQGQIRLTC 309

Query: 2167 RRIN 2178
+ N
Sbjct: 310 SKAN 313

Score = 103 bits (258), Expect = 1e-19
Identities = 67/170 (39%), Positives = 85/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI AA 1330
+QGCD S+LLD GE+ A PN S RGF+VI NIK+ VE +C VSCADILA+ A
Sbjct: 66 VQGCDASVLLDSG----GEQGAIPNAGSLRGFDVIANIKAQVEAICKQTVSCADILAVGA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R SV + LGGP+W V LG
Sbjct: 122 RHSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNIPAPTS-NLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ + S + AN+ +PA S NL+QLI F G + ++VALSG I
Sbjct: 139 RRDSTSGSAALANSIDLPAASFNLSQLIGSFDNKGFTATEMVALSGAHTI 188

Score = 73.2 bits (178), Expect = 2e-10
Identities = 39/70 (55%), Positives = 47/70 (67%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L + + A+AQLS FY SCPN S++KS V +A+ KE RMGASL
Sbjct: 1 MASSVSGLLLMLCMAAV----ASAQLSATFYDTSCPNALSTIKSAVTAAVKKENRMGASL 56

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 57 LRLHFHDCFV 66

>gb|ABK23423.1| unknown [Picea sitchensis]
Length = 318

Score = 168 bits (426), Expect = 4e-39
Identities = 81/124 (65%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNE+NI+T+ A + CPRT G DN L+PLDL TP +FD +Y+ NL
Sbjct: 197 QARCTSFARIYNESNIDTSLATAVKPKCPRTGG--DNTLSPLDLATPITFDKHYCNLR 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNGGSTDS V YSTN F +DFAAAM+ MG+I PLTG++G+IR+NC
Sbjct: 255 SKKGLLHSDQQLFNGGSTDSQVTTYSTNQNNFFTFDFAAAMVMGNIKPLTGTSGQIRRNC 314

Query: 2167 RRIN 2178
R+ N
Sbjct: 315 RKS N 318

Score = 149 bits (377), Expect = 2e-33
Identities = 86/169 (50%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+ GCDGSILLDD S+FTGEK A PN NS RG++VID IK+ VE C GVVSCADI+AIAA
 Sbjct: 70 VNGCDGSILLDDNSTFTGEKTATPNNSVIRGYDVIDTIKTQVEAACSGVVSCADIVAIAA 129

 Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV + LGGPTW V LG
 Sbjct: 130 RDSV-----VALGGPTWTVLLG 146

 Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
 RRD+ TAS +AAN+ IP+P SNL+ LIS F + LS KDLVALSG I
 Sbjct: 147 RRDSTTASFNAANSSIPSPASNLSTLISSFRSHNLSPKDLVALSGAHTI 195

Score = 66.6 bits (161), Expect = 2e-08
 Identities = 33/64 (51%), Positives = 44/64 (68%), Gaps = 2/64 (3%)
 Frame = +1

Query: 598 ICLALFVL--IWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
 I + LF++ I + QL++ FY SCP S V++ V+ A++KE RMGASLLRL FHD
 Sbjct: 8 IPIVLFIIICIPNIVHGLTSTFYSESCPRALSIVQAAVEQAVAKERRMGASLLRLHFHD 67

 Query: 772 CFVN 783
 CFVN
 Sbjct: 68 CFVN 71

>ref|NP_001060629.1| Os07g0677300 [Oryza sativa (japonica cultivar-group)]
 sp|Q0D3N0.1|PER2_ORYSJ RecName: Full=Peroxidase 2; Flags: Precursor
 dbj|BAA03911.1| peroxidase [Oryza sativa Japonica Group]
 dbj|BAC79528.1| peroxidase [Oryza sativa Japonica Group]
 dbj|BAC83104.1| peroxidase [Oryza sativa Japonica Group]
 tpe|CAH69354.1| TPA: class III peroxidase 112 precursor [Oryza sativa (japonica
 cultivar-group)]
 dbj|BAF22543.1| Os07g0677300 [Oryza sativa Japonica Group]
 dbj|BAG93552.1| unnamed protein product [Oryza sativa Japonica Group]
 gb|EEE67816.1| hypothetical protein OsJ_25570 [Oryza sativa Japonica Group]
 Length = 314

Score = 168 bits (426), Expect = 4e-39
 Identities = 76/124 (61%), Positives = 99/124 (79%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
 QA+C NFR R+YNETNI+++FA + +CPR +GSGD+NLAPLD TP +FD+ Y+ NL+
 Sbjct: 191 QAQCQNFDRRLYNETNIDSSFATALKANCPRTSGSGDSNLAPLDTTPNAFDSAYYTNLL 250

 Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 KLLHSDQ LFNGGSTD+ VR +S+N F+S F AAM+KMG+ISPLTG+ G+IR NC
 Sbjct: 251 SNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTAAMVKGNIPLTGTGQIRLNC 310

Query: 2167 RRIN 2178

++N

Sbjct: 311 SKVN 314

Score = 121 bits (303), Expect = 8e-25

Identities = 72/169 (42%), Positives = 89/169 (52%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+QGCD S+LL E+NA PN S RGF V+DNIK+ VE +C VSCADILA+AA

Sbjct: 69 VQGCDASVLLSGQ-----EQNAGPNAGSLRGFNVDNIKTQVEAICSQTVSCADILAVAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGP+W V LG

Sbjct: 124 RDSV-----VALGGPSWTVLLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TA++S AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 141 RRDSTTANESQANTDLPAPSSSLAELIGNFSRKGLDVTDMVALSGAHTI 189

Score = 70.5 bits (171), Expect = 2e-09

Identities = 36/70 (51%), Positives = 49/70 (70%)

Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750

MAS S +++ L + + +A+AQLS FY SCPN S++KS V +A++ E RMGASL

Sbjct: 1 MAS-ASSVSLMLLVAAAMASAASAQLSATFYDTSCPNALSTIKSAVTA AVNSEPRMGASL 59

Query: 751 LRLFFHDCFV 780

+RL FHDCFV

Sbjct: 60 VRLHFHDCFV 69

>gb|ACJ11762.1| class III peroxidase [Gossypium hirsutum]

Length = 323

Score = 168 bits (425), Expect = 5e-39

Identities = 80/124 (64%), Positives = 101/124 (81%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FR RIYNETNI++ FA + + +CP S GDN+L+PLD + TSFDN YFKNL

Sbjct: 202 QARCTTFRTRIYNETNIDSTFATSLRANCP--SNGGDNSLSPLDTTSSTSF DNAYFKNLQ 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLF+GGSTDS V YS+N G+F++DFA AM+KMG++SPLTG++G+IR NC
Sbjct: 260 GQKGLLHSDQQLFSGGSTDSQVNAYSSNLGSFTTDFANAMVKMGNLSPLTGTSGQIRTNC 319

Query: 2167 RRIN 2178
R+ N
Sbjct: 320 RKAN 323

Score = 152 bits (384), Expect = 3e-34
Identities = 87/169 (51%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILATAA 1330
+ GCDGSILLDDT++ TGEK A PN NSARGFEVID IKS VE +CPGVVSCADI+A+AA
Sbjct: 75 VNGCDGSILLDDTANMTGEKTAVPNSNSARGFEVIDTIKSQVESLCPGVVSCADIVAVAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 135 RDSV-----VALGGPSWIVLLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LI+ FS G + K++VALSG+ I
Sbjct: 152 RRDSTTASLSAANSNIPAPTLNLSGLITAFSNKGFTAKEMVALSGSHTI 200

Score = 72.0 bits (175), Expect = 5e-10
Identities = 39/75 (52%), Positives = 48/75 (64%)
Frame = +1

Query: 559 SKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRM 738
SK S R + + LF+L+ A AQLS+ FY +CP S++KS V SA+S E RM
Sbjct: 3 SKTCSPSNKLRFLLGMVFLLM-NMATAQLSSTFYSTTCPRALSTIKSAVNSAVSNEARM 61

Query: 739 GASLLRLFFHDCFVN 783
GASL RL FHDCFVN
Sbjct: 62 GASLPRLHFHDCFVN 76

>gb|ABK25962.1| unknown [Picea sitchensis]
Length = 323

Score = 168 bits (425), Expect = 5e-39
Identities = 79/124 (63%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARC NFRA IYN+TNI + ++ + + CP T+GSGDNNL+PLD +PT+FD Y+ NL
 Sbjct: 200 QARCFNFRAHIYNDTNILSTYSTSLRSKCPPTNGSGDNNLSPLDYVSPTAFDKNYYCNLK 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
 KKGLLHSDQ+LFNGGSTDS V Y++N F SDFAAAM+KMG+I PLTG++G+IRKNC
 Sbjct: 260 IKKGLLHSDQELFNGGSTDSQVTTYASNQNIFFSDFAAAMVKGNIKPLTGTSGQIRKNC 319

Query: 2167 RRIN 2178
 R+ N
 Sbjct: 320 RKPN 323

Score = 153 bits (387), Expect = 1e-34
 Identities = 87/169 (51%), Positives = 102/169 (60%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
 + GCDGS+LLDD+S TGEK A PN NSARGF+VID IKS VEK C GVVSCADILAIAA
 Sbjct: 73 VNGCDGSVLLDDSSKITGEKTAVPNANSARGFDVIDTIKSQVEKSCSGVVSCADILAIAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RDSV + LGGP+W V LG
 Sbjct: 133 RDSV-----VELGGPSWTVLLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TAS+S ANN IP PTS+L+++IS F A GLS K++VAL+G I
 Sbjct: 150 RRDSTTASKSGANNIPPTSSLSKIISLFQAQGLSAKEMVALAGAHTI 198

Score = 69.3 bits (168), Expect = 3e-09
 Identities = 36/65 (55%), Positives = 45/65 (69%), Gaps = 4/65 (6%)
 Frame = +1

Query: 601 CLALFVLIWGS----ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFH 768
 C+A+ V I S ++ QLS+ FY SCP S VK+ V+ A++KE RMGASLLRL FH
 Sbjct: 10 CIAVMVFIICSIANLSHGQLSSTFYDKSCPAALS VVKA AVKQAVAKEQRMGASLLRLHFH 69

Query: 769 DCFVN 783
 DCFVN
 Sbjct: 70 DCFVN 74

>gb|EAZ05133.1| hypothetical protein OsI_27326 [Oryza sativa Indica Group]
 Length = 324

Score = 168 bits (425), Expect = 5e-39
 Identities = 77/124 (62%), Positives = 97/124 (78%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLA LD TP +FDN Y+ NL+

Sbjct: 200 QAQCQNFRDRIYNETNIDSAFATQRQANCPRPTGSGDSNLAALDTTTPNAFDNAYYSNLL 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C

Sbjct: 260 SNKGLLHSDQVLFNNGGSADNTVRNFASNAAFSSAFTTAMVKMGNISPLTGTGGQIRLSC 319

Query: 2167 RRIN 2178

++N

Sbjct: 320 SKVN 323

Score = 116 bits (290), Expect = 2e-23

Identities = 71/167 (42%), Positives = 86/167 (51%)

Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AARD

Sbjct: 80 GCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAARD 134

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 135 SV-----VALGGPSWTVLLGRR 151

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 152 DSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 198

Score = 71.6 bits (174), Expect = 7e-10

Identities = 34/69 (49%), Positives = 46/69 (66%)

Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F

Sbjct: 7 SSLSLMLLVAAAMASVASAQLSATFYDTSCP NALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFVNVIY 792

HDCFV +

Sbjct: 67 HDCFVQASF 75

>ref|NP_001046400.1| Os02g0240100 [Oryza sativa (japonica cultivar-group)]

Length = 335

Score = 168 bits (425), Expect = 5e-39
Identities = 74/123 (60%), Positives = 101/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFR R+YN+TNI+ AFA R++ CP GSGD++LAPLD QT FDN Y++NL+
Sbjct: 211 SQCANFRDRVYNDTNIDPAFAALRRRGCPAAPGSGDSSLAPLDAQTNVFDNAYYRNLLA 270

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I PLTG+ G+IR++CR
Sbjct: 271 QRGLLHSDQELFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNIKPLTGAAGQIRRSR 330

Query: 2170 RIN 2178
+N
Sbjct: 331 AVN 333

Score = 134 bits (337), Expect = 9e-29
Identities = 80/171 (46%), Positives = 97/171 (56%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 81 VQGCDASILDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRNVELLCPGVVSCADIVAL 140

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 141 AARDSTAL-----LGGPSWAVP 157

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS SAAN+ +PAP+S+L LI+ F GLS +D+ ALSG I
Sbjct: 158 LGRRDSTTASLSAANDLPAPSSDLATLIAGFGNKGLSPRDMTALSGAHTI 208

Score = 70.1 bits (170), Expect = 2e-09
Identities = 42/82 (51%), Positives = 52/82 (63%), Gaps = 4/82 (4%)
Frame = +1

Query: 547 LVCLSKLTMASFCSRLTICLALFVLIWGSANA----QLSTNFYHSCPNLFSSVKSTVQS 714
L+ + ++TMAS S CL F L+ +A A QLST FY SCP L V++TV
Sbjct: 1 LIKICEITMASRSS-WHCCLLAFFLLSSAAGAAYGQQLSTTFYAASCP TLQVVVRATVLG 59

Query: 715 AISKETRMGASLLRLFFHDCFV 780
A+ E RMGASL+RLFFHDCFV
Sbjct: 60 ALLAERRMGASLVRLLFFHDCFV 81

>gb|AAC49818.1| peroxidase [Oryza sativa Indica Group]
Length = 317

Score = 168 bits (425), Expect = 5e-39
Identities = 77/124 (62%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR RIYNETNI++AFA RQ +CPR +GSGD+NLA LD TP +FDN Y+ NL+
Sbjct: 193 QAQCQNFDRRIYNETNIDSAFATQRQANCPRPTGSGDSNLAALDTTTPNAFDNAYYSNLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGGS D+ VR +++N FSS F AM+KMG+ISPLTG+ G+IR +C
Sbjct: 253 SNKGLLHSDQVLFNGGSADNTRNFASNAAAFSSAFTTAMVKMGNISPLTGTGQGIIRLSC 312

Query: 2167 RRIN 2178
++N
Sbjct: 313 SKVN 316

Score = 118 bits (296), Expect = 5e-24
Identities = 72/169 (42%), Positives = 88/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VIDN K+ VE +C VSCADILA+AA
Sbjct: 71 VQGCDASVLLSGQ-----EQNAGPNVGSRLRGFSVIDNAKARVEAICNQTVSCADILAVAA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 126 RDSV-----VALGGPSWTVLLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN +PAP+S+L +LI FS GL D+VALSG I
Sbjct: 143 RRDSTTASEALANTDLPAPSSSLAELIGNFSRKGLDATDMVALSGAHTI 191

Score = 71.2 bits (173), Expect = 9e-10
Identities = 34/65 (52%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S L++ L + + A+AQLS FY SCPN S++KS + +A++ E RMGASLLRL F
Sbjct: 7 SSLSLMLLVAAAMASVASAQLSATFYDTSCPNALSTIKSVITA AVNSEARMGASLLRLHF 66

Query: 766 HDCFV 780

HDCFV
Sbjct: 67 HDCFV 71

>dbj|BAD28869.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69272.1| TPA: class III peroxidase 30 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAG98261.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAF08314.2| Os02g0240100 [Oryza sativa Japonica Group]
Length = 327

Score = 168 bits (425), Expect = 5e-39
Identities = 74/123 (60%), Positives = 101/123 (82%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++C NFR R+YN+TNI+ AFA R++ CP GSGD++LAPLD QT FDN Y++NL+
Sbjct: 203 SQCANFRDRVYNDTNIDPAFAALRRRGCPAAPGSGDSSLAPLDAQTNVFDNAYYRNLLA 262

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I PLTG+ G+IR++CR
Sbjct: 263 QRGLLHSDQELFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNIKPLTGAAGQIRRSCR 322

Query: 2170 RIN 2178
+N
Sbjct: 323 AVN 325

Score = 134 bits (337), Expect = 9e-29
Identities = 80/171 (46%), Positives = 97/171 (56%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 73 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRNVELLCPGVVSCADIVAL 132

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 133 AARDSTAL-----LGGPSWAVP 149

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS SAAN+ +PAP+S+L LI+ F GLS +D+ ALSG I
Sbjct: 150 LGRRDSTTASLSAANSIDLAPSSDLATLIAGFGNKGLSPRDMTALSGAHTI 200

Score = 66.6 bits (161), Expect = 2e-08

Identities = 36/64 (56%), Positives = 42/64 (65%), Gaps = 4/64 (6%)
Frame = +1

Query: 601 CLALFVLIWGSANA----QLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFH 768
CL F L+ +A A QLST FY SCP L V++TV A+ E RMGASL+RLFFH
Sbjct: 10 CLLAFFLLSSAAGAAYGQQLSTTFYAASCPTLQVVVRATVLGALLAERRMGASLVRLFFH 69

Query: 769 DCFV 780
DCFV
Sbjct: 70 DCFV 73

>ref|XP_002274693.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 324

Score = 167 bits (424), Expect = 7e-39
Identities = 85/125 (68%), Positives = 96/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP +G GD+NLA LDL TP SFDN YFKNL
Sbjct: 200 QARCVTFRDRIYDNGTDIDAGFASTRRRRCPADNGDGDNNLAALDLVTPNSFDNYYFKNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GGSTDSIV YS N TFSSDFA AM+KMGGDI PLTG+ GEIR+
Sbjct: 260 IQKKGLLQSDQVLFSGGSTDSIVSEYSKNRKTFSDFALAMVKMGDIEPLTGAAGEIREF 319

Query: 2164 CRRIN 2178
C IN
Sbjct: 320 CNAIN 324

Score = 136 bits (343), Expect = 2e-29
Identities = 76/169 (44%), Positives = 100/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD+SS EKNA N NSARG+EVI ++KS VE +CPG+VSCADILA+AA
Sbjct: 73 VQGCDASILLDDSSSIQSEKNAPNNLSARGYEVHDKVKSQVESICPGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW VKLG
Sbjct: 133 RDA-----SVAVGPTWTVKLG 149

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S ++ +P+ +L++LIS F + GLST+D+VALSG+ I
Sbjct: 150 RRDSTTSGLSQVSSNLPSFRDSLRLISLFGSKGLSTRDMVALSGSHTI 198

Score = 63.2 bits (152), Expect = 2e-07
Identities = 31/73 (42%), Positives = 46/73 (63%), Gaps = 3/73 (4%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS---ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMG 741
M S C + + VL+ S AQLS++FY ++CP S++++ + A+S+E RM
Sbjct: 1 MGSIAGNYGACIFVAVLLILSIMPCEAQLSSSFYDNTCPKALSTIRTATRKAVSRERRMA 60

Query: 742 ASLLRLFFHDCFV 780
ASL+RL FHDCFV
Sbjct: 61 ASLIRLHFHDCFV 73

>gb|EEC82680.1| hypothetical protein OsI_27324 [Oryza sativa Indica Group]
Length = 318

Score = 167 bits (424), Expect = 7e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 195 QAQCQNFRDRLYNETNIDAAFAAALKASCPRTGSGDGNLAPLDTTPTAFDNAYYTNLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 255 SNKGLLHSDQVLFNGGAVDGGVRSYASGPSRFRDFAAAMVKMGNIAPLTGTGQGIQLVC 314

Query: 2167 RRIN 2178
++N
Sbjct: 315 SKVN 318

Score = 130 bits (327), Expect = 1e-27
Identities = 73/165 (44%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 68 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 128 RDSV-----VALGGPSWRVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645

RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 145 RRDSTTASLALANSDLPPPSFDVANLTAAFAAKGLSQADMVALSG 189

Score = 64.3 bits (155), Expect = 1e-07
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYSRSCPRALAIIRAGVRAAVAQEPRMGASLLRLHFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>ref|NP_001060626.1| Os07g0676900 [Oryza sativa (japonica cultivar-group)]
dbj|BAF22540.1| Os07g0676900 [Oryza sativa Japonica Group]
Length = 333

Score = 167 bits (424), Expect = 7e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+
Sbjct: 210 QAQCQNFRDRLYNETNIDAAFAAALKASCPRTSGSGDGNLAPLDTTPTAFDNAYYT NLL 269

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C
Sbjct: 270 SNKGLLHSDQVLFNGGAVDGGVRSYASGPSRFRDFAAAMVKMGNIAPLTGTGQGI RLV C 329

Query: 2167 RRIN 2178
++N
Sbjct: 330 SKVN 333

Score = 130 bits (327), Expect = 1e-27
Identities = 73/165 (44%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA
Sbjct: 83 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAV AA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGP+W V LG
Sbjct: 143 RDSV-----VALGGPSWRVLLG 159

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG

Sbjct: 160 RRDSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 204

Score = 68.6 bits (166), Expect = 6e-09

Identities = 38/74 (51%), Positives = 50/74 (67%), Gaps = 1/74 (1%)

Frame = +1

Query: 562 KLTMAFCS-RLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRM 738

+LTMAS S L +CLAL + G QLS FY SCP + +++ V++A+++E RM

Sbjct: 13 RLTMASCLSVLLLLCLALAGSVSGQ---QLSATFYSRSCPRALAIIRAGVRAAVAQEPRM 69

Query: 739 GASLLRLFFHDCFV 780

GASLLRL FHDCFV

Sbjct: 70 GASLLRLHFHDCFV 83

>emb|CAH10840.1| peroxidase [Picea abies]

Length = 320

Score = 167 bits (424), Expect = 7e-39

Identities = 81/124 (65%), Positives = 99/124 (79%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ TPT+FDN Y+ NL

Sbjct: 199 QSRCAFFRTRIYNESNINAAAFATSVKPNCP--SAGGDNTLSPLDVVTPTTFDNKYYSNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIRKNC 2166

+KGLLHSDQQLFNGGSTDS V YSTN +F +DFAAAM+KMG+ISPLTG++G+IRKNC

Sbjct: 257 VQKGLLHSDQQLFNGGSTDSQVTTYSTNQNSFFTFDFAAAMVKMGNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178

R+ N

Sbjct: 317 RKAN 320

Score = 151 bits (381), Expect = 7e-34

Identities = 87/169 (51%), Positives = 99/169 (58%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AA 1330

+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA

Sbjct: 72 VNGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDS+ + L GPTW V LG

Sbjct: 132 RDSI-----VELQGPTWTVM LG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS SAANN IP+P S+L+ LI+ F GLSTKDLVALSG I

Sbjct: 149 RRDSPATSLAANNIPSPASSLSTLITSFQNHGLSTKDLVALSGAHTI 197

Score = 69.3 bits (168), Expect = 3e-09
Identities = 34/70 (48%), Positives = 46/70 (65%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGS-----ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + ++ S N QLS+ FY SCP + S VK+ V+ A++KE RMGASL+

Sbjct: 4 RTLVCIGVMVALLCSININAVNGQLSSTFYAKSCP RVQSIVKTVVKQAVAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783
RL FHDCFVN

Sbjct: 64 RLHFHDCFVN 73

>dbj|BAC83101.1| putative peroxidase precursor [Oryza sativa Japonica Group]
gb|EEE67813.1| hypothetical protein OsJ_25567 [Oryza sativa Japonica Group]
Length = 318

Score = 167 bits (424), Expect = 7e-39
Identities = 77/124 (62%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+

Sbjct: 195 QAQCQNFRDRLYNETNIDAAFAAALKASCP RPTSGSGDGNLAPLDTTPTAFDNAYYTNLL 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C

Sbjct: 255 SNKGLLHSDQVLFNGGAVDGVRSYASGPSRFR R DFAAAMVKMGNIAPLTGTGGQIRLVC 314

Query: 2167 RRIN 2178
++N

Sbjct: 315 SKVN 318

Score = 130 bits (327), Expect = 1e-27
Identities = 73/165 (44%), Positives = 94/165 (56%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AA

Sbjct: 68 VQGCDASVLLNDTANFTGEQGANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 128 RDSV-----VALGGPSWRVLLG 144

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRD+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG

Sbjct: 145 RRDSTTASLALANSDLPPPSFDVANLTASFAAKGLSQADMVALSG 189

Score = 64.3 bits (155), Expect = 1e-07

Identities = 32/63 (50%), Positives = 43/63 (68%)

Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771

L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD

Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYSRSCPRLAIIRAGVRAAVAQEPRMGASLLRLHFHD 65

Query: 772 CFV 780

CFV

Sbjct: 66 CFV 68

>tpe|CAH69351.1| TPA: class III peroxidase 109 precursor [Oryza sativa (japonica
cultivar-group)]

Length = 322

Score = 167 bits (424), Expect = 7e-39

Identities = 77/124 (62%), Positives = 95/124 (76%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QA+C NFR R+YNETNI+ AFA + SCPR +GSGD NLAPLD TPT+FDN Y+ NL+

Sbjct: 199 QAQCQNFRDRLYNETNIDAAFAAALKASCPRPTGSGDGNLAPLDTTPTAFDNAYYTNNL 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFS SDFAAAMIKMGDISPLTGSNGEIRKNC 2166

KGLLHSDQ LFNGG+ D VR Y++ P F DFAAAM+KMG+I+PLTG+ G+IR C

Sbjct: 259 SNKGLLHSDQVLFNGGAVDGQVRSYASGPSRFR R DFAAAMVKMGNIAPLTGTGQGI R LVC 318

Query: 2167 RRIN 2178

++N

Sbjct: 319 SKVN 322

Score = 128 bits (321), Expect = 6e-27
Identities = 72/163 (44%), Positives = 92/163 (56%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE C VSCADILA+AARD
Sbjct: 74 GCDASVLLNDTANFTGEQG ANPNVGSIRGFNVVDNIKAQVEAACKQTVSCADILAVAARD 133

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 134 SV-----VALGGPSWRVLLGRR 150

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
D+ TAS + AN+ +P P+ ++ L + F+A GLS D+VALSG
Sbjct: 151 DSTTASLALANS DLPPPSFDVANLTASFAAKGLSQADMVALSG 193

Score = 64.3 bits (155), Expect = 1e-07
Identities = 32/63 (50%), Positives = 43/63 (68%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L +CLAL + G QLS FY SCP + +++ V++A+++E RMGASLLRL FHD
Sbjct: 9 LLLCLALAGSVSGQ---QLSATFYSRSCPRA LAIIRAGVRAAVAQEPRMGASLLRLHFHD 65

Query: 772 CFV 780
CFV
Sbjct: 66 CFV 68

>ref|XP_002451848.1| hypothetical protein SORBIDRAFT_04g008620 [Sorghum bicolor]
gb|EES04824.1| hypothetical protein SORBIDRAFT_04g008620 [Sorghum bicolor]
Length = 278

Score = 167 bits (423), Expect = 9e-39
Identities = 79/124 (63%), Positives = 100/124 (80%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG-DNNLAPLDLQTPTSFDNYYFKNLV 1986
++C NFR IYN+T+I+ AFA RQ+SCP G+G D NLA LD+QT FDN Y++NL+
Sbjct: 153 SQCQNFGRGHIYNDTDIDAAFAALRQRSCPAAPGTGGDTNLAALDVQTQLVFDNAYYRNLL 212

Query: 1987 QKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGISPLTGSGNGEIRKNC 2166
K+GLLHSDQ+LFNGGS D++VR YS+NP F+SDFAAAMIKMGI+ISPLTG+ G+IR NC
Sbjct: 213 AKRGLLHSDQELFNNGSQDALVRQYSSNPALFASDFAAAMIKMGNISPLTG TAGQIRANC 272

Query: 2167 RRIN 2178
R +N
Sbjct: 273 RVVN 276

Score = 134 bits (338), Expect = 7e-29
Identities = 78/169 (46%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCDGSILLDD SF GEK A PN NS RGF+VID IK+ VE +CPGVVSCADI+A+AA
Sbjct: 25 VQGCDGSILLDDVGSFVGEKGAGPNVNSVRGFDVIDQIKTNVELICPGVVSCADIVALAA 84

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
R F + LGGP+W V LG
Sbjct: 85 R-----FGTFLLGGPSWAVPLG 101

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P+P S L L++ F GLS DL ALSG I
Sbjct: 102 RRDSTTASLTANSDLPSASGLATLVTAFGNKGLSPGDLTALSGAHTI 150

Score = 39.3 bits (90), Expect = 3.8
Identities = 17/22 (77%), Positives = 19/22 (86%)
Frame = +1

Query: 715 AISKETRMGASLLRLFFHDCFV 780
A+ E RMGASL+RLFFHDCFV
Sbjct: 4 ALLAERRMGASLVRLFFHDCFV 25

>gb|ACN33811.1| unknown [Zea mays]
Length = 320

Score = 167 bits (423), Expect = 9e-39
Identities = 77/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR IYN+TNI FA + + +CPR +GSGD NLAPLD TP SFDN Y+ NL+
Sbjct: 197 QAQCKNFRDHIYNDTNINQGFASSLKANCPRPTGSGDGNLAPLDTTTPYSFDNAYYSNLL 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++N FSS FAAAM+KMG++SPLTGS G+IR C
Sbjct: 257 SQKGLLHSDQELFNGGSTDNVTRNFASNSAAFSSAFAAAMVKMGNLSPLTGSQGGQIRLTC 316

Query: 2167 RRIN 2178

+N
Sbjct: 317 STVN 320

Score = 118 bits (296), Expect = 5e-24
Identities = 72/171 (42%), Positives = 89/171 (52%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD S+LL D ++ FTGE+ A PN S RGF+VI NIK+ VE VC VSCADILA+
Sbjct: 68 VQGCDAVLLADNAATGFTGEQGAAPNAGSLRGFDVIANIKAQVEAVCKQTVSCADILAV 127

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDSV + LGGP+W V
Sbjct: 128 AARDSV-----VALGGPSWTVP 144

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS S AN+ +P P NL QLI+ F G + ++ LSG I
Sbjct: 145 LGRRDSTTASLSLANSIDLPPFFNLGQLITAFGNKGFTATEMATLSGAHTI 195

Score = 75.1 bits (183), Expect = 6e-11
Identities = 36/65 (55%), Positives = 45/65 (69%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
S ++ CL L + + A+AQLS FY SCPN S++K V +A+ KE RMGASLLRL F
Sbjct: 4 SSVSSCLLLLCLAAVASAQLSPTFYDSSCPNALSTIKIAVNAAVQKENRMGASLLRLHF 63

Query: 766 HDCFV 780
HDCFV
Sbjct: 64 HDCFV 68

>gb|ABR18139.1| unknown [Picea sitchensis]
Length = 327

Score = 167 bits (423), Expect = 9e-39
Identities = 83/124 (66%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR RIYNE+NI FA R+ +CP T G DNNLAPLDL TPT+FDN Y+ NL
Sbjct: 206 QARCTNFRNRIYNESNIALLFAGLRKANCPVTGG--DNNLAPLDLFTPTAFDINSYNNLQ 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ GLLHSDQQLF GGSTD+ V Y+ +P F +DFAAAM+KMG+I PLT +NGEIRKNC

Sbjct: 264 FQNGLLHSDQQLFKGGSTDNRVSFYAVHPDAFFNDFAAAMVKMGNIKPLTVNNGEIRKNC 323

Query: 2167 RRIN 2178
R+IN

Sbjct: 324 RKIN 327

Score = 162 bits (410), Expect = 3e-37
Identities = 91/169 (53%), Positives = 105/169 (62%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEK ANPN NS RGF+VID IK+ VE C GVVSCADI+AIAA
Sbjct: 79 VNGCDGSILLDDTSTFTGEKTANPNNSVRGFDVIDTIKTQVEATCSGVVSCADIVAIAA 138

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 139 RDSV-----VQLGGPTWTVMLG 155

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ +AS+SAANN IP PTSNL+ LIS F A GL+T+D+VALSG+ I
Sbjct: 156 RRDSTSASKSAANNNIPPTSNSALISFFQAQGLTTEDMVALSGSHTI 204

Score = 76.3 bits (186), Expect = 3e-11
Identities = 39/78 (50%), Positives = 52/78 (66%), Gaps = 4/78 (5%)
Frame = +1

Query: 562 KLTMAFCS---RLTICLALFVLIWG-SANAQLSTNFYYHSCPNLFSSVKSTVQSAISKE 729
++ MA F + R+ +C++L V++ S QL +FY SCPN+ S V S V A++KE
Sbjct: 3 RIVMAFFSTMGIRIACISLLVIVCSTSVYGGQLCPDFYDKSCPNVLSIVNSVVMQAVAKE 62

Query: 730 TRMGASLLRLFFHDCFVN 783
RMGASLLRL FHDCFVN
Sbjct: 63 KRMGASLLRLHFHDCFVN 80

>sp|A2YPX3.2|PER2_ORYSI RecName: Full=Peroxidase 2; Flags: Precursor
gb|AAC49821.1| peroxidase [Oryza sativa Indica Group]
gb|EEC82682.1| hypothetical protein OsI_27327 [Oryza sativa Indica Group]
Length = 314

Score = 167 bits (422), Expect = 1e-38
Identities = 75/124 (60%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QA+C NFR R+YNETNI+++FA + +CPR +GSGD+NLAPLD TP +FD+ Y+ NL+
Sbjct: 191 QAQCQNFRDRLYNETNIDSSFATALKANCPRPTGSGDSNLAPLDTTTPNAFDSAYYTNLL 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFNGGST+ VR +S+N F+S F AM+KMG+ISPLTG+ G+IR NC

Sbjct: 251 SNKGLLHSDQVLFNGGSTDNTVRNFSSNTAAFNSAFTVAMVKGNISPLTGTQGQIRLNC 310

Query: 2167 RRIN 2178

++N

Sbjct: 311 SKVN 314

Score = 121 bits (303), Expect = 8e-25
Identities = 72/169 (42%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF V+DNIK+ VE +C VSCADILA+AA

Sbjct: 69 VQGCDAVLLSGQ-----EQNAGPNAGSLRGFNVVDNIKTQVEAICSQTVSCADILAVAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 124 RDSV-----VALGGPSWTVLLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TA++S AN +PAP+S+L +LI FS GL D+VALSG I

Sbjct: 141 RRDSTTANESQANTDLPAPSSSLAELIGNFSRKGLDVTDMVALSGAHTI 189

Score = 70.5 bits (171), Expect = 2e-09
Identities = 36/70 (51%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S +++ L + + +A+AQLS FY SCPN S++KS V +A++ E RMGASL

Sbjct: 1 MAS-ASSVSLMLLVAAAMASAASAQLSATFYDTSCPNALSTIKSAVTA AVNSEPRMGASL 59

Query: 751 LRLFFHDCFV 780

+RL FHDCFV

Sbjct: 60 VRLHFHDCFV 69

>ref|XP_002461208.1| hypothetical protein SORBIDRAFT_02g042850 [Sorghum bicolor]
gb|EER97729.1| hypothetical protein SORBIDRAFT_02g042850 [Sorghum bicolor]
Length = 319

Score = 166 bits (421), Expect = 2e-38

Identities = 76/124 (61%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR IYN+TNI +AFA + + +CPR++GSGD NLAPLD TP FDN Y+ NL+

Sbjct: 196 QAQCQFFRDHIYNDTNINSAFATSLKANCPRSTGSGDGNLAPLDTTPYKFDNAYYSNLL 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGBISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGSTD+ VR +++N FSS FAAAM+KMG++SPLTGS G+IR C

Sbjct: 256 NQKGLLHSDQELFNGGSTDNTVRNFASNSAAFSSAFSAAMVKGMLSPLTGSQGQIRLTC 315

Query: 2167 RRIN 2178

++N

Sbjct: 316 SKVN 319

Score = 118 bits (296), Expect = 5e-24
Identities = 71/171 (41%), Positives = 89/171 (52%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD S+LL D ++ FTGE+ A PN S RGF+VI NIK+ VE +C VSCADILA+

Sbjct: 67 VQGCDA SVLLADNAATGFTGEQGALPNAGSLRGFDVIANIKTQVEAICKQTVSCADILAV 126

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDSV + LGGP+W V

Sbjct: 127 AARDSV-----VALGGPSWTVP 143

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

LGRRD+ TAS S AN+ +P P+ NL QLI F G + ++ LSG I

Sbjct: 144 LGRRDSTTASLSANSDLPSPFNLEQLIKAFGNKGFTATEMATLSGAHTI 194

Score = 74.7 bits (182), Expect = 8e-11
Identities = 36/59 (61%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

L LF+ + A+AQLS FY SCPN S++KS V +A+ KE RMGASLLRL FHDCFV

Sbjct: 9 LLLFLCLAAVASAQLSPTFYDTSCPNALSTIKSAVNAAVQKENRMGASLLRLHFHDCFV 67

>ref|XP_002320417.1| predicted protein [Populus trichocarpa]
gb|EEE98732.1| predicted protein [Populus trichocarpa]
Length = 316

Score = 166 bits (421), Expect = 2e-38

Identities = 82/123 (66%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT FR RIYN+TNI+ +FA TR+ SCP + GD LAPLD T T FDN Y+ NLV

Sbjct: 197 ARCTTFRNRIYNDTNIDASFATRRASCP--ASGGDATLAPLD-GTQTRFDNYYTNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YSTN TF+ DFAAAM+KMG+ISPLTG NGEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSTNGATFARDFAAAMVKMGNISPLTGRNGEIRRNCR 313

Query: 2170 RIN 2178

+N

Sbjct: 314 VVN 316

Score = 157 bits (396), Expect = 1e-35
Identities = 89/165 (53%), Positives = 100/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDT++FTGEKNANPNRNSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDGSILLDDTATFTGEKNANPNRNSARGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + GGP+W V LG

Sbjct: 129 RDGVVL-----RGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDARTASQSAAN+ IP+P S+L LIS FSA GLS D+ ALSG

Sbjct: 146 RRDARTASQSAANSQIPSPASSLATLISMFSAKGLSAGDMTALSG 190

Score = 62.8 bits (151), Expect = 3e-07
Identities = 32/78 (41%), Positives = 45/78 (57%)
Frame = +1

Query: 550 VCLSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKE 729

+C+ L +SFCS AQLS FY +CPNL + V++ + A++ +

Sbjct: 10 LCVVPLLASSFCS-----AQLSATFYASTCPNLQTIVRNAMTGAVNGQ 52

Query: 730 TRMGASLLRLFFHDCFVN 783

R+ AS+LRLFFHDCFVN

Sbjct: 53 PRLAASILRLFFHDCFVN 70

>ref|NP_001130666.1| hypothetical protein LOC100191769 [Zea mays]

gb|ACF78975.1| unknown [Zea mays]
Length = 324

Score = 166 bits (421), Expect = 2e-38
Identities = 77/123 (62%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFRA IYN+T+I+ AFA RQ++CP G+GD++LAPLD+QT FDN Y++NL+
Sbjct: 200 SQCQNFRAHIYNDTDIDPAFASLRQRTCPAAPGTGDSSLAPLDVQTQLVFDNAYYRNLLA 259

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLL SDQ LFNGGS D++VR YS NP F+SDFA AMIKMG+ISPLTG+ G+IR NCR
Sbjct: 260 KRGLLRSDQALFNGGSQDALVRQYSANPALFASDFANAMIKMGNISPLTGTAGQIRANCR 319

Query: 2170 RIN 2178
+N
Sbjct: 320 VVN 322

Score = 134 bits (338), Expect = 7e-29
Identities = 77/169 (45%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCDGSILLDD SF GEK A PN NS RGF+VID IK+ VE +CPGVVSCADI+A+AA
Sbjct: 72 VQGCDGSILLDDVGSFVGEKGAGPNVNSLRGFDVIDQIKANVELICPGVVSCADIVALAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + LGGP+W V LG
Sbjct: 132 RDGTFL-----LGGPSWAVPLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P+P S L L++ F GL DL ALSG I
Sbjct: 149 RRDSTTASLALANS DLPSPVSGLAALLA AFGNKGLGPGDLTALSGAHTI 197

Score = 63.9 bits (154), Expect = 1e-07
Identities = 36/72 (50%), Positives = 48/72 (66%), Gaps = 2/72 (2%)
Frame = +1

Query: 571 MASFCSRLTICLA--LFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGA 744
MASF + LA LF+L + QLS++FY +CP L V++T+ +A+ E RMGA
Sbjct: 1 MASFRTSWHCLLAACLFLLASAAHQQLSSSFYAATCPTLELIVRTTMTLALLAERRMGA 60

Query: 745 SLLRLFFHDCFV 780
SL+RLFFHDCFV

Sbjct: 61 SLVRLFFHDCFV 72

>ref|NP_200648.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9LV1.1|PER68_ARATH RecName: Full=Peroxidase 68; Short=Atperox P68; Flags: Precursor
dbj|BAA96931.1| peroxidase [Arabidopsis thaliana]
dbj|BAC42892.1| putative peroxidase [Arabidopsis thaliana]
gb|AAP40354.1| putative peroxidase [Arabidopsis thaliana]
Length = 325

Score = 166 bits (421), Expect = 2e-38
Identities = 82/124 (66%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARC FR+RIYN TNI+ +FA +R++SCP +GSGDNN A LDL+TP FD YF LV
Sbjct: 202 QARCVTFRSRIYNSTNIDLSFALSRRRSCPAATGSGDNNAILDLRTPEKFDGSYFMQLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
+GLL SDQ LFNGGSTDSIV YS + F DF AAMIKMGDISPLTGSNG+IR++C
Sbjct: 262 NHRGLTSDQVLFGNGGSTDSIVVSYSRSVQAFYRDFVAAMIKMGDISPLTGSNGQIRRSC 321

Query: 2167 RRIN 2178
RR N
Sbjct: 322 RRPN 325

Score = 144 bits (362), Expect = 1e-31
Identities = 85/170 (50%), Positives = 99/170 (58%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILATAA 1330
+ GCD SILLDDT SF GEK A PN NS RG+EVID IKS VE++CPGVVSCADILAI A
Sbjct: 74 VNGCDASILLDDTRSFLGEKTAGPNNSVRYEVIDAIKSRVERLCPGVVSCADILAITA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + +GG W+VKLG
Sbjct: 134 RDSVLL-----MGGRGWSVKLG 150

Query: 1511 RRDARTASQSAANNGI-PAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+G+ P PTS L+ LI+ F A GLS +D+VALSG I
Sbjct: 151 RRDSITASFSTANSGLVPPPTSTLDNLINLFRANGLSPRDMVALSGAHTI 200

Score = 73.2 bits (178), Expect = 2e-10
Identities = 36/66 (54%), Positives = 47/66 (71%), Gaps = 1/66 (1%)
Frame = +1

Query: 589 RLTICLALFVLIWGS-ANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFF 765
R + LF+++ GS A AQL T+FY SCP+L +V+ VQ ++KE R+ ASLLRLFF
Sbjct: 10 RAAFVLLFIVMLGSQAQAQLRTDFYSDSCPSLLPTVRRVVQREVAKERRIAASLLRLFF 69

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 70 HDCFVN 75

>ref|XP_002338628.1| predicted protein [Populus trichocarpa]
gb|EEF10179.1| predicted protein [Populus trichocarpa]
Length = 183

Score = 166 bits (420), Expect = 2e-38
Identities = 83/124 (66%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR G NLAPLDL TP SFDN YFKNL+
Sbjct: 62 QAQCFTFRDRIYNASNIDAGFASTRKRRCPRAGGQA--NLAPLDLVTPNSFDNYYFKNLM 119

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLL SDQ LFNGGSTDSIV YS NP FSSDFA+AMIKMGDI PLTGS G+IR+ C
Sbjct: 120 RNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPKFSSDFASAMIKMGDIRPLTGSAGQIRRIC 179

Query: 2167 RRIN 2178
+N
Sbjct: 180 SAVN 183

Score = 65.5 bits (158), Expect = 5e-08
Identities = 31/57 (54%), Positives = 43/57 (75%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
+GGP+W VK GRRD+ TAS++ AN +PA L++LISRF GL+ +D+VALSG+
Sbjct: 1 VGGPSWAVKFGRRDSTASRTLANAELPAFFDRLDRLISRFAQKGLTARDMVALSGS 57

>ref|XP_002336344.1| predicted protein [Populus trichocarpa]
gb|EEE73229.1| predicted protein [Populus trichocarpa]
Length = 316

Score = 166 bits (420), Expect = 2e-38
Identities = 83/124 (66%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR G NLAPLDL TP SFDN YFKNL+
Sbjct: 195 QAQCFTFRDRIYNASNIDAGFASTRKRRCPRAGGQA--NLAPLDLVTPNSFDNYYFKNLM 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNP GTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLL SDQ LFNGGSTDSIV YS NP FSSDFA+AMIKMGDI PLTGS G+IR+ C
Sbjct: 253 RNKGLLQSDQVLFNGGSTDSIVSEYSRNP AKFSSDFASAMIKMGDIRPLTGSAGQIRRIC 312

Query: 2167 RRIN 2178
+N
Sbjct: 313 SAVN 316

Score = 135 bits (339), Expect = 5e-29
Identities = 76/166 (45%), Positives = 97/166 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLD+TSS EK A N+NSARG+EVID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 68 VQGCDASILLDETSSIKSEKTAGANKNSARGYEVIDKAKAEVEKICPGVVSCADIIAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP+W VKLG
Sbjct: 128 RDA-----SAYVGGPSWAVKLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS + A +PA + +L +LISRF GL+ +D+VALSG+
Sbjct: 145 RRDSTTASPTLAITELPAFSDDLGRLISRFQQKGLTARDMVALSGS 190

Score = 63.5 bits (153), Expect = 2e-07
Identities = 26/50 (52%), Positives = 40/50 (80%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+ A+LS+ FY+ SCPN S++++ ++AI++E RM ASL+RL FHDCFV
Sbjct: 19 ACQAKLSSTFYHKSCPNAESAIRTAIRTAIRERRMAASLIRLHFHDCFV 68

>emb|CAA71493.1| peroxidase [Spinacia oleracea]
Length = 309

Score = 166 bits (420), Expect = 2e-38
Identities = 76/123 (61%), Positives = 99/123 (80%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRSTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989

ARC +FR IYN+T+I+ F TR+ +CP ++ +G+ NLAPLDLQ+PT FDN Y+KNL+
Sbjct: 187 ARCVSFRHHIYNDTDIDANFEATRKNVNCPLSNNTGNTNLAPLDLQSP TKFDNSYYKNLIA 246

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GLLHSDQ+L+NGGS D++V YS + F+ DF AA+IKMG+ISPLTGS+GEIRKNCR

Sbjct: 247 KRGLLHSDQELYNGGSQDALVTRYSKSNAFAKDFVAAIIKMGNISPLTGSSGEIRKNCR 306

Query: 2170 RIN 2178

IN

Sbjct: 307 FIN 309

Score = 131 bits (329), Expect = 7e-28

Identities = 79/170 (46%), Positives = 95/170 (55%), Gaps = 1/170 (0%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S+LLDDTS+FTGEK A NRN S RGFEVID+IK+ VE C VSCADILA+A

Sbjct: 58 VNGCDASLLDDTSTFTGEKTAISNRNNSVRGFEVIDSIKTNVEASCKATVSCADILALA 117

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V + LGGP+W V L

Sbjct: 118 ARDGVFL-----LGGPSWKVPL 134

Query: 1508 GRRDARTASQSAANGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

GRRDARTAS +AA N +P +S+L+ L + F+ GLS KD+ ALSG I

Sbjct: 135 GRRDARTASLTAA NNLPASSLSNLTTLFNNKGLSPKDMTALSGAHTI 184

Score = 70.9 bits (172), Expect = 1e-09

Identities = 32/50 (64%), Positives = 39/50 (78%)

Frame = +1

Query: 634 ANAQLSTNFYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFVN 783

+NAQLS+ Y SCPNL V+ T++ A+ KE RMGAS+LRLFFHDCFVN

Sbjct: 10 SNAQLSSKHYASSCPNLEKIVRKT MKQAVQKEQRMGASILR LFFHDCFVN 59

>gb|AA53172.1| peroxidase [Populus alba x Populus tremula var. glandulosa]

Length = 316

Score = 166 bits (420), Expect = 2e-38

Identities = 81/123 (65%), Positives = 99/123 (80%)

Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT FR RIYN+TNI+ +FA TR+ SCP + GD LAPLD T T FDN Y+ NLV

Sbjct: 197 ARCTTFRNRIYNDTNIDASFATRRASCP--ASGGDATLAPLD-GTQTRFDNNYYTNLVA 253

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++VR YSTN TF+ DFAAAM++MG+ISPLTG+NGEIR+NCR

Sbjct: 254 RRGLLHSDQELFNGGSQDALVRTYSTNGATFARDFAAAMVRMGNISPLTGTNGEIRRNCR 313

Query: 2170 RIN 2178

+N

Sbjct: 314 VVN 316

Score = 159 bits (402), Expect = 3e-36
Identities = 90/165 (54%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDT++FTGEKNANPNRNSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDGSILLDDTATFTGEKNANPNRNSARGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG

Sbjct: 129 RDGVVL-----LGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDARTASQSAAN+ IP+P S+L LIS FSA GLS D+ ALSG

Sbjct: 146 RRDARTASQSAANSQIPSPASSLATLISMFSAGLSAGDMTALSG 190

Score = 63.2 bits (152), Expect = 2e-07
Identities = 32/78 (41%), Positives = 45/78 (57%)
Frame = +1

Query: 550 VCLSKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKE 729
+C+ L +SFCS AQLS FY +CPNL + V++ + A++ +

Sbjct: 10 LCIVPLLASSFCS-----AQLSATFYASTCPNLQTIVRNAMTGAVNGQ 52

Query: 730 TRMGASLLRLFFHDCFVN 783

R+ AS+LRLFFHDCFVN

Sbjct: 53 PRLAASILRLFFHDCFVN 70

>ref|XP_002509738.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]

gb|EEF51125.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]

Length = 320

Score = 166 bits (419), Expect = 3e-38
Identities = 80/125 (64%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ CP SGSGD+NLAPLDL TP FDN YF+NL
Sbjct: 196 QAQCVTFRGRIYNNASDIDAGFAATTRSQCPAASGSGDSNLAPLDLVTNIFDNNYFRNL 255

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LF+GG+TDSIV YS + FSSDFA+AM+KMG+ISPLTGS G+IR+
Sbjct: 256 IQKKGLLQSDQVLFSGGATDSIVNQYSRDSVFSDFASAMVKMGNISPLTGSQQGIRRV 315

Query: 2164 CRRIN 2178
C +N
Sbjct: 316 CNVVN 320

Score = 137 bits (346), Expect = 8e-30
Identities = 77/169 (45%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AA 1330
+QGCDGSILLDDT + TGEK A N NS RGF+VIDNIKS +E CPG+VSCADI+A+AA
Sbjct: 69 VQGCDGSILLDDTPTMTGEKTARNNANSVRGFDVIDNIKSQLESRCPGIVSCADIVAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GP+W+V LG
Sbjct: 129 RDA-----SVAASGPSWSVNLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS+S A++ +PA T +L++L S F + GLS +D+VALSG I
Sbjct: 146 RRDSTTASRLADSNLPAFTDSLRLTSLFGSKGLSQRDMVALSGAHTI 194

Score = 70.1 bits (170), Expect = 2e-09
Identities = 32/67 (47%), Positives = 49/67 (73%), Gaps = 2/67 (2%)
Frame = +1

Query: 586 SRLTICLALFVLIWGS--ANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRL 759
SRL++ + ++I+ S AQLS+NFY ++CP+ S++K + +A+S+E RM ASL+RL
Sbjct: 3 SRLSLLCMVLMIFSSLPCKAQLSSNFYDNTCPSALSTIKGAISTAVSREQRMAASLIRL 62

Query: 760 FFHDCFV 780
FHDCFV
Sbjct: 63 HFHDCFV 69

>ref|XP_002453592.1| hypothetical protein SORBIDRAFT_04g008630 [Sorghum bicolor]
gb|EES06568.1| hypothetical protein SORBIDRAFT_04g008630 [Sorghum bicolor]
Length = 321

Score = 165 bits (418), Expect = 4e-38
Identities = 76/123 (61%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A C +FR IYN+TN++ AFA RQ++CP SGSGD NLAPLD+QT FDN Y++NL+
Sbjct: 197 AECEDFRGHIYNDTNVDPFAALRQRNCPAESGSGDTNLAPLDVQTRYVFDNAYYRNLMV 256

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D++V+ YST+PG F+S F AAMIKMG+I LTGS G+IR +CR
Sbjct: 257 RQGLLHSDQELFNGGSQDALVQQYSTDPGLFASHFVAAMIKMGNIGTLTGSQGGIRADCR 316

Query: 2170 RIN 2178
+N
Sbjct: 317 VVN 319

Score = 135 bits (339), Expect = 5e-29
Identities = 81/169 (47%), Positives = 92/169 (54%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCDGSILLDD SF GEK A PN S RG+EVID IK+ VE VCPGVVSCADI+A+AARD
Sbjct: 72 GCDGSILLDDAGSFVGEKTALPNA-SIRGYEVIDQIKANVEAVCPGVVSCADIVALAARD 130

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
++ GGPTW V LGRR
Sbjct: 131 GTVLL-----GGPTWAVPLGRR 147

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHISH 1663
D+ TAS S AN+ IPAPT NL+ LI F GLS D+ ALSG I +
Sbjct: 148 DSTTASLSQANS DIPAPTLNLDLILAFGKKGLSPADMTALSGAHTIGY 196

Score = 60.8 bits (146), Expect = 1e-06
Identities = 34/70 (48%), Positives = 40/70 (57%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MA L CL L + QL+ FY SCP L V++T+ AI + RMGASL
Sbjct: 1 MACSFRALLHCLLALSLCSTAYGGQLTPTFYALSCP ALEPIVRTTMTKAI INDRRMGASL 60

Query: 751 LRLFFHDCFV 780

LRLFFHDCFV
Sbjct: 61 LRLFFHDCFV 70

>gb|ACN60163.1| class III peroxidase [Tamarix hispida]
Length = 320

Score = 164 bits (415), Expect = 8e-38
Identities = 77/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT+FRARIYNETNI ++FA++ Q +CP T G DNNL+PLD +PT+FD Y+ +L+
Sbjct: 199 QARCTSFARIYNETNINSSFAKSLQANCPSTGG--DNNLSPLDTSSPTTFDVGYYTDLI 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQL+NGGSTDS V YS++ TF +DF +MI MG+ISPLTGS G++R NC
Sbjct: 257 GQKGLLHSDQQLYNGGSTDSQVTSYSSSSSTFLTDFGTSMINMGNISPLTGSRGQVRTNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKTN 320

Score = 125 bits (313), Expect = 5e-26
Identities = 78/170 (45%), Positives = 89/170 (52%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGS-ILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S + K A PN S RGF+V+D IKS VE VCPGVV CADILA+A
Sbjct: 71 VNGCDASGSIRRHCQLHRKRKTAQPNNGSLRGFDVVDTIKSKVESVCPGVVPCADILAVA 130

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGG +W V L
Sbjct: 131 ARDSV-----VALGGKSWGVL 147

Query: 1508 GRRDARTASQAANN GIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS SAAN GIPAPT NL+ LI+ FS +GLSTKDLV LSG I
Sbjct: 148 GRRDSTTASLSAANTGIPAPTLNLSGLITSFSNVGLSTKDLVVLGAHTI 197

>ref|XP_002450134.1| hypothetical protein SORBIDRAFT_05g001030 [Sorghum bicolor]
gb|EES09122.1| hypothetical protein SORBIDRAFT_05g001030 [Sorghum bicolor]
Length = 317

Score = 163 bits (413), Expect = 1e-37
Identities = 76/124 (61%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC NFR RIY+E NI+T+ A + + +CP +G DNN++PLD TP FDN+Y+KNL+
Sbjct: 196 QARCVNFRDRIYSEANIDTSLATSLKNCNPKTG--DNNISPLDASTPYVFDNFYKLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKG+LHSDQQLFNGGS DS YS+N F +DF+ AM+KM +ISPLTGS+G+IRKNC
Sbjct: 254 NKKGVLHSDQQLFNGGSADSQTTTYSSNMAKFFTFSTAMLKMSNISPLTGSSGQIRKNC 313

Query: 2167 RRIN 2178
RR+N
Sbjct: 314 RRVN 317

Score = 147 bits (370), Expect = 1e-32
Identities = 81/165 (49%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDT +FTGEK A PN NS RGF+VID+IK+ +E++CP VVSCADI+A+AA
Sbjct: 69 VNGCDGSVLLDDTPTFTGEKTAVPNNNSLRGFDVIDSIKAQLERICPVVSCADIVAA 128

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 129 RDSV-----VALGGPTWAVNLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS AANN IPAPT +L L FS GLS D++ALSG
Sbjct: 146 RRDSL TASLDAANNDIPAPTLDLTLTKSFSNKGLSASDMIALSG 190

Score = 68.9 bits (167), Expect = 4e-09
Identities = 36/71 (50%), Positives = 47/71 (66%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS LALF ++QL+ NFY SCPN ++++ V+SA+++E RMGASL
Sbjct: 1 MASHKPLTCSVLALFFAA-SLVSSQLNANFYDKSCPNAlyTIQTAVRSaVARENRMGASL 59

Query: 751 LRLFFHDCFVN 783
LRL FHDCFVN
Sbjct: 60 LRLHFHDCFVN 70

>gb|AAC05277.1| peroxidase FLXPER4 [Linum usitatissimum]
Length = 305

Score = 163 bits (413), Expect = 1e-37
Identities = 81/124 (65%), Positives = 103/124 (83%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYN+TNI+ AFA TR+ +CP+ +G+G N LAPLD TPT FDN Y+++LV
Sbjct: 185 QARCTTFRQRIYNDTNIDPAFATTRRGNC PQ-AGAGAN-LAPLD-GTPTQFDNRYQQDLV 241

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSGEIRKNC 2166
++GLLHSDQ+LFN G+ D++VR YS N TF++DFAAAM++MG+ISPLTG+NGEIR NC
Sbjct: 242 ARRGLLHSDQELFNNGTQDALVRTYSNNAATFATDFAAAMVRMGNISPLTGNGEIRFNC 301

Query: 2167 RRIN 2178
RR N
Sbjct: 302 RRPN 305

Score = 144 bits (362), Expect = 1e-31
Identities = 80/169 (47%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGS+LLDDT++FTGEKNA PN+NS RGF++ID IK+ VE C VSCADILA+AA
Sbjct: 58 VNGCDGSLLDDTATFTGEKNAGPNQNSVRGFDI IDTIKTRVEAACNATVSCADILALAA 117

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V +V GGPTW V LG
Sbjct: 118 RDGVVLV-----GGPTWTVP LG 134

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAAN IPAP S+L + + F+ GL+ +D+ LSG I
Sbjct: 135 RRDARTASQSAANAQIPAPGSSLGTITNLFTNKGLTARDVTILSGAHTI 183

Score = 65.1 bits (157), Expect = 6e-08
Identities = 29/55 (52%), Positives = 39/55 (70%)
Frame = +1

Query: 619 LIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
L+ S +AQL+ NFY SCP L + V++ + A++ E RM AS+LRL FHDCFVN
Sbjct: 5 LLASSGSAQLAANFYATSCPTLLTIVRNAMTQAVNSENMAASILRLHFHDCFVN 59

>ref|XP_002269343.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 331

Score = 163 bits (412), Expect = 2e-37

Identities = 81/125 (64%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QARC FR RIY N T+I+ FA TR++ CP +G+GD+NLAPL+L TP SFDN YFKNL
Sbjct: 207 QARCVTFRDRIYDNGTDIDAGFASTRRRRC PANNGGDDNLAPLELVTPNSFDNYYFKNL 266

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAIKMGDISPLTGSNGEIRKN 2163
+++KGLL SDQ LF+GGSTD+IV YS +P TF SDFA+AM+KMGDI LTGS G IRK
Sbjct: 267 IRRKGLLQSDQVLFSGGSTDTIVNEYSKSPKTFRSDFASAMVKMGDIEALTGSAGVIRKF 326

Query: 2164 CRRIN 2178
C IN
Sbjct: 327 CNVIN 331

Score = 132 bits (332), Expect = 3e-28
Identities = 76/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILLDD+SS EKNA N NS RG+EVIDNIKS VE +CPGVVSCADI+A+AA
Sbjct: 80 VQGC DASILLDDSSSIQSEKNAPNNLNSVRGYEVIDNIKSKVESLCPGVVSCADIVAVAA 139

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ VS GPTW V+LG
Sbjct: 140 RDASVAVS-----GPTWTVRLG 156

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T+ S A +P+ +L++L+S F + GLS +D+VALSG+ I
Sbjct: 157 RRDSTTSGLSQAATNLPSFRDSLDKLVSLFGSKGLSARDMVALSGSHTI 205

Score = 63.5 bits (153), Expect = 2e-07
Identities = 31/69 (44%), Positives = 46/69 (66%), Gaps = 1/69 (1%)
Frame = +1

Query: 577 SFC SRLTICLALFVLIWGS-ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
S S I LA+F+++ A LS FY H+CP +++++ V++A+S+E RM ASL+
Sbjct: 12 SCISPACIFLAVFLILSNMPCEAHLSPTFYDHTCPRALTTIQTAVRTAVSRERRMAASLI 71

Query: 754 RLFFHDCFV 780
RL FHDCFV
Sbjct: 72 RLHFHDCFV 80

>gb|EAY85148.1| hypothetical protein OsI_06503 [Oryza sativa Indica Group]

Length = 323

Score = 163 bits (412), Expect = 2e-37
Identities = 74/123 (60%), Positives = 98/123 (79%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLVQ 1989
++C NFR RIYN+TNI+ AFA R+ CP GSGD +LAPLD T FDN Y++NL+
Sbjct: 199 SQCANFRDRIYNDTNIDPAFAALRRGGCPAAPGSGDTS LAPLDALTQNVFDNAYYRNLLA 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++V+ YS+NP F++DFAAAMIKMG+I+PLTG+ G+IR++CR
Sbjct: 259 QRGLLHSDQVLFNGGSQDALVQQYSSNPALFAADFAAAMIKMGNINPLTGAAGQIRRSCR 318

Query: 2170 RIN 2178
+N
Sbjct: 319 AVN 321

Score = 139 bits (349), Expect = 4e-30
Identities = 80/171 (46%), Positives = 99/171 (57%), Gaps = 2/171 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1324
+QGCD SILLDD +SF GEK A PN NS RG++VID IK VE +CPGVVSCADI+A+
Sbjct: 69 VQGCDASILLDDVPATSFVGEKTAFPNVNSVRGYDVIDQIKRRVELLC PGVVSCADIVAL 128

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 129 AARDSTAL-----LGGPSWEVP 145

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
LGRRD+ TAS SAAN+ +PAP+S+L L++RF + GLS +D+ ALSG I
Sbjct: 146 LGRRDSTTASLSAANS DLPAPSSDLATLVARFGSKGLSPRDMTALSGAHTI 196

Score = 69.7 bits (169), Expect = 3e-09
Identities = 35/60 (58%), Positives = 41/60 (68%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
CL F L+ +A QLST FY SCP L V++TV S + E RMGASL+RLFFHDCFV
Sbjct: 10 CLLAFFLLSSAACGQLSTTFYAASCPTQLLVVRATVLSTLLAERRMGASLRLFFHDCFV 69

>ref|XP_002269301.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 213

Score = 162 bits (411), Expect = 2e-37
Identities = 81/124 (65%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q RC FR RIYN T+I+ FA TR++ CP +G+GD NLAPL+L TP SFDN YFKNL+
Sbjct: 90 QGRCVTFRDRIYNGTDIDAGFASTRRRRCPADNGNGDANLAPLELVTPNSFDNYYFKNLI 149

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q+KGLL SDQ LF+GGSTDSIV YS +P TF SDFA+AM+KMGI PLT S G IRK
Sbjct: 150 QRKGLLQSDQVLFSGGSTDSIVNEYSKSPKTFRSDFASAMLMGDIPLTRSAGVIRKFY 209

Query: 2167 RRIN 2178
IN
Sbjct: 210 NVIN 213

Score = 62.0 bits (149), Expect = 5e-07
Identities = 30/60 (50%), Positives = 42/60 (70%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
+ GPTW VKLGRRD+ T+ S A +P+ +L++LIS F + GLS +D+VALSG+ I
Sbjct: 29 VSGPTWTVKLGRRDSTTSGLSLAATNLPSPFRDSLKLISLFGSKGLSARDMVALSGSHTI 88

>gb|AAD37428.1|AF149278_1 peroxidase 3 precursor [Phaseolus vulgaris]
Length = 324

Score = 162 bits (411), Expect = 2e-37
Identities = 78/126 (61%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSG--DNNLAPLDLQTPTSFDNYYFKN 1980
+ARC + +RIYNE NIE+ FA+ RQ++CPR S DNN+APL+ +TP FDN Y+KN
Sbjct: 199 KARCAVYGSRIYNEKNIESLFAKARQKNCPRNSNGTPKDNNVAPLEFKTPNHFDNYYKN 258

Query: 1981 LVQKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ KKGLLHSDQ LF+GGSTDS+VR YS + F SDF AMIKMG+I PLTGSNG+IR+
Sbjct: 259 LINKKGLLHSDQVLFDDGGSTDSLVRAYSNDQRAFESDFVTAMIKMGNIKPLTGSNGQIRR 318

Query: 2161 NCRRIN 2178
C R N
Sbjct: 319 LCGRPN 324

Score = 126 bits (317), Expect = 2e-26
Identities = 79/170 (46%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLD SS EK A PN S RG+EVID IKS VE +CPG+VSCADI+AIAA
Sbjct: 74 VNGCDGSVLLDGPSS---EKTAPPNDKSLRGYEVIDAIKSKVEALCPGIVSCADIVAIAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV I LGGP W VKLG
Sbjct: 131 RDSVNI-----LGGPFWKVKLG 147

Query: 1511 RRDARTA-SQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ T Q A++ +P+P S+L+ LIS F GLS KD+VALSG I
Sbjct: 148 RRDSTGFFQLASSGALPSPASSLDTLISSFKDQGLSAKDMVALSGAHTI 197

Score = 83.6 bits (205), Expect = 2e-13
Identities = 42/67 (62%), Positives = 50/67 (74%), Gaps = 1/67 (1%)
Frame = +1

Query: 586 SRLTICLALFVL-IWGSANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLF 762
S T +A F L + GS++AQLS NFY CP + +VKS VQSA++KE RMGASLLRLF
Sbjct: 9 STTTFAIAFFTLFLIGSSSAQLSENFYAKKCPKVLVAVKSVVQSAVAKEPRMGASLLRLF 68

Query: 763 FHDCFVN 783
FHDCFVN
Sbjct: 69 FHDCFVN 75

>ref|XP_002334243.1| predicted protein [Populus trichocarpa]
gb|EEF07510.1| predicted protein [Populus trichocarpa]
Length = 317

Score = 162 bits (410), Expect = 3e-37
Identities = 80/124 (64%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RI+++ NI+ FA TR++ CP D+ LAPLDL TP SFDN YFKNL+
Sbjct: 196 QAQCFTFRDRIHSDNNIDAGFASTRKRCPLVGS--DSTLAPLDLVTPNSFDNYYFKNLM 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
QKKGLL SDQ+LF+GGSTDSIV YS NP FSSDFA+AMIKMGDISPLTG+ G+IR+ C
Sbjct: 254 QKKGLLQSDQELFSGGSTDSIVSEYSRNPAKFSSDFASAMIKMGDISPLTGTAGQIRRIC 313

Query: 2167 RRIN 2178
+N

Sbjct: 314 SAVN 317

Score = 133 bits (335), Expect = 1e-28
Identities = 76/166 (45%), Positives = 95/166 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD SILLD+TSS EK A N NS RG+EVID KS VEK+CPGVVSCADI+A+AA
Sbjct: 69 VQGCDASILLDETSSIQSEKTAGGNNSVRGYEVIDKAKSKVEKICPGVVSCADIIAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP+W VKLG
Sbjct: 129 RDA-----SAYVGGPSWAVKLG 145

Query: 1511 RRDARTASQSAANN GIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS + A +PA + +L +LISRF GL+ +D+VALSG+
Sbjct: 146 RRDSTTASPTLAITELPAFSDDLGR LISRFQKGLTARDMVALSGS 191

Score = 62.0 bits (149), Expect = 5e-07
Identities = 28/57 (49%), Positives = 42/57 (73%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
LF+L + A+LS+ FY SCP S++++ ++AI++E RM ASL+RL FHDCFV
Sbjct: 13 LFLSTTACQAKLSSAFYDKSCPKAESAIRTAIRTAIRERRMAASLIRLHFHDCFV 69

>ref|XP_002438530.1| hypothetical protein SORBIDRAFT_10g021630 [Sorghum bicolor]
gb|EER89897.1| hypothetical protein SORBIDRAFT_10g021630 [Sorghum bicolor]
Length = 329

Score = 162 bits (409), Expect = 4e-37
Identities = 73/126 (57%), Positives = 100/126 (79%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS--GSGDNNLAPLDLQTPTSFDNYYFKN 1980
QARCT FR+RIY +TNI FA RQQ+CP+ S G+GD LAP+D++TP +FDN Y++N
Sbjct: 204 QARCTTFRSRIYGD TNINATFASLRQQTCPQASDGGAGDAALAPIDVRTPEAFDNAYYQN 263

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ ++GL HSDQ+LFNGGS D++V+ YS N F++DFA AM++MG ISPLTG+ GE+R
Sbjct: 264 LMARQGLFHSDQQLFNGGSQDALVKKYSGNAAMFAADFAKAMVRMG AISPLTGTQGEVRL 323

Query: 2161 NCRRIN 2178
+CR++N

Sbjct: 324 DCRKVN 329

Score = 141 bits (356), Expect = 5e-31
Identities = 79/165 (47%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 77 VNGCDASILLDDTATFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW V LG
Sbjct: 137 RDAVNLL-----GGPTWTVYLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDARTASQS AN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 154 RRDARTASQSDANGNLPGPSLTLVTMFGNKGLSARDMTALSG 198

Score = 69.3 bits (168), Expect = 3e-09
Identities = 35/66 (53%), Positives = 48/66 (72%), Gaps = 2/66 (3%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQ--LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
LT+ L +L+ G+A A LST+FY CPN+ S V++ + SA++ E RMGAS+LR+FF
Sbjct: 13 LTVA AVL SLLMAGAAAAGGLSTSFYSKKCPNVQSIVRAGMASAVAAEKRMGASILRMFF 72

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 73 HDCFVN 78

>ref|XP_002281755.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 162 bits (409), Expect = 4e-37
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD+QT FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIQTMNKFDNYYQNLM 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR YS N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TQRGLLHSDQELFNGGSQDALVRTYSANNALFFGDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 RRIN 2178

R +N

Sbjct: 314 RVVN 317

Score = 152 bits (383), Expect = 4e-34

Identities = 85/169 (50%), Positives = 101/169 (59%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA

Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACKATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD V + LGGP+W V LG

Sbjct: 129 RDGVVL-----LGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ ALSG+ I

Sbjct: 146 RRDARTANQSAANNLPPFANLSALISGFAAKGLNADDMTALSGSHTI 194

Score = 70.9 bits (172), Expect = 1e-09

Identities = 37/71 (52%), Positives = 47/71 (66%)

Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750

MASF + + + VL S NAQLS NFY +CPN+ V+ + A+ +E RMGAS+

Sbjct: 1 MASFTNSFVFSIISVLAC-SINAQLSPNFYASTCPNVQKIVRVEMVQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783

LRLFFHDCFVN

Sbjct: 60 LRLFFHDCFVN 70

>ref|XP_002437128.1| hypothetical protein SORBIDRAFT_10g021610 [Sorghum bicolor]

gb|EER88495.1| hypothetical protein SORBIDRAFT_10g021610 [Sorghum bicolor]

Length = 314

Score = 161 bits (408), Expect = 5e-37

Identities = 76/125 (60%), Positives = 98/125 (78%), Gaps = 1/125 (0%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFART-RQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983

QARCT FR+RIY +TNI +FA RQQ+CP++ G G NLAP+D+QTPT FD Y+ NL

Sbjct: 191 QARCTTFRSRIYGDTNINASF AAALRQQTCPQSGGDG--NLAPMDVQTPTRFDTDYTNL 248

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GL HSDQ+LFNGGS D++VR YS NP F+SDF AAMIKMG++ LTG+ G+IR+N
Sbjct: 249 LSQRGLFHSDQELFNGGSQDALVRQYSANPSLFSDFMAAMIKMGNVGVLTGTAGQIRRN 308

Query: 2164 CRRIN 2178
CR +N
Sbjct: 309 CRVVN 313

Score = 134 bits (336), Expect = 1e-28
Identities = 80/169 (47%), Positives = 92/169 (54%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCDGSILLD GEK A PN NSARGFEVID IK+ VE CPGVVSCADILA+AA
Sbjct: 68 VQGCDGSILLDAG----GEKTAGPNANSARGFEVIDTIKTNVEAACPGVVSCADILALAA 123

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD ++ G PTWNV LG
Sbjct: 124 RDGTNLLGG-----PTWNVPLG 140

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P T++L LIS FS GLS +D+ ALSG I
Sbjct: 141 RRDSTTASASLANSLPQSTASLGTLSLFSRQGLSARDMTALSGAHTI 189

Score = 71.6 bits (174), Expect = 7e-10
Identities = 36/60 (60%), Positives = 42/60 (70%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYYHSCP NLFS SVKSTVQSAISKETRMGASLLR LFFHDCFV 780
CL L+ A+ AQLST FY SCPNL S V+ + A+S + RMGASLLR LFFHDCFV
Sbjct: 9 CLVAISLLSCVAHAQLSTTFYASSCPNLQ SIVRRAMIQALSNDQRMGASLLR LFFHDCFV 68

>ref|XP_002517727.1| Cationic peroxidase 1 precursor, putative [Ricinus communis]
gb|EEF44659.1| Cationic peroxidase 1 precursor, putative [Ricinus communis]
Length = 264

Score = 160 bits (406), Expect = 9e-37
Identities = 79/124 (63%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YNETNI++A A + + CP T+GS D+NL+PLD +P FDN YFKNLV
Sbjct: 143 QARCLMFRGRLYNETNIDSALATSLKSDCP-TTGS-DDNLSPLDATSPVIFDNSYFKNLV 200

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLF+GGST+S V+ YST+P TF +DFA AMIKMG +SPLTG++G+IR +C
Sbjct: 201 NNKGLLHSDQQLFSGGSTNSQVKTYSTDPFTFYADFANAMIKMGKLSPLTGTGQIRTDC 260

Query: 2167 RRIN 2178
R++N
Sbjct: 261 RKNV 264

Score = 140 bits (354), Expect = 9e-31
Identities = 80/170 (47%), Positives = 98/170 (57%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTS--SFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIA 1327
+ GCD S+LLDD S SFTGEK A PN NS RGF+VID IKS VE +CPGVVSCADILA+A
Sbjct: 15 VNGCDASVLLDDISPSFTGEKTAGPNANSLRGFDVIDTIKSQVESICPGVVSCADILAVA 74

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 75 ARDSV-----VALGGPSWQVEL 91

Query: 1508 GRRDARTASQAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
GRRD+ TAS AAN +P+P +L+ LIS S G + K++VAL+G+ I
Sbjct: 92 GRRDSTTASYDAANTDLPSPMLDSDLISALSRKGFTAKEMVALAGSHTI 141

>ref|NP_001057822.1| Os06g0547400 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54122.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69328.1| TPA: class III peroxidase 86 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF19736.1| Os06g0547400 [Oryza sativa Japonica Group]
gb|EEC80780.1| hypothetical protein OsI_23305 [Oryza sativa Indica Group]
gb|EEE65851.1| hypothetical protein OsJ_21628 [Oryza sativa Japonica Group]
Length = 324

Score = 160 bits (406), Expect = 9e-37
Identities = 74/124 (59%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR+RIY E NI +FA RQQ+CPR+ G D NLAP D+QTP +FDN Y++NLV
Sbjct: 203 RAQCQFFRSRIYTERNINASFASLRQQTCPRSSG--DANLAPFDVQTPDAFDNAYYQNLV 260

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D +VR YSTNP FSSDF +AM+KMG++ P +G+ E+R NC
Sbjct: 261 SQRGLLHSDQELFNGGSQDGLVRQYSTNPSQFSSDFVSAMVKGMLLPSSGTATEVRLNC 320

Query: 2167 RRIN 2178

R++N

Sbjct: 321 RKNV 324

Score = 149 bits (375), Expect = 3e-33

Identities = 84/169 (49%), Positives = 99/169 (58%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

+ GCDGSILLDDTS+FTGEK+A PN NSARGFEVID IK+ VE C VSCADILA+AA

Sbjct: 76 VNGCDGSILLDDTSTFTGEKSAGPNANSARGFEVIDAIKTQVEASCKATVSCADILALAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD V ++ GGPTW+V LG

Sbjct: 136 RDGVNLL-----GGPTWSVALG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

R+D+RTASQSAAN+ +P P S+L LIS F GLS +D+ ALSG I

Sbjct: 153 RKDSRTASQSAANSNLPGPSLATLISMFGNQGLSARDMTALSGAHTI 201

Score = 73.2 bits (178), Expect = 2e-10

Identities = 36/63 (57%), Positives = 47/63 (74%), Gaps = 1/63 (1%)

Frame = +1

Query: 598 ICLALFVLIWGSANAQ-LSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774

+ + + VL+ G+A AQ LS NFY +CPNL + V+S + SA+ E RMGAS+LRLFFHDC

Sbjct: 15 VAVVVAVLLGGAAEAQQLSPNFYSRTCPLATIVRSGMASAVRTEPRMGASILRLFFHDC 74

Query: 775 FVN 783

FVN

Sbjct: 75 FVN 77

>ref|XP_002285724.1| PREDICTED: hypothetical protein [Vitis vinifera]

Length = 318

Score = 160 bits (405), Expect = 1e-36

Identities = 78/124 (62%), Positives = 99/124 (79%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L

Sbjct: 196 KARCTSFNRNHIYNDTIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLK 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+L+NGGSTDSIV YS N TF D A AM+KMG+ISPLTG+NG+IR NC
Sbjct: 253 EKKGLLHSDQELYNGGSTDSIVETYSINTATFFRDVANAMVKMGNISPLTGNGQIRTNC 312

Query: 2167 RRIN 2178
R++N
Sbjct: 313 RKNV 316

Score = 155 bits (391), Expect = 5e-35
Identities = 86/167 (51%), Positives = 100/167 (59%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 71 GCDASILLDDTATFTGEKTAGPNNNSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 130

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V+LGRR
Sbjct: 131 SV-----VALGGPTWTVRLGR 147

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS SAA +P P NL+QLIS FS GL+TK++V LSGT I
Sbjct: 148 DSTTASFSAAARTDLPGNLNLSQLISAFSKKGLTTKEMVVLSTHTI 194

Score = 66.6 bits (161), Expect = 2e-08
Identities = 32/58 (55%), Positives = 41/58 (70%), Gaps = 1/58 (1%)
Frame = +1

Query: 610 LFVLIWGSANAQ-LSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+F L+ G A+A LS NFY SCP ++++ V A++KE RMGASLLRL FHDCFV
Sbjct: 12 IFSLLGMAHAHYLSPNFYARSCPRALPTIRTAVNKAVAKEKRMGASLLRLHFHDCFV 69

>ref|XP_002521867.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF40503.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 326

Score = 160 bits (405), Expect = 1e-36
Identities = 83/125 (66%), Positives = 96/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSQRPTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T I+ FA TR++SCP G D NLAPLDL TP SFDN YFKNL

Sbjct: 204 QAQCFTFRDRIYSNGTEIDAGFASTRKRSCPAVGG--DANLAPLDLVTPNSFDNNYFKNL 261

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ L +GGSTDIV GYS +P TFSSDFA+AMIKMG+I PLTG+ G+IR+

Sbjct: 262 MQRKGLLESDQILLSGGSTDSIVSGYSRSPSTFSSDFAAMIKMGNIDPLTGTAGQIRRI 321

Query: 2164 CRRIN 2178

C IN

Sbjct: 322 CSAIN 326

Score = 137 bits (344), Expect = 1e-29
Identities = 75/165 (45%), Positives = 99/165 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LLD+TS+ EK A PN++SARG+EVID K+ VEK+CPGVVSCADIL++AA

Sbjct: 77 IQGCDASVLLDETSTIESEKTALPNKDSARGYEVIDKAKTEVEKICPGVVSCADILSVAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RDS S +GGP+W V LG

Sbjct: 137 RDS-----SAYVGGPSWTVMLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645

RRD+ TAS++ AN+ +P+ L++LISRF + GLS +D+VALSG

Sbjct: 154 RRDSTTASRTLANSFELPSFKDGLDRLISRFQSKGLSARDMVALSG 198

Score = 60.8 bits (146), Expect = 1e-06
Identities = 27/56 (48%), Positives = 44/56 (78%), Gaps = 1/56 (1%)
Frame = +1

Query: 616 VLIWGSA-NAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

+LI G+A +AQL++ FY CPN S+++++++I+ E RM ASL+RL FHDCF+

Sbjct: 22 LLILGTACHAQLTSTFYDSLCPNALSTIRTSIRNSIAAERRMAASLIRLHFHDCF 77

>emb|CAH10841.1| peroxidase [Picea abies]
Length = 320

Score = 160 bits (405), Expect = 1e-36
Identities = 78/124 (62%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ TP F+N Y+ NL

Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKANCP--SAGGDNTLSPLDVVTPIKFNNKYGNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLFNGGSTDS V YSTN +F +DFAAAM+KM +ISPLTG++G+IRKNC
Sbjct: 257 IQKGLLHSDQQLFNGGSTDSQVTAYSTNQNSFFTDFAAAMVKMSNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 154 bits (388), Expect = 1e-34
Identities = 89/169 (52%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA
Sbjct: 72 VSGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GPTW V LG
Sbjct: 132 RDSV-----VELQGPTWTVM LG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAANN IP+P S+L+ LIS F GLSTKDLVALSG I
Sbjct: 149 RRDSTTASLSAANNIPSPASSLSALISSFKGHGLSTKDLVALSGAHTI 197

Score = 62.8 bits (151), Expect = 3e-07
Identities = 33/70 (47%), Positives = 43/70 (61%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGSAN-----AQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + + S N QLS+ FY SCP S VK V+ A++KE RMGASL+
Sbjct: 4 RNLLCIGIMAVFVCSININAVSGQLSSTFYDKSCPRAQSIVKRVVKQALAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783
RL FHDCFV+
Sbjct: 64 RLHFHDCFVS 73

>gb|EEE67814.1| hypothetical protein OsJ_25568 [Oryza sativa Japonica Group]
Length = 135

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 12 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTTPYSFDNAYYSNLL 71

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 72 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQGQIRLSC 131

Query: 2167 RRIN 2178
++N
Sbjct: 132 SKVN 135

>tpe|CAH69352.1| TPA: class III peroxidase 110 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 313

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 190 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTTPYSFDNAYYSNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 250 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQGQIRLSC 309

Query: 2167 RRIN 2178
++N
Sbjct: 310 SKVN 313

Score = 127 bits (319), Expect = 1e-26
Identities = 74/175 (42%), Positives = 94/175 (53%)
Frame = +2

Query: 1118 AS*ILMSKH*QMCGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV 1297
AS + + H GCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C
Sbjct: 53 ASLLRLHFHDC FVGCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQT 112

Query: 1298 VSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI* 1477
VSCADILA+AARDSV +
Sbjct: 113 VSCADILAVAARDSV-----VA 129

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNLISRF SALGLSTKDLVALS 1642
LGGP+W V LGRRD+ TAS +ANN +P P +L LI F G S D+VALS

Sbjct: 130 LGGPSWTVGLGRRDSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALS 184

Score = 67.0 bits (162), Expect = 2e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTAAVNNEPRMGASLLRLHFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>ref|NP_001060627.1| Os07g0677100 [Oryza sativa (japonica cultivar-group)]
dbj|BAC83102.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAF22541.1| Os07g0677100 [Oryza sativa Japonica Group]
dbj|BAG95220.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 315

Score = 160 bits (404), Expect = 1e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFDN Y+ NL+
Sbjct: 192 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTPYSFDNAYYSNLL 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR ++N FSS F++AM+KM ++ PLTGS G+IR +C
Sbjct: 252 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLTGSQQGQIRLSC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 132 bits (331), Expect = 4e-28
Identities = 74/169 (43%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AA
Sbjct: 65 VQGCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVGLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 RRDSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 190

Score = 67.0 bits (162), Expect = 2e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTAANNNEPRMGASLLRLHFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>gb|ABD66594.1| peroxidase [Litchi chinensis]
Length = 234

Score = 159 bits (403), Expect = 2e-36
Identities = 88/169 (52%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDTS+F GEK A PN NS RGF V+D IK+ +EK CPGVVSCAD+LAIAA
Sbjct: 4 VDGCDGSLLDDTSTFVGEKTAVPNNNSVRGFNVVDQIKAKLEKACPGVVSCADLLAIAA 63

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 64 RDSV-----VHLGGPSWTVRLG 80

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD++TAS++ AN IP PTSNL+ LIS FSA GLS KDLVALSG I
Sbjct: 81 RRDSKTASRALANTSIPPPTSNSALISSFSAQGLSLKDLVALSGAHTI 129

Score = 113 bits (283), Expect = 2e-22
Identities = 54/98 (55%), Positives = 69/98 (70%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARCT+FR IYN+TNI+++FA + ++ CPR+ DN LA LD QTP FD Y+ NL++
Sbjct: 132 ARCTSFRGHIYNDTNIDSSFAMSLRRKCPRSGN--DNALANLDRQTPFCFDKLYDNLLK 189

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAA 2103
KKGLLHSDQ+LF GGS D V+ Y+ N F DFA A

Sbjct: 190 KKGLLHSDQELFKGGSADPFVKKYANNTSAFFKDFAGA 227

>emb|CBI19219.1| unnamed protein product [Vitis vinifera]
Length = 446

Score = 159 bits (403), Expect = 2e-36
Identities = 81/138 (58%), Positives = 105/138 (76%), Gaps = 1/138 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L

Sbjct: 194 KARCTSFNRNHIYNDTIDPFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLK 250

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+L+NGGSTDSIV YS N TF D A AM+KMG+ISPLTG+NG+IR NC

Sbjct: 251 EKKGLLHSDQELYNGGSTDSIVETYSINTATFFRDVANAMVKMGNISPLTGTTNGQIRTNC 310

Query: 2167 RRIN*F-DSVLNIKGPTH 2217

R+I + + I+ PT+

Sbjct: 311 RKIQCIGPTPIEIRNPTN 328

Score = 155 bits (391), Expect = 5e-35
Identities = 86/167 (51%), Positives = 100/167 (59%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG+EVID IKS VE +CPGVVSCADI+A+AARD

Sbjct: 69 GCDASILLDDTATFTGEKTAGPNNNSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 128

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V+LGRR

Sbjct: 129 SV-----VALGGPTWTVRLGR 145

Query: 1517 DARTASQSAANNGIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS SAA +P P NL+QLIS FS GL+TK++V LSGT I

Sbjct: 146 DSTTASFSAAARTDLPNPNLSQLISAFSKGLTTKEMVVLSTGHTI 192

Score = 65.1 bits (157), Expect = 6e-08
Identities = 31/57 (54%), Positives = 40/57 (70%), Gaps = 1/57 (1%)

Frame = +1

Query: 610 LFVLIWGSANAQ-LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCF 777
+F L+ G A+A LS NFY SCP ++++ V A++KE RMGASLLRL FHDCF
Sbjct: 12 IFSLLLGMAHAHYLSPNFYARSCPRLPTIRTAVNKAVAKEKRMGASLLRLHFHDCF 68

>ref|XP_002334317.1| predicted protein [Populus trichocarpa]
gb|EEF08174.1| predicted protein [Populus trichocarpa]
Length = 224

Score = 159 bits (403), Expect = 2e-36
Identities = 80/124 (64%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR D LAPLDL TP SFDN YFKNL+
Sbjct: 103 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGS--DATLAPLDLVT PNSFDNYYFKNLM 160

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS+G+IR+ C
Sbjct: 161 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSSGQIRRIC 220

Query: 2167 RRIN 2178
+N
Sbjct: 221 SAVN 224

Score = 99.4 bits (246), Expect = 3e-18
Identities = 59/140 (42%), Positives = 77/140 (55%)
Frame = +2

Query: 1229 NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARDSVQIVSGQTTNKNTLN*I IKLYIS 1408
NSARG+ VID K+ VEK+CPGVVSCADI+A+AARD+
Sbjct: 2 NSARGYNVIDKAKTEVEKICPGVVSCADIIA VAARDA----- 38

Query: 1409 KLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQL 1588
S +GGP++ VKLGRRD+ TAS++ AN +PA +L L
Sbjct: 39 -----SAYVGGPSYAVKLGRRDSTTASRTLANAELPAFFESLESL 78

Query: 1589 ISRFSALGLSTKDLVALSGT 1648
ISRF GL+ +D+VALSG+
Sbjct: 79 ISRFQKKGLTARDMVALSGS 98

>emb|CAN73051.1| hypothetical protein [Vitis vinifera]
Length = 297

Score = 159 bits (403), Expect = 2e-36
Identities = 77/124 (62%), Positives = 97/124 (78%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD+QT FDN Y++NL
Sbjct: 176 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIQTMNKFDNKYYENLE 233

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 234 AQRGLFHSDQELFNGGSQDALVRAYSANNALFFXDFAAAMVKMSNISPLTGTNGEIRSNC 293

Query: 2167 RRIN 2178
R +N
Sbjct: 294 RVVN 297

Score = 151 bits (382), Expect = 5e-34
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 49 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 108

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 109 RDGVVL-----LGGPSWTVPLG 125

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ ALSG+ I
Sbjct: 126 RRDARTANQSAANNLPPFANLSALISGFAAKGLNADDMTALSGSHTI 174

Score = 62.4 bits (150), Expect = 4e-07
Identities = 28/49 (57%), Positives = 36/49 (73%)
Frame = +1

Query: 637 NAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
N +LS NFY +CPN+ V+ + A+ +E RMGAS+LRLFFHDCFVN
Sbjct: 2 NYKLSPNFYASTCPNVQKIVRVEMVQAVIREPRMGASILRLFFHDCFVN 50

>gb|EEE67818.1| hypothetical protein OsJ_25573 [Oryza sativa Japonica Group]
Length = 323

Score = 159 bits (402), Expect = 3e-36

Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+

Sbjct: 200 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYYRNLLS 259

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR +++++ F + FA AM+KMG+ISPLTG+ G+IR C

Sbjct: 260 NKGLLHSDQELFSGSTDNVRSFASAAAFGAATAMVKMGNISPLTGTQGQIRLICS 319

Query: 2170 RIN 2178

+N

Sbjct: 320 AVN 322

Score = 94.7 bits (234), Expect = 8e-17
Identities = 68/168 (40%), Positives = 85/168 (50%), Gaps = 1/168 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AARD

Sbjct: 79 GCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAARD 132

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W+V LGRR

Sbjct: 133 SV-----VALGGPSWSVPLGRR 149

Query: 1517 DARTASQSAANNGIPAP-TSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ A+ +A AP T +L QLIS +++ GLS DLVALSG I

Sbjct: 150 DSTGAATAAQVISSLAPSTDLSAQLISAYASKGLSATDLVALSGAHTI 197

Score = 67.8 bits (164), Expect = 1e-08
Identities = 39/70 (55%), Positives = 46/70 (65%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL

Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTSCPRAMSIKSTVTA AVNNEPRMGASL 58

Query: 751 LRLFFHDCFV 780

LRL FHDCFV

Sbjct: 59 LRLHFHDCFV 68

>gb|EEE56633.1| hypothetical protein OsJ_06032 [Oryza sativa Japonica Group]

Length = 303

Score = 159 bits (402), Expect = 3e-36
Identities = 74/123 (60%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 179 AQCQFFRGGHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 238

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 239 RRGLLHSDQELFNGGSQDERVKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 298

Query: 2170 RIN 2178
+N
Sbjct: 299 VVN 301

Score = 95.9 bits (237), Expect = 3e-17
Identities = 48/70 (68%), Positives = 54/70 (77%), Gaps = 2/70 (2%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD S F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+
Sbjct: 80 VQGCDASILLDDVPSKGFVGEKTAGPNTNSIRGYEVIDKIKANVEAACPGVVSCADILAL 139

Query: 1325 AARDSVQIVS 1354
AAR+ V +VS
Sbjct: 140 AAREGVNLVS 149

Score = 60.5 bits (145), Expect = 2e-06
Identities = 34/76 (44%), Positives = 47/76 (61%), Gaps = 7/76 (9%)
Frame = +1

Query: 574 ASFC SRLTICLALFVLIWGSANA-----QLSTNFYYHSCP NLFSSVKSTVQSAISKET 732
+S +R + LAL + + SA A ++ ++Y SCP L + V+ T+ SAI E
Sbjct: 5 SSTTTRFCLLLALVLPMISSAAAGDDALPLPMTPSYYRKSCPTLEAIVRGTMLSAIKAER 64

Query: 733 RMGASLLRLFFHDCFV 780
RMGAS+LRLFFHDCFV
Sbjct: 65 RMGASILRLFFHDCFV 80

>ref|XP_002281731.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 317

Score = 159 bits (402), Expect = 3e-36
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATRRSTCP-VSG-GNSNLAPLDIRTMNRFDNIIYYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGTNGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 151 bits (381), Expect = 7e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGV-----VQLGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I
Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 7e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSIIISLLACSLNQLSPNFYASTCPNVQNVIRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>gb|EAZ05136.1| hypothetical protein OsI_27329 [Oryza sativa Indica Group]
Length = 338

Score = 159 bits (402), Expect = 3e-36
Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+
Sbjct: 215 ARCRGFRTRLYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYYRNLLS 274

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C
Sbjct: 275 NKGLLHSDQELFSNGSTDNTVRSFASSAAAFGAATAMVKMGNISPLTGTQGGIRLICS 334

Query: 2170 RIN 2178
+N
Sbjct: 335 AVN 337

Score = 96.7 bits (239), Expect = 2e-17
Identities = 69/169 (40%), Positives = 86/169 (50%), Gaps = 1/169 (0%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAIAR 1333
QGCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AAR
Sbjct: 93 QGCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAAR 146

Query: 1334 DSVQIVSGQTNTKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W+V LGR
Sbjct: 147 DSV-----VALGGPSWSVPLGR 163

Query: 1514 RDARTASQSAANNGIPAP-TSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RD+ A+ +A AP T +L QLIS +++ GLS DLVALSG I
Sbjct: 164 RDSTGAATAAQVISSLAPSTDLSLAQLISAYASKGLSATDLVALSGAHTI 212

Score = 69.3 bits (168), Expect = 3e-09
Identities = 45/93 (48%), Positives = 55/93 (59%), Gaps = 1/93 (1%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL
Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPTFYDTSCPRAMSIKSTVTAAVNNEPRMGASL 58

Query: 751 LRLFFHDCFVNV-IYLHLLPLTYKYAKLTYSSS 846

LRL FHDCFV +L P+ + Y L SS
Sbjct: 59 LRLHFHDCFVQARFHLTNHPVFFFYFDLMPKSS 91

>ref|NP_001046402.1| Os02g0240500 [Oryza sativa (japonica cultivar-group)]
dbj|BAD28874.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69270.1| TPA: class III peroxidase 28 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF08316.1| Os02g0240500 [Oryza sativa Japonica Group]
Length = 334

Score = 159 bits (402), Expect = 3e-36
Identities = 74/123 (60%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 210 AQCQFFRGHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 269

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 270 RRGLLHSDQELFNGGSQDERVKKYSTDPDFLAFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 329

Query: 2170 RIN 2178
+N
Sbjct: 330 VVN 332

Score = 134 bits (336), Expect = 1e-28
Identities = 76/173 (43%), Positives = 96/173 (55%), Gaps = 2/173 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSS--FTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD S F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+
Sbjct: 80 VQGCDASILLDDVPSKGFVGEKTAGPNTNSIRGYEVIDKIKANVEAACPGVVSCADILAL 139

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AAR+ V + LGGP+W V
Sbjct: 140 AAREGVNL-----LGGPSWEVP 156

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHISH 1663
LGRRD+ TAS+S A++ +P P+S+L L++ F GL+ +D+ ALSG I +
Sbjct: 157 LGRRDSTTASKSEADSLPGPSSSLADLVAAFGKKGLAPRDMTALSGAHTIGY 209

Score = 60.5 bits (145), Expect = 2e-06

Identities = 34/76 (44%), Positives = 47/76 (61%), Gaps = 7/76 (9%)
Frame = +1

Query: 574 ASFCSRLTICLALFVLIWGSANA-----QLSTNFYHSCPNLFSSVKSTVQSAISKET 732
+S +R + LAL + + SA A ++ ++Y SCP L + V+ T+ SAI E
Sbjct: 5 SSTTTRFCLLLALVLPMISSAAAGDDALPLPMTPSYYRKSCPTLEAIVRGTMLSAIAER 64

Query: 733 RMGASLLRLFFHDCFV 780
RMGAS+LRLFFHDCFV
Sbjct: 65 RMGASILRLFFHDCFV 80

>ref|NP_001060630.1| Os07g0677400 [Oryza sativa (japonica cultivar-group)]
gb|AAC49820.1| peroxidase [Oryza sativa Indica Group]
dbj|BAC79530.1| peroxidase [Oryza sativa Japonica Group]
dbj|BAD30310.1| peroxidase [Oryza sativa Japonica Group]
tpe|CAH69355.1| TPA: class III peroxidase 113 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF22544.1| Os07g0677400 [Oryza sativa Japonica Group]
Length = 314

Score = 159 bits (402), Expect = 3e-36
Identities = 72/123 (58%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC FR R+YNETNI+ AFA + +CP T GSGD NLAPLD TPT+FDN Y++NL+
Sbjct: 191 ARCRGFRTRYNETNIDAAFAAALKANCPATPGSGDGNLAPLDTTPTAFDNAYYRNLLS 250

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KGLLHSDQ+LF+ GSTD+ VR ++++ F + FA AM+KMG+ISPLTG+ G+IR C
Sbjct: 251 NKGLLHSDQELFNSGSTDNTVRSFASAAAFGAATAMVKMGNISPLTGTQGGIRLICS 310

Query: 2170 RIN 2178
+N
Sbjct: 311 AVN 313

Score = 97.1 bits (240), Expect = 2e-17
Identities = 69/170 (40%), Positives = 87/170 (51%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAIAA 1330
+QGCD SILL E+NA PN S RG++VID+IK+ +E VC VSCADIL +AA
Sbjct: 68 VQGCDASILLAGN-----ERNAAPNF-SVRGYDVIDSIKTQIEAVCKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W+V LG

Sbjct: 122 RDSV-----VALGGPSWSVPLG 138

Query: 1511 RRDARTASQAANNIGIPAP-TSNLNQLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ A+ +A AP T +L QLIS +++ GLS DLVALSG I

Sbjct: 139 RRDSTGAATAAQVISSLAPSTD SLAQLISAYASKGLSATDLVALSGAHTI 188

Score = 67.8 bits (164), Expect = 1e-08
Identities = 39/70 (55%), Positives = 46/70 (65%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS S L + L L L+ +A A LS FY SCP S +KSTV +A++ E RMGASL
Sbjct: 1 MAS-ASSLGLLLMLAALV-STATAHLSPFYDTSCPRAMSIKSTVTA AVNNEPRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAA59487.1| peroxidase [Triticum aestivum]
gb|ACF08093.1| class III peroxidase [Triticum aestivum]
Length = 319

Score = 159 bits (401), Expect = 3e-36
Identities = 72/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI+TAF A + + +CPR +GSGD++LAPLD TP +FDN Y++NL+
Sbjct: 196 QAQCQNFDRRLYNETNIDTAFATSLRANCPRPTGSGDSSLAPLDTTTPNAFDNAYYRNLM 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DF AAM+ MG+ISPLTG+ G++R +C
Sbjct: 256 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFN RDFRAAMVSMGNISPLTGTGQGVRLSC 315

Query: 2167 RRIN 2178
R+N
Sbjct: 316 SRVN 319

Score = 131 bits (329), Expect = 7e-28
Identities = 76/169 (44%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD SILL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA

Sbjct: 69 VQGCASILLSDTATFTGEQAGPNAGSIRGMNVIDNIKAQVEAVCTQTVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 129 RDSV-----VALGGPSWTVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P P+ ++ L + F+A GLS D+VALSG I

Sbjct: 146 RRDSTTASLSLANSDLPPPSFDVANLTANFAAKGLSVTDMVALSGAHTI 194

Score = 60.5 bits (145), Expect = 2e-06
Identities = 35/73 (47%), Positives = 44/73 (60%), Gaps = 1/73 (1%)
Frame = +1

Query: 565 LTMASFCs-RLTICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMG 741
+ MAS S L +CLA ++AQLS FY SCP + ++ V +A+ E RMG

Sbjct: 3 MAMASSLSVLLLLCLA-----APSSAQLSPRFYARSCPRAQAIIRRGVAAAVRSERRMG 56

Query: 742 ASLLRLFFHDCFV 780
ASLLRL FHDCFV

Sbjct: 57 ASLLRLHFHDCFV 69

>gb|AAB02554.1| cationic peroxidase [Stylosanthes humilis]
Length = 320

Score = 159 bits (401), Expect = 3e-36
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYNE+NI+ ++A++ Q +CP S GD+NL+P D+ TP FDN Y+ NL

Sbjct: 198 QARCTTFRTRIYNESNIDPSYAKSLQGNCP--SVGGDSNLSPFDVTPNKFNDAYYINLK 255

Query: 1987 QKKGLLHSDQQLFNGG-STDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
KKGLLH+DQQLFNGG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR N

Sbjct: 256 NKKGLLHADQQLFNGGGSTDSQVTAYSNNAAATFNTDFGNAMIKMGNLSPLTGTSGQIRTN 315

Query: 2164 CRRIN 2178
CR+ N

Sbjct: 316 CRKTN 320

Score = 152 bits (384), Expect = 3e-34
Identities = 85/169 (50%), Positives = 103/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+QGCD S+LLDDTS+FTGEK A PN NSARGF+VID IKS VE +CPGVVSCADILA+AA
Sbjct: 71 VQGCDASVLLDDTSTFTGEKTAFPNVNSARGFDVIDTIKSQVESLCPGVVSCADILALAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+WNV+LG
Sbjct: 131 RDSV-----VALGGPSWNVQLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS ++AN+ +P P+ NL+ LIS FS G + K+LV LSG I
Sbjct: 148 RRDSTASLNSANSDLPGPSFNLSGLISAFSKKGFTAKELVTLSGAHTI 196

Score = 75.1 bits (183), Expect = 6e-11
Identities = 35/62 (56%), Positives = 45/62 (72%), Gaps = 1/62 (1%)
Frame = +1

Query: 598 ICLALFVLI-WGSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRLFFHDC 774
+C +F+ + G + QLS+NFY CPN S++KS V SA+SKE R+GASLLRL FHDC
Sbjct: 10 VCFIIFMCLNIGLGGSQLSSNFYATKCPNALSTIKSAVNSAVSKEARLGASLLRLHFHDC 69

Query: 775 FV 780
FV
Sbjct: 70 FV 71

>sp|P16147.2|PERX_LUPPO RecName: Full=Peroxidase
emb|CAA36066.1| peroxidase [Lupinus polyphyllus]
prf||1805332A peroxidase:ISOTYPE=basic isozyme
Length = 158

Score = 159 bits (401), Expect = 3e-36
Identities = 79/124 (63%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+ C F+ RIYN+TNI+T FA +RQ +CP ++G G+ NLAPLD TP FDN Y+K+LV
Sbjct: 36 QSECQFFKTRIYNDTNIDTNFATSRQANCPFSAG-GETNLAPLDSLTPNRFDNYYKDLV 94

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+GLLHSDQ LFNGGS D++VR YSTN F SDFAAA++KM ISPLTG GEIRKNC
Sbjct: 95 SNRGLLHSDQVLFNGGSQDTLVRTYSTNNVKKFSDFAAAIVKMSKISPLTG IAGEIRKNC 154

Query: 2167 RRIN 2178
R IN
Sbjct: 155 RVIN 158

>dbj|BAA77389.1| peroxidase 3 [Scutellaria baicalensis]
Length = 318

Score = 159 bits (401), Expect = 3e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIYN+TNI AFA + +CPR+ G DNNLAPLD +P F+N Y++NL+
Sbjct: 197 QARCTTFRGRIYNDTNINGAFATGLRANCPRSGG--DNNLAPLDNVSPARFNNDYYRNLI 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSNGEIRKNC 2166
+GLLHSDQ+LFN G+ D+ VR YSTN F +DFA AM+KM ++SPLTG+NG+IR+NC
Sbjct: 255 GLRGLLHSDQQLFNNGTADAQVRAYSTNSAAFFNDFANAMVKMSNLSPLTGTTNGQIRRNC 314

Query: 2167 RRIN 2178
RR N
Sbjct: 315 RRTN 318

Score = 135 bits (341), Expect = 3e-29
Identities = 76/169 (44%), Positives = 94/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD S+LLDD + FTGEK A PN NS RGF+VIDNIK+ VE CP +VSC+DIL++AA
Sbjct: 70 VNGCDASVLLDDRTGFTGEKTAGPNANSLRGFDVIDNIKTLVEGSCPNIVSCSDILSVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V V GGP+W V LG
Sbjct: 130 RDGVVAV-----GGPSWAVALG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS +AAN IP P NLN LI+ FS G + +++VALSG+ I
Sbjct: 147 RRDSTTASLNAANTQIPGPGLNLNALITSFSNKGFTAREMVALSGSHTI 195

Score = 87.4 bits (215), Expect = 1e-14
Identities = 42/71 (59%), Positives = 53/71 (74%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MASF S + L L +L+ G +NAQLS NFY +CPNL + +++ V SA+S +TRMGASL
Sbjct: 1 MASFVSEFSTRMLVL LLLIGVSNAQLSANFYNTTCPNLLTIIRNAVNSAVSSDTRMGASL 60

Query: 751 LRLFFHDCFVN 783

LRL FHDCFVN
Sbjct: 61 LRLHFHDCFVN 71

>ref|XP_002461207.1| hypothetical protein SORBIDRAFT_02g042840 [Sorghum bicolor]
gb|EER97728.1| hypothetical protein SORBIDRAFT_02g042840 [Sorghum bicolor]
Length = 318

Score = 158 bits (400), Expect = 4e-36
Identities = 73/124 (58%), Positives = 93/124 (75%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++C NFRA IYN+TN+ AFA R+ SCP +G GD NL PLD T T+FDN Y+ NL+
Sbjct: 195 SQCKNFRAHIYNDTNVNVAFATLRKVSPPAAAGDGDGNTPLDTATSTAFDNAYYTNLLS 254

Query: 1990 KKGLLHSDQQLFN-GGSTDSIVRGYSTNPGETSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ GLLHSDQQLFN GG+TD +VR Y++ P F+ DF AAMI+MG+ISPLTG G+IR+ C
Sbjct: 255 RSGLLHSDQQLFNNGGATDGLVRYASTPTRFNRDFTAAIRMGNISPLTGRQGIIRAC 314

Query: 2167 RRIN 2178
R+N
Sbjct: 315 SRVN 318

Score = 138 bits (347), Expect = 6e-30
Identities = 79/169 (46%), Positives = 98/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DT++FTGE+ ANPN S RGF V+DNIK+ VE VCPGVVSCADILA+AA
Sbjct: 67 VQGCDASVLLNDTATFTGEQTANPNVGSIRGFGVVDNIKAQVEAVCPGVVSCADILAVAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 127 RDSV-----VALGGPSWRVLLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +PAP+ +L L + F+ LS DLVALSG I
Sbjct: 144 RRDSTTASLALANSDDLPAISLDLANLTAAFAKKRLSRTDLVALSGAHTI 192

Score = 67.0 bits (162), Expect = 2e-08
Identities = 30/49 (61%), Positives = 38/49 (77%)
Frame = +1

Query: 634 ANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

A+AQLS FY SCP +++KS V +A+++E RMGASLLRL FHDCFV
Sbjct: 19 ASAQLSATFYSRSCPRALATIKSAVTAAVAQEPRMGASLLRLHFHDCFV 67

>gb|EEC82684.1| hypothetical protein OsI_27330 [Oryza sativa Indica Group]
Length = 309

Score = 158 bits (400), Expect = 4e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 187 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 244

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 245 SNKGLLHSDQVLFNNGGSTDNTVRNFASNAAFSSAFATAMVNMGNIAPKTGTNGQIRLSC 304

Query: 2167 RRIN 2178
++N
Sbjct: 305 SKVN 308

Score = 102 bits (254), Expect = 4e-19
Identities = 64/167 (38%), Positives = 85/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AARD
Sbjct: 67 GCDASVLLSGN-----EQDAPPNKDSL RGYGVDSIKAQIETVCNQTVSCADILTVAARD 121

Query: 1337 SVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V LGRR
Sbjct: 122 SV-----VALGGPTWTVPLGRR 138

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 DSTGASAALAI SDLPFTASLQELVDAFAKGLSVTDMVALSGAHTI 185

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/61 (54%), Positives = 43/61 (70%), Gaps = 2/61 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC

Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTAAVNSEPRMGASLLRLHFHDC 65

Query: 775 F 777

F

Sbjct: 66 F 66

>gb|AAW52720.1| peroxidase 6 [Triticum monococcum]

Length = 322

Score = 158 bits (400), Expect = 4e-36

Identities = 73/123 (59%), Positives = 95/123 (77%)

Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

++C NFR IYN TNI+ AFA R+++CP + +GD NLAP D+QT FDN Y++NLV

Sbjct: 199 SQCLNFRDHIYNGTNIDPAFATLRKRTCPAQAPNGDKNLAPFDVQTQLLFDNAYYRNLV 258

Query: 1990 KKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169

K+GLL+SDQ LFNGGS D++VR Y NP F+SDF AMIKMG+I+PLTG+ G+IR+NCR

Sbjct: 259 KRGLLNSDQVLFNNGSQDALVRQYVANPALFASDFVTAMIKMGNINPLTGTAGQIRRNCR 318

Query: 2170 RIN 2178

+N

Sbjct: 319 VVN 321

Score = 131 bits (329), Expect = 7e-28

Identities = 76/169 (44%), Positives = 92/169 (54%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330

+QGCDGSILLDD SF GEK A PN +S RG+EVID IK VE +CPG+VSCADI A+AA

Sbjct: 71 VQGCDGSILLDDVGSFVGKTAFPNVDSVRGYEVIDEIKKNVELLCPGIVSCADIAALAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD + LGGP+W+V LG

Sbjct: 131 RDGTFL-----LGGPSWSVPLG 147

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS + AN+ +PAP+ +L LI F LS +DL ALSG I

Sbjct: 148 RRDSTTASLTEANS DLPAPSLSLGLLIKAFDKKQLSPQDLTALSGAHTI 196

Score = 64.3 bits (155), Expect = 1e-07

Identities = 33/60 (55%), Positives = 39/60 (65%)

Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNI FSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
CL L+ SA QLS +FY SCP L V++T+ A+ E RMGASLLRL FHD CFV
Sbjct: 12 CLLALFLLSSSAYGQLSPSFYAKSCPTLQLIVRATMIKALLAERRMGASLLRLHFHDCFV 71

>gb|AAQ55292.1| class III peroxidase GvPx2b [Vitis vinifera]
Length = 255

Score = 158 bits (400), Expect = 4e-36
Identities = 76/124 (61%), Positives = 100/124 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR IYN+T+I+ AFA ++Q+ CPR+ G D+NL+PLD T T FDN YF+ L
Sbjct: 135 KARCTSRNHIYNDTIDPAFAASKQKICPRSGG--DDNLSPLD-GTTTVFDNVYFRGLE 191

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQ L+NGGSTDS+V+ YS + TF +D A AM++MGDISPLTG+NG+IR NC
Sbjct: 192 EKKGLLHSDQVLYNGGSTDSL VKTYSIDTATFFTDVANAMVRMGDISPLTG TNGQIRTNC 251

Query: 2167 RRIN 2178
R++N
Sbjct: 252 RKNV 255

Score = 147 bits (372), Expect = 8e-33
Identities = 83/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLD T++FTGEK A PN NS RG+EVID IKS V +CPGVVSCADI+A+AARD
Sbjct: 10 GCDASILLDGTATFTGEKTAGPNNSVRGYEVIDTIKSQVGS LCPGVVSCADIVAVAARD 69

Query: 1337 SVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNV KLGR R 1516
SV I+ GGPTW V+LGRR
Sbjct: 70 SVVIL-----GGPTWTVRLGR R 86

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS SAA +P P +L+QLIS FS GL+TK++V LSGT I
Sbjct: 87 DSTTASFS AAGTDLPGPNLSLSQLISAFSKKGLTTKEMVVLSGTHTI 133

>gb|AAF65464.2|AF247700_1 peroxidase POC1 [Oryza sativa Indica Group]
Length = 311

Score = 158 bits (400), Expect = 4e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+

Sbjct: 189 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR ++N FSS FA AM+ MG+I+P TG+NG+IR +C

Sbjct: 247 SNKGLLHSDQVLFNNGSTDNTVRNFASNAAFSSAFATAMVNMGNIAPKTGTNGQIRLSC 306

Query: 2167 RRIN 2178

++N

Sbjct: 307 SKVN 310

Score = 104 bits (260), Expect = 7e-20

Identities = 65/169 (38%), Positives = 87/169 (51%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AA

Sbjct: 67 VQGCDASVLLSGN-----EQDAPPNKDSL RGYGVIDS IKAQIEAVCNQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG

Sbjct: 122 RDSV-----VALGGPTWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ AS + A + +P T++L +L+ F+ GLS D+VALSG I

Sbjct: 139 RRDSTGASAAALASDLPPFTASLQELVDAFAKKGLSVTDMVALSGAHTI 187

Score = 68.2 bits (165), Expect = 8e-09

Identities = 34/62 (54%), Positives = 44/62 (70%), Gaps = 2/62 (3%)

Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774

C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC

Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTA AVNSEPRMGASLLRLHFHDC 65

Query: 775 FV 780

FV

Sbjct: 66 FV 67

>ref|XP_002311022.1| predicted protein [Populus trichocarpa]

gb|EEE88389.1| predicted protein [Populus trichocarpa]

Length = 319

Score = 158 bits (399), Expect = 6e-36
Identities = 79/124 (63%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + + LAPLDL TP SFDN YFKNL+
Sbjct: 197 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSN--STLAPLDLVTPNSFDNYYFKNLM 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 255 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPAPFKSDFGSAMIKMGDIGLLTGSAGQIRRIC 314

Query: 2167 RRIN 2178
+N
Sbjct: 315 SAVN 318

Score = 126 bits (316), Expect = 2e-26
Identities = 74/166 (44%), Positives = 94/166 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLD+T S EK A N NSARG+ VID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 70 VQGCASILLDETLSIQSEKTALGNLNSARGYNVIDKAKTEVEKICPGVVSCADIIAVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP++ VKLG
Sbjct: 130 RDA-----SAYVGGPSYAVKLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGT 1648
RRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 147 RRDSTTASRTLANAELPAFFESLES LISRFBQKKGLTARDMVALSGS 192

Score = 62.4 bits (150), Expect = 4e-07
Identities = 28/57 (49%), Positives = 40/57 (70%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR LFFHDCFV 780
+ L+ + AQLS FY SCPN S++++ ++SAI+ + RM ASL+RL FHDCFV
Sbjct: 14 MLFLLNTACQAQLSPAFYDSSCPNAISAIRTAIRSAIASDRRMAASLIRLHFHDCFV 70

>gb|EEE67819.1| hypothetical protein OsJ_25574 [Oryza sativa Japonica Group]
Length = 309

Score = 158 bits (399), Expect = 6e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 187 QACSTFRGRIYNETNIDSAFATQRQANCPTSG--DMNLAPLDTTANAFDNAYYTNNL 244

Query: 1987 QKKGLLHSDQQLFNNGSTDSIVRGYSTNPGTFSSDFAAAMIKMGISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 245 SNKGLLHSDQVLFNNGSTDNTVRNFASNAEFSSAFATAMVNMGNIAPKTGTNGQIRLSC 304

Query: 2167 RRIN 2178
++N
Sbjct: 305 SKVN 308

Score = 102 bits (254), Expect = 4e-19
Identities = 64/167 (38%), Positives = 85/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AARD
Sbjct: 67 GCDASVLLSGN-----EQDAPPNKDSLRYGVIDSIIKAQIEAVCNQTVSCADILTVAARD 121

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V LGRR
Sbjct: 122 SV-----VALGGPTWTVPLGR 138

Query: 1517 DARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
D+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 DSTGASAAALASDLPPFTASLQELVDAFAKGLSVTDMVALSGAHTI 185

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/61 (54%), Positives = 43/61 (70%), Gaps = 2/61 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC
Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTA AVNSEPRMGASLLRLHFHDC 65

Query: 775 F 777
F
Sbjct: 66 F 66

>ref|NP_001147216.1| LOC100280824 [Zea mays]
gb|ACG26145.1| peroxidase 52 precursor [Zea mays]
Length = 318

Score = 158 bits (399), Expect = 6e-36
Identities = 72/124 (58%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT FR RIY +T+I +FA RQQ+CPR+ G G NLAP+D+QTP FD YF NL+
Sbjct: 196 QARCTTFRGRIYGD TDINASFAALRQQTCPRSGGDG--NLAPIDVQTPVRFD TAYFTNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++VR YS + F++DF AAMI+MG++ LTG+ G+IR+NC
Sbjct: 254 SRRGLFHSQQLFNGGSQDALVRQYSASASLFNADFVAAMIRMGNVGVLGTAGQIRRNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 134 bits (338), Expect = 7e-29
Identities = 83/169 (49%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGSILLD GEK A PN NS RGFEVID IK VE CPGVVSCADILA+AA
Sbjct: 73 VQGCDGSILLDAG----GEKTAGPNLSVRGFEVIDTIKRNVEAACPGVVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD TNL LGGPTW+V LG
Sbjct: 129 RDG-----TNL-----LGGPTWSVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S AN+ +P PT++L LIS F GLS +D+ ALSG I
Sbjct: 146 RRDSTTASASLANSLPPPTASLGTLLSLFGRQGLSPRDMTALSGAHTI 194

Score = 73.2 bits (178), Expect = 2e-10
Identities = 40/75 (53%), Positives = 49/75 (65%)
Frame = +1

Query: 556 LSKLTMASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETR 735
+ +L MAS L CL + L+ A+AQLS FY SCPNL S V++ + A+ E R
Sbjct: 1 MQLLAMAS--PTLMQCLVVVSLSCVAHAQLSPTFYASSCPNLQSIVRAAMTQAVGSEQR 58

Query: 736 MGASLLRLFFHDCFV 780
MGASLLRLFFHDCFV
Sbjct: 59 MGASLLRLFFHDCFV 73

>ref|NP_001060631.1| Os07g0677500 [Oryza sativa (japonica cultivar-group)]
dbj|BAC79531.1| peroxidase POC1 [Oryza sativa Japonica Group]
dbj|BAD30311.1| peroxidase POC1 [Oryza sativa Japonica Group]
tpe|CAH69356.1| TPA: class III peroxidase 114 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF22545.1| Os07g0677500 [Oryza sativa Japonica Group]
Length = 311

Score = 158 bits (399), Expect = 6e-36
Identities = 75/124 (60%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI++AFA RQ +CPRTSG D NLAPLD T +FDN Y+ NL+
Sbjct: 189 QAQCSTFRGRIYNETNIDSAFATQRQANCPRTSG--DMNLAPLDTTANAFDNAYYTNNL 246

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFN GSTD+ VR +++N FSS FA AM+ MG+I+P TG+NG+IR +C
Sbjct: 247 SNKGLLHSDQVLFNNGGSTDNTVRNFASNAEFSSAFATAMVMGNIAPKTGTNGQIRLSC 306

Query: 2167 RRIN 2178
++N
Sbjct: 307 SKVN 310

Score = 104 bits (260), Expect = 7e-20
Identities = 65/169 (38%), Positives = 87/169 (51%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E++A PN++S RG+ VID+IK+ +E VC VSCADIL +AA
Sbjct: 67 VQGCDASVLLSGN-----EQDAPPNKDSLRYGVVIDSIKAQIEAVCNQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 122 RDSV-----VALGGPTWTVPPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ AS + A + +P T++L +L+ F+ GLS D+VALSG I
Sbjct: 139 RRDSTGASAAALISDLPPFTASLQELVDAFAKKGLSVTDMVALSGAHTI 187

Score = 68.2 bits (165), Expect = 8e-09
Identities = 34/62 (54%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L V++ +A+AQLS FY SCP S +KS V +A++ E RMGASLLRL FHDC
Sbjct: 6 CISLLVVVALATAASAQLSATFYDTSCPRAMSIKSAVTA AVNSEPRMGASLLRLHFHDC 65

Query: 775 FV 780
FV
Sbjct: 66 FV 67

>pdb|1SCH|A Chain A, Peanut Peroxidase
pdb|1SCH|B Chain B, Peanut Peroxidase
Length = 294

Score = 158 bits (399), Expect = 6e-36
Identities = 76/124 (61%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CT FR RIYNE+NI+ +A++ Q +CP S GD NL+P D+ TP FDN Y+ NL
Sbjct: 173 QAQCTAFRTRIYNESNIDPTYAKSLQANCP--SVGGDTNLSPFDVTPNKF DNAYYINLR 230

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR NC
Sbjct: 231 NKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNC 290

Query: 2167 RRIN 2178
R+ N
Sbjct: 291 RKTN 294

Score = 152 bits (385), Expect = 2e-34
Identities = 87/169 (51%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+QGCD S+LLDDTS+FTGEK A PN NS RGFEVID IKS VE +CPGVVSCADILA+AA
Sbjct: 46 VQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAA 105

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGG +WNV LG
Sbjct: 106 RDSV-----VALGGASWNVLLG 122

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S+AN+ +PAP NL+ LIS FS G +TK+LV LSG I

Sbjct: 123 RRDSTTASLSSANSDLPAFFNLISAFSNKGFTTKELVTLGAHTI 171

Score = 68.9 bits (167), Expect = 4e-09
Identities = 31/45 (68%), Positives = 36/45 (80%)
Frame = +1

Query: 646 LSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
LS+NFY CPN S++KS V SA++KE RMGASLLRL FHDCFV
Sbjct: 2 LSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFV 46

>sp|P22195.2|PER1_ARAHY RecName: Full=Cationic peroxidase 1; AltName: Full=PNPC1; Flags:
Precursor
gb|AAB06183.1| cationic peroxidase [Arachis hypogaea]
Length = 316

Score = 158 bits (399), Expect = 6e-36
Identities = 76/124 (61%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CT FR RIYNE+NI+ +A++ Q +CP S GD NL+P D+ TP FDN Y+ NL
Sbjct: 195 QAQCTAFRTRIYNESNIDPTYAKSLQANCP--SVGGDTNLSPFDVTPNKFBNAYYINLR 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQLFNG STDS V YS N TF++DF AMIKMG++SPLTG++G+IR NC
Sbjct: 253 NKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNC 312

Query: 2167 RRIN 2178
R+ N
Sbjct: 313 RKTN 316

Score = 152 bits (385), Expect = 2e-34
Identities = 87/169 (51%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSTFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LLDDTS+FTGEK A PN NS RGFEVID IKS VE +CPGVVSCADILA+AA
Sbjct: 68 VQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAA 127

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGG +WNV LG
Sbjct: 128 RDSV-----VALGGASWNVLLG 144

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S+AN+ +PAP NL+ LIS FS G +TK+LV LSG I
Sbjct: 145 RRDSTTASLSSANSDDLPAFFNL SGLISAFSNKGFTTKELVTL SGAHTI 193

Score = 77.0 bits (188), Expect = 2e-11
Identities = 35/57 (61%), Positives = 44/57 (77%)
Frame = +1

Query: 610 LFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+F+ + G +AQLS+NFY CPN S++KS V SA++KE RMGASLLRL FHD CFV
Sbjct: 12 IFMCLIGLGS AQLSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFV 68

>gb|ACU22965.1| unknown [Glycine max]
Length = 322

Score = 157 bits (398), Expect = 7e-36
Identities = 78/124 (62%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+ FR RIYNETNI+++FA + Q +CP S GD+NLAPLD T FDN YFK+L
Sbjct: 202 QAKCSTFRTRIYNETNIDSSFATSLQANCP--SVGGDSNLAPLDSNQNT-FDNAYFKDLQ 258

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLH+DQ LFNGGSTDS V GY+++P +F++DFA AM+KMG+ISPLTGS+GEIR NC
Sbjct: 259 SQKGLLHTDQVLFNGGSTDSQVNGYASDPSSFNTDFANAMVKMGNISPLTGSSGEIRTNC 318

Query: 2167 RRIN 2178
+ N
Sbjct: 319 WKTN 322

Score = 134 bits (338), Expect = 7e-29
Identities = 78/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL+DTSSFTGE+ A N NS RGF VIDNIKS VE +CPGVVSCADIL +AA
Sbjct: 75 VQGCDASVLLNDTSSFTGEQTAAGNVNSIRFGVIDNIKSQVESLCPGVVSCADILTVAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 135 RDSV-----VALGGPSWTVQLG 151

Query: 1511 RRDARTASQSAANN GIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S+AN+ +P +L QL F GL+T ++VALSG

Sbjct: 152 RRDSTTASLSSANSDLPRFDLSLQQLSDNFQNKGLTTAEMVALSG 196

Score = 76.6 bits (187), Expect = 2e-11
Identities = 40/75 (53%), Positives = 51/75 (68%), Gaps = 5/75 (6%)
Frame = +1

Query: 571 MASFCSRLT-----ICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETR 735
MAS C +T I LF+ G +++QLS++FY +CPN S++KS V SA+S E R
Sbjct: 1 MASSCFSMITPIFKIRFFLFLCFIGISSQLSSDFYSTTCPNALSTIKSAVDSAVSNEAR 60

Query: 736 MGASLLRLFFHDCFV 780
MGASLLRL FHDCFV
Sbjct: 61 MGASLLRLHFHDCFV 75

>ref|XP_002311955.1| predicted protein [Populus trichocarpa]
gb|EEE89322.1| predicted protein [Populus trichocarpa]
Length = 187

Score = 157 bits (398), Expect = 7e-36
Identities = 79/124 (63%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + + LAPLDL TP SFDN YFKNL+
Sbjct: 65 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSN--STLAPLDLVT PNSFDNYYFKNLM 122

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 123 QNKGLLQSDQVLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSAGQIRRIC 182

Query: 2167 RRIN 2178
+N
Sbjct: 183 SAVN 186

Score = 63.2 bits (152), Expect = 2e-07
Identities = 31/57 (54%), Positives = 43/57 (75%)
Frame = +2

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGT 1648
+GGP++ VKLGRRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 4 VGGPSYAVKLGRRDSTASRTLANAELPAFFESLESISRFAQKKGLTARDMVALSGS 60

>gb|AAM61588.1| peroxidase [Arabidopsis thaliana]

Length = 316

Score = 157 bits (398), Expect = 7e-36
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYN +NI+T+FA +++++CP TSGSGDN A LD+++P FD+ ++K L+
Sbjct: 193 RAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYKQLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLL SDQ LFN G TDS+V YS N F DFA AMIKMGDISPLTGSNG+IR+NC
Sbjct: 253 SKKGLLSDQQLFNGGPTDSLVIAYSHNLNAFYRDFARAMIKMGDISPLTGSNGQIRQNC 312

Query: 2167 RRIN 2178
RR N
Sbjct: 313 RRPN 316

Score = 150 bits (378), Expect = 2e-33
Identities = 85/170 (50%), Positives = 103/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGS+LLDDT SF GEK + P+ NS RGFEVID IK VEK+CPG+VSCADILAI A
Sbjct: 65 VNGCDGSLLDDTSPFLGEKTSGPSNNSVRGFEVIDKIKFKVEKMCPGIVSCADILAITA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 125 RDSVLL-----LGGPGWSVKLG 141

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ +AAN+G IP P + L+ LI+RF A GLST+D+VALSG+ I
Sbjct: 142 RRDSTTANFAAANSVIPPPIITTLNLINRFKAQGLSTRDMVALSGSHTI 191

Score = 72.8 bits (177), Expect = 3e-10
Identities = 32/62 (51%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777
+ L + +++ + AQL+ +FY SCP+LF V+ V+ A+++E RMGASLLRLLFFHDCF
Sbjct: 5 VLLMMIMMLASQSEAQLNRDFYKESCPSLFLVVRVVKRAVAREPRMGASLLRLLFFHDCF 64

Query: 778 VN 783
VN
Sbjct: 65 VN 66

>ref|NP_200647.1| peroxidase, putative [Arabidopsis thaliana]
sp|Q9LVL2.1|PER67_ARATH RecName: Full=Peroxidase 67; Short=Atperox P67; AltName: Full=ATP44;
Flags: Precursor
dbj|BAA96930.1| peroxidase [Arabidopsis thaliana]
Length = 316

Score = 157 bits (398), Expect = 7e-36
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQSCPRSTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYN +NI+T+FA +++++CP TSGSGDN A LD+++P FD+ ++K L+
Sbjct: 193 RAQCVTFRNRIYNASNIDTSFAISKRRNCPATSGSGDNKKANLDVRSPDRFDHGFYKQLL 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGETFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLL SDQ LFN G TDS+V YS N F DFA AMIKMGDISPLTGSNG+IR+NC
Sbjct: 253 SKKGLLTSQVLFNNGPTDSLVIAYSHNLNAFYRDFARAMIKMGDISPLTGSNGQIRQNC 312

Query: 2167 RRIN 2178
RR N
Sbjct: 313 RRPN 316

Score = 149 bits (377), Expect = 2e-33
Identities = 85/170 (50%), Positives = 102/170 (60%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAIAA 1330
+ GCDGS+LLDDT SF GEK + P+ NS RGFEVID IK VEK+CPG+VSCADILAI A
Sbjct: 65 VNGCDGSLLDDTSPFLGEKTSGPSNNSVRGFEVIDKIKFKVEKMCPGIVSCADILAITA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W+VKLG
Sbjct: 125 RDSVLL-----LGGPGWSVKLG 141

Query: 1511 RRDARTASQSAANNG-IPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ +AAN+G IP P + L+ LI+RF A GLST+D+VALSG I
Sbjct: 142 RRDSTTANFAAANSVIPPPIITLSNLINRFKAQGLSTRDMVALSGAHTI 191

Score = 72.8 bits (177), Expect = 3e-10
Identities = 32/62 (51%), Positives = 46/62 (74%)
Frame = +1

Query: 598 ICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDCF 777

+ L + +++ + AQL+ +FY SCP+LF V+ V+ A+++E RMGASLLRLFFHDCF
Sbjct: 5 VLLMMIMMLASQSEAQLNRDFYKESCPSLFLVVRVVKRAVAREPRMGASLLRLFFHDCF 64

Query: 778 VN 783

VN

Sbjct: 65 VN 66

>ref|XP_002460939.1| hypothetical protein SORBIDRAFT_02g037840 [Sorghum bicolor]
gb|EER97460.1| hypothetical protein SORBIDRAFT_02g037840 [Sorghum bicolor]
Length = 325

Score = 157 bits (397), Expect = 1e-35
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C N++ARIYN+ NI AFA + + CP G G N APLD TP +FDN Y+ +LV

Sbjct: 204 QAQCQNYQARIYNDANINAAFAASLRAGCPAGGGGGAN--APLDASTPNAFDNAYYGDLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGST +VR Y+ + FSSDFAAAM+KMG I +TGS+GE+R+NC

Sbjct: 262 AQQGLLHSDQELFNGGSTDGLVRSYAASSARFSSDFAAAMVKMGIGVITGSSGEVRRNC 321

Query: 2167 RRIN 2178

RR+N

Sbjct: 322 RRVN 325

Score = 139 bits (349), Expect = 4e-30
Identities = 76/165 (46%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV VSCADILAI AA 1330
+QGCD S+LLDDT +FTGEK+A PN S RGF VID IK+ +E +CP VSCADILA+AA

Sbjct: 77 VQGCDA SVLLDDTGNFTGEKSAGPNAGSLRGFGVIDTIKALLEALCPRTVSCADILAVAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG

Sbjct: 137 RDSV-----VALGGPSWTVQLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645

RRD+ TAS S AN +P+P S+L+ L++ F+ GLS+ D+VALSG

Sbjct: 154 RRDSTTASLSTANTDLPSPASSLSTLLAAFARKGLSSTDMVALSG 198

Score = 64.7 bits (156), Expect = 8e-08

Identities = 30/65 (46%), Positives = 43/65 (66%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
S+L++ + + +A AQLS FY SCP ++K+ V++A+ + RMGASLLRL F
Sbjct: 13 SKLSVLILALATVVAARAQLSPTFYASSCPAALVTIKTAVRAALVLD RRMGASLLRLHF 72

Query: 766 HDCFV 780
HDCFV
Sbjct: 73 HDCFV 77

>ref|XP_002334018.1| predicted protein [Populus trichocarpa]
gb|EEE77880.1| predicted protein [Populus trichocarpa]
Length = 307

Score = 157 bits (397), Expect = 1e-35
Identities = 79/124 (63%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR RIYN +NI+ FA TR++ CPR + LAPLDL TP SFDN YFKNL+
Sbjct: 186 QAQCFTFRERIYNHSNIDAGFASTRRRRCPRVGSNA--TLAPLDLVTPNSFDNYYFKNLM 243

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
Q KGLL SDQ LFNGGSTDSIV YS NP F SDF +AMIKMGDI LTGS G+IR+ C
Sbjct: 244 QNKGLLQSDQQLFNGGSTDSIVSEYSRNPFRSDFGSAMIKMGDIGLLTGSAGQIRRIC 303

Query: 2167 RRIN 2178
+N
Sbjct: 304 SAVN 307

Score = 127 bits (319), Expect = 1e-26
Identities = 74/166 (44%), Positives = 95/166 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLD+T+S EK A N NSARG+ VID K+ VEK+CPGVVSCADI+A+AA
Sbjct: 59 VQGCDASILLDETTSIQSEKTALGNLNSARGYNVIDKAKTEVEKICPGVVSCADIIAVAA 118

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S +GGP++ VKLG
Sbjct: 119 RDA-----SAYVGGPSYAVKLG 135

Query: 1511 RRDARTASQAANNIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
RRD+ TAS++ AN +PA +L LISRF GL+ +D+VALSG+
Sbjct: 136 RRDSTTASRTLANAELPAFFESLESISRFGKKGLTARDMVALSGS 181

Score = 60.5 bits (145), Expect = 2e-06
Identities = 27/50 (54%), Positives = 36/50 (72%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
+ AQLS FY SCPN S++ + ++SAI+ + RM ASL+RL FHDCFV
Sbjct: 10 ACQAQLSPAIFYDSSCPNALSAGTAIRSAIASDRRMAASLIRLHFHDCFV 59

>gb|EAY85151.1| hypothetical protein OsI_06506 [Oryza sativa Indica Group]
Length = 335

Score = 157 bits (397), Expect = 1e-35
Identities = 73/123 (59%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C FR IYN+TN++ FA R++ CP SGSGD+NLAPLD T +FDN Y+++LV
Sbjct: 211 AQCQFFRGHIYNDTNVDPLFAAERRRRCPAASGSGDSNLAPLDDMTALAFDNAYYRDLVG 270

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ+LFNGGS D V+ YST+P F+ DF AAMIKMG I PLTG+ G+IRKNCR
Sbjct: 271 RRGLLHSDQELFNGGSQDERVKYSTDPDLFAGDFVAAMIKMGKICPLTGAAGQIRKNCR 330

Query: 2170 RIN 2178
++
Sbjct: 331 VVS 333

Score = 138 bits (347), Expect = 6e-30
Identities = 76/171 (44%), Positives = 95/171 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD SILLDD F GEK A PN NS RG+EVID IK+ VE CPGVVSCADILA+AA
Sbjct: 83 VQGCDASILLDDVQGFVGEKTAGPNANSIRGYEVIDKIKANVEAACPGVVSCADILALAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
R+ V + LGGP+W V LG
Sbjct: 143 REGVNL-----LGGPSWEVPLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHISH 1663
RRD+ TAS+S A++ +P P+S+L LI+ F GL+ +D+ ALSG I +
Sbjct: 160 RRDSTTASKSEADSLPGPSSSLADLIAAFGKKGLAPRDMTALSGAHTIGY 210

Score = 58.2 bits (139), Expect = 8e-06
Identities = 26/45 (57%), Positives = 34/45 (75%)
Frame = +1

Query: 646 LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
++ ++Y SCP L + V+ T+ SAI E RMGAS+LRLFFHDCFV
Sbjct: 39 MTPSYRKSCPTLEAIVRGTMVSAIKAERRMGASILRLFFHDCFV 83

>emb|CAH10842.1| peroxidase [Picea abies]
Length = 320

Score = 157 bits (397), Expect = 1e-35
Identities = 77/124 (62%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYNE+NI AFA + + +CP S GDN L+PLD+ T FDN Y+ NL
Sbjct: 199 QSRCAFFRTRIYNESNINAAFATSVKANCP--SAGGDNTLSPLDVVTSIKFDNKYYGNLK 256

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KLLHSDQQLFNGG TDS V YSTN +F +DFAAAM+KM +ISPLTG++G+IRKNC
Sbjct: 257 IQKGLLHSDQQLFNGGPTDSQVTAYSTNQNSFFTDFAAAMVKMSNISPLTGTSGQIRKNC 316

Query: 2167 RRIN 2178
R+ N
Sbjct: 317 RKAN 320

Score = 151 bits (382), Expect = 5e-34
Identities = 88/169 (52%), Positives = 98/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDD ++FTGEK A PN NSARGF+VID IK+ VE C GVVSCADIL IAA
Sbjct: 72 VNGCDGSILLDDNATFTGEKTAGPNANSARGFDVIDTIKTQVEAACSGVVSCADILTIAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GPTW V LG
Sbjct: 132 RDSV-----VELQGPTWTVM LG 148

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS S ANN IP+P S+L+ LIS F GLSTKDLVALSG I
Sbjct: 149 RRDSTASLSDANNIPASSLSALISSFKHGLSTKDLVALSGAHTI 197

Score = 65.5 bits (158), Expect = 5e-08
Identities = 34/70 (48%), Positives = 43/70 (61%), Gaps = 5/70 (7%)
Frame = +1

Query: 589 RLTICLALFVLIWGSAN-----AQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
R +C+ + + S N QLS+ FY SCP S VK V+ A++KE RMGASL+
Sbjct: 4 RTLLCIGVMAVFVCSININAVSGQLSSTFYDKSCPRAQSIVKRNVKQAVAKEKRMGASLV 63

Query: 754 RLFFHDCFVN 783
RL FHDCFVN
Sbjct: 64 RLHFHDCFVN 73

>emb|CBI22007.1| unnamed protein product [Vitis vinifera]
Length = 425

Score = 157 bits (396), Expect = 1e-35
Identities = 75/121 (61%), Positives = 97/121 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C FR+RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFRSRIYNDTNIDPNFAATTRSTCP-VSG-GNSNLAPLDIRTMNRFDNIYYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGNGEIRSNC 313

Query: 2167 R 2169
R
Sbjct: 314 R 314

Score = 151 bits (381), Expect = 7e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAREKVCPCGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 129 RDGV-----VQLGGPSWTVPGL 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I

Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 7e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSIISLLACSLNGQLSPNFYASTCPNVQNIVRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|XP_002283995.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 316

Score = 157 bits (396), Expect = 1e-35
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSFGSDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+
Sbjct: 195 KAQCIKFRYRIYNETNVDAFAKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++SPLTG++GEIR NC
Sbjct: 252 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTTFFTDVANAMVKMGNLSPLTGTGDEIRTNC 311

Query: 2167 RRIN 2178
R+IN
Sbjct: 312 RKIN 315

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 101/167 (60%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V++GRR
Sbjct: 130 SV-----VALGGPTWTVMGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I
Sbjct: 147 DSTTASLSTANADLPAPTSDDLVLTSLSFKGFTTQEMVALSGHTI 193

Score = 74.3 bits (181), Expect = 1e-10
Identities = 38/70 (54%), Positives = 48/70 (68%)
Frame = +1

Query: 571 MASFC SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSFFCMFSFLL--GMAHAQLSPNFYASSCPRALSTIRTAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>emb|CAN81400.1| hypothetical protein [Vitis vinifera]
Length = 317

Score = 157 bits (396), Expect = 1e-35
Identities = 75/124 (60%), Positives = 98/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C F +RIYN+TNI+ FA TR+ +CP SG G++NLAPLD++T FDN Y++NL+
Sbjct: 196 QAQCFTFXSRIYNDTNIDPNFAATTRSTCP-VSG-GNSNLAPLDIRTMRFDNIYYQNLN 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N F DFAAAM+KM +ISPLTG+NGEIR NC
Sbjct: 254 TRRGLLHSDQELFNGGSQDALVRTYNANNALFFRDFAAAMVKMSNISPLTGNGEIRSNC 313

Query: 2167 RRIN 2178
R +N
Sbjct: 314 RVVN 317

Score = 150 bits (380), Expect = 9e-34
Identities = 84/169 (49%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDT IKTRVEAACNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W + LG
Sbjct: 129 RDGV-----VQLGGPSWTIPLG 145

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
RRDARTASQSAANN IP+P ++L+ LIS F+A GL+ +D+ ALSG+ I
Sbjct: 146 RRDARTASQSAANNEIPSPLASLSALISGFAAKGLNARDMTALSGSHTI 194

Score = 71.6 bits (174), Expect = 7e-10
Identities = 35/71 (49%), Positives = 49/71 (69%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MASF + + ++ L+ S N QLS NFY +CPN+ + V+ ++ A+ +E RMGAS+
Sbjct: 1 MASFTNSFVV-FSIISLLACSINGQLSPNFYASTCPNVQNIVRVAMRQAVIREPRMGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>emb|CAN63655.1| hypothetical protein [Vitis vinifera]
Length = 272

Score = 157 bits (396), Expect = 1e-35
Identities = 76/124 (61%), Positives = 99/124 (79%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+
Sbjct: 151 KAQCIKFRYRIYNETNVDAAFASKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 207

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++SPLTG++GEIR NC
Sbjct: 208 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTTFFTDVANAMVKGMLSPLTGTGDEIRTNC 267

Query: 2167 RRIN 2178
R+IN
Sbjct: 268 RKIN 271

Score = 150 bits (379), Expect = 1e-33
Identities = 83/168 (49%), Positives = 102/168 (60%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVS CADILAI AAR 1333

QGCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AAR
 Sbjct: 25 QGCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAAAR 84
 Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
 DSV + LGGPTW V++GR
 Sbjct: 85 DSV-----VALGGPTWTVQMGR 101
 Query: 1514 RDARTASQSAANNIPAPTSNLNLISRFSAALGLSTKDLVALSGTKHI 1657
 RD+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I
 Sbjct: 102 RDSTTASLSTANADLPAPTSDDLVLTSLSNKGFTTQEMVALSGTHTI 149

>gb|AAA20472.1| peroxidase [Cenchrus ciliaris]
 Length = 307

Score = 156 bits (395), Expect = 2e-35
 Identities = 75/125 (60%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
 Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRSTSGSDNNLAPLDLQTPTSFNYYFKNLV 1986
 QARCT FR RIY +TNI+ +FA +QQ+CPR+ G G NLAP+D QTP FDN Y+ NLV
 Sbjct: 188 QARCTTFRGRIYGDNTIDASFAALQQQTCPRSGGDG--NLAPIDAQTPARFDNAYYTNLV 245
 Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAMIKMGDISPLTGSN-GEIRKN 2163
 ++GL HSDQ+LFNGGS D++VR YS++P F+SDF AAMIKMG+I G+N G++R+N
 Sbjct: 246 SRRGLFHSDQELFNGGSQDALVRQYSSSPSQFNSDFVAAMIKMGNI----GANAGQVRRN 301
 Query: 2164 CRRIN 2178
 CR +N
 Sbjct: 302 CRVVN 306

Score = 108 bits (271), Expect = 4e-21
 Identities = 71/168 (42%), Positives = 83/168 (49%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
 +QGCD SIL S GEK+A PN NS RG+EVID IK VE CPGVVSCA I+ +AA
 Sbjct: 68 VQGCDASIL----SRSGGEKSAGPNANSVRGYEVIDTIKKNVEAACPGVVSCATIVPLAA 123
 Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 R ++ G PTWNV LG
 Sbjct: 124 RPGPNLLGG-----PTWNVPLG 140
 Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSAALGLSTKDLVALSGTKH 1654
 RRD+ TA S AN +P PTS L LIS F LS +D++ALSG H
 Sbjct: 141 RRDSTAMLSTANQNLPPPTS-LGTLISLFGG-RLSARDMIALSGAHH 186

Score = 73.6 bits (179), Expect = 2e-10
Identities = 35/60 (58%), Positives = 44/60 (73%)
Frame = +1

Query: 601 CLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLRFFHDCFV 780
CL L+ +A+ AQLST FY SCPNL + V++ + A+S E RMGAS+LRLFFHDCFV
Sbjct: 9 CLLAISLLSFTAHAQLSTTFYASSCPNLQTVVRAAMTQAVSSEPRMGASILRFFHDCFV 68

>gb|ACF08096.1| class III peroxidase [Triticum aestivum]
Length = 313

Score = 156 bits (394), Expect = 2e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL
Sbjct: 188 QAQCQNFRDRLYNETNINSGFATSLKANCPQPTGSGDRNLANLDVSTPYSDNAYYSNLK 247

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R
Sbjct: 248 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKMGNLSPLTGSQGGVRL 307

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 308 SCSKVN 313

Score = 101 bits (252), Expect = 6e-19
Identities = 64/169 (37%), Positives = 83/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGFEVID+IK+ +E +C VSCADIL +AA
Sbjct: 66 VQGCDAVLLSGM-----EQNAFPNVMSLRGFEVIDSIKAKLETMCKQTVSCADILTVAA 120

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 121 RDSV-----VALGGPSWTVPGL 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P P +L L F G + D+VALSG I
Sbjct: 138 RRDSTNANEAVANSDDLPPFFDLVNLQSFQDGKFTVTDMAVALSGAHTI 186

Score = 72.4 bits (176), Expect = 4e-10
Identities = 36/72 (50%), Positives = 50/72 (69%)
Frame = +1

Query: 565 LTMAFCSRLTICLALFVLIWGSANAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGA 744
+ +S + L +CLA+ +A+AQLS FY +CPN +++KS V +A++KE RMGA
Sbjct: 1 MASSSLSAVLLLCLAV-----AASAQLSPTFYDTTCPNALATIKAHTAAVNKENRMGA 54

Query: 745 SLLRLLFFHDCFV 780
SLLRL FHDCFV
Sbjct: 55 SLLRLHFHDCFV 66

>ref|XP_002461211.1| hypothetical protein SORBIDRAFT_02g042870 [Sorghum bicolor]
gb|EER97732.1| hypothetical protein SORBIDRAFT_02g042870 [Sorghum bicolor]
Length = 321

Score = 156 bits (394), Expect = 2e-35
Identities = 74/125 (59%), Positives = 95/125 (76%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPSFNYYFKNL 1983
QA+C FR IYN+TNI +AFA + Q +CPR +GSGD+ LAPLD +PT+FDN YF NL
Sbjct: 196 QAQCRFFRDHIYNDTNINSAFAASLQANCPRPANGSGDSTLAPLDAASPTAFDNAYFSNL 255

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ KGLLHSDQQLFNGGSTDS VR ++++ FS+ FA AM+ MG+I+P TGS G+IR
Sbjct: 256 MSHKGLLHSDQQLFNGGSTDSTVRSFASSASAFSNAFATAMVMGNIAPKTGSQQGQIRVT 315

Query: 2164 CRRIN 2178
C ++N
Sbjct: 316 CSKVN 320

Score = 121 bits (303), Expect = 8e-25
Identities = 71/165 (43%), Positives = 88/165 (53%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+ GCD S+LL DT SFTGE+ A PN+NS RGF VID+IK+ VE VC VSCADILA+AA
Sbjct: 69 VDGCDASVLLADTGSTGEQAIPNKNLSLGRFVIDSIKTQVEAVCNQTVSCADILAVAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V +G
Sbjct: 129 RDSV-----VALGGPSWTVLVG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645

RRD+ TAS+ A +P P+ +L L F+ LS D+VALSG
Sbjct: 146 RRDSTTASKDNAERDLPPPSFDLANLTRSFANKNLSVTDMMVALSG 190

Score = 71.2 bits (173), Expect = 9e-10
Identities = 33/66 (50%), Positives = 47/66 (71%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLFF 765
SRL++ + + + +A AQLS+ FY SCP +++KS V +A++ E RMGASLLRL F
Sbjct: 5 SRLSLLVAILALATAATAQLSSTFYDTSCPKALATIKSAVTAAVNNEARMGASLLRLHF 64

Query: 766 HDCFVN 783
HDCFV+
Sbjct: 65 HDCFVD 70

>sp|Q02200.1|PERX_NICSY RecName: Full=Lignin-forming anionic peroxidase; Flags: Precursor
gb|AAA34050.1| anionic peroxidase [Nicotiana sylvestris]
Length = 322

Score = 156 bits (394), Expect = 2e-35
Identities = 82/125 (65%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIY N T+I+ FA TR++ CP+ +G NLAPLDL TP FDN YFKNL
Sbjct: 200 QAQCFLFRDRIYSNGTDIDAGFASTRRRQCPQEGENG--NLAPLDLVTPNQFDNYYFKNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+QKKGLL SDQ LFNGGSTD+IV YS + FSSDFAAAMIKMGDISPL+G NG IRK
Sbjct: 258 IQKKGLLQSDQVLFNGGSTDNIVSEYSNSARAFSSDFAAAMIKMGDISPLSGQNGIIRKV 317

Query: 2164 CRRIN 2178
C +N
Sbjct: 318 CGSVN 322

Score = 134 bits (337), Expect = 9e-29
Identities = 76/169 (44%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLD+T S EK A PN SARGF +I++ K VEK+CPGVVSCADIL +AA
Sbjct: 73 VQGCDASILLDETSPSIESEKTALPNLGSARGFGIIEDAKREVEKICPGVVSCADILTVA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RD+ S +GGP+W VKLG
Sbjct: 133 RDA-----SAAVGGPSWTVKLG 149

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS++ A +P P LN+LIS F++ GLST+D+VALSG I

Sbjct: 150 RRDSTTASKTLAETDLPGPFDPNRLISSFASKGLSTRDMVALSGAHTI 198

Score = 64.7 bits (156), Expect = 8e-08
Identities = 32/68 (47%), Positives = 47/68 (69%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLR 756

SF ++ I +L +L +AQLS FY ++CPN ++++++V+ AIS E RM ASL+R

Sbjct: 7 SFRAKAAI-FSLLLLSCMQCHAQLSATFYDNTCPNALNTIRTSVRQAISSERRMAASLIR 65

Query: 757 LFFHDCFV 780

L FHDCFV

Sbjct: 66 LHFHDCFV 73

>ref|XP_002437129.1| hypothetical protein SORBIDRAFT_10g021620 [Sorghum bicolor]
gb|EER88496.1| hypothetical protein SORBIDRAFT_10g021620 [Sorghum bicolor]

Length = 313

Score = 155 bits (393), Expect = 3e-35
Identities = 73/124 (58%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

QARCT FR+RIY +TNI +FA RQQ+CP++ G G NLA +D QTPT FD Y+ NL+

Sbjct: 191 QARCTTFRSRIYGDTNINASFAALRQQTCPQSGGDG--NLASIDEQTPTRFDTDYTNLM 248

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

++GL HSDQ+LFNGGS D++VR YS + F+SDF AAMIKMG++ LTG+ G+IR+NC

Sbjct: 249 LQRGLFHSDQELFNGGSQDALVRQYSASSSLFNSDFVAAMIKMGNVGVLGTAGQIRRNC 308

Query: 2167 RRIN 2178

R +N

Sbjct: 309 RVVN 312

Score = 128 bits (322), Expect = 5e-27
Identities = 76/169 (44%), Positives = 90/169 (53%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330

Sbjct: 66 VQGCDAVLLSGM-----EQNAIPNVMSLRGFEVIDSIKAQLETMCKQTVSCADILTVAA 120

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG

Sbjct: 121 RDSV-----VALGGPSWTVPLG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++AANN +P P +L L F G + D+VALSG I

Sbjct: 138 RRDSTNANEEAANLPPPFDFLVNLTQSFGDKGFTVTDMVALSGAHTI 186

Score = 72.4 bits (176), Expect = 4e-10
Identities = 36/72 (50%), Positives = 50/72 (69%)
Frame = +1

Query: 565 LTMASFCRLTICLALFVLIWGSANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGA 744
+ +S + L +CLA+ +A+AQLS FY +CPN +++KS V +A++KE RMGA

Sbjct: 1 MASSSLSAVLLLCLAV-----AASAQLSPTFYDTTCPNALATIKAHTAAVNKENRMGA 54

Query: 745 SLLRLFFHDCFV 780
SLLRL FHDCFV

Sbjct: 55 SLLRLHFHDCFV 66

>gb|ACI03401.1| peroxidase 1 [Litchi chinensis]
Length = 318

Score = 155 bits (392), Expect = 4e-35
Identities = 87/169 (51%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI 1330
+ GCDGS+LLDDTS+F GEK A PN S RGF V+D IK+ +EK CPGVVSCAD+LAI 1330

Sbjct: 69 VNGCDGSLLDDTSTFVGEKTAVPNNISVRGFNVVDQIKAKLEKACPGVVSCADLLAI 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG

Sbjct: 129 RDSV-----VHLGGPSWKVRLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ AN IP PTSNL+ LIS FSA GLS KDLVALSG+ I

Sbjct: 146 RRDSTTASRALANTSIPPPTSNSALISSFSAQGLSLKDLVALSGSHTI 194

Score = 150 bits (379), Expect = 1e-33
Identities = 70/123 (56%), Positives = 91/123 (73%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT+FR +YN+TNI+++FA++ ++ CPR+ DN LA LD QTP FD Y+ NL++
Sbjct: 197 ARCTSFRGHVYNDTNIDSSFAQLRRKCPRSGN--DNVLANLDRQTPFCFDKLYYDNLLK 254

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKGLLHSDQQLF GGS D V+ Y+ N F DFA AM+KMG+I PLTG G+IR NCR
Sbjct: 255 KKGLLHSDQQLFKGGSadPFVKKYANNTSAFFKDFAGAMVKMGNIKPLTGRAGQIRINCR 314

Query: 2170 RIN 2178
++N
Sbjct: 315 KVN 317

Score = 63.9 bits (154), Expect = 1e-07
Identities = 31/50 (62%), Positives = 34/50 (68%)
Frame = +1

Query: 634 ANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGASLLRFFHDCFVN 783
AN QL NFY +CP S V V +AI ETR+GASLLRL FHDCFVN
Sbjct: 21 ANGQLCPNFYESTCPQALSIVHKGVAIAIKNETRIGASLLRLHFHDCFVN 70

>ref|XP_002284007.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 316

Score = 155 bits (392), Expect = 4e-35
Identities = 76/124 (61%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C+ FR RIYNETNI+ FA ++Q CP S GD NL+ LD +T T FDN YF NL+
Sbjct: 195 KAQCSKFRDRIYNETNIDATFATSKQAICP--SSGDENLSDL-ETTTVFDNVYFTNLI 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQLFNG STDS+V YS + TF +D A+AM+KMG++SPLTG++GEIR NC
Sbjct: 252 EKKGLLHSDQQLYNGNSTDSMVETYSNDSTTFFTDVASAMVKMGNLSPLTGTGGEIRTNC 311

Query: 2167 RRIN 2178
R IN
Sbjct: 312 RAIN 315

Score = 151 bits (381), Expect = 7e-34
Identities = 83/167 (49%), Positives = 102/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTANFTGEKTAGPNNNSVRGYDV IDTIKSMESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW V+LGRR
Sbjct: 130 SV-----VALGGPTWTVQLGRR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V LSGT I
Sbjct: 147 DSTTASFSTANS DLPAPTS DLDALISLFSNKGFTTQEMVVLSGHTI 193

Score = 70.9 bits (172), Expect = 1e-09
Identities = 35/70 (50%), Positives = 50/70 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+++Y SCP+ S++++ V +A++ E+RMGASL
Sbjct: 1 MASLSLFSLFCMFSFLL--GMAHAQLSSDYSSSCPSALSTIQTAVNNAVADES RMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>ref|XP_002323054.1| predicted protein [Populus trichocarpa]
gb|EEF04815.1| predicted protein [Populus trichocarpa]
Length = 317

Score = 155 bits (392), Expect = 4e-35
Identities = 74/124 (59%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCT F RI NETNI+++F + Q C T NN PLD+ +PTSFD+ Y++NL+
Sbjct: 199 QARCTTFLTRINNETNIDSSFKTSTQAQCQNT-----NNFVPLDVTSP TSFDSAYYRNLL 253

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQQLF+GGSTD+ VR YS+N F +DFA AMIKMG++SPLTG+NG+IR NC
Sbjct: 254 NQKGLLHSDQQLFSGGSTDAQVRAYSSNQAAFRTDFANAMIKMGNLSPLTG TNGQIRTNC 313

Query: 2167 RRIN 2178
R+ N
Sbjct: 314 RKAN 317

Score = 119 bits (297), Expect = 4e-24
Identities = 73/170 (42%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD S+LLD GEK A N NS RGFEVID+IK+ +E CPGVVSCADIL++AA
Sbjct: 76 VNGCDASVLLDG-----GEKTAPANTNSLRGFEVIDSIKTQLESSCPGVVSCADILSVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V+LG
Sbjct: 131 RDSV-----VALGGPSWQVQLG 147

Query: 1511 RRDARTA-SQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA S S NN +P+P +++ LIS FS G + K++VALSG+ I
Sbjct: 148 RRDSATAGSVSDVNNVPSPALSVSGLISAFSNGFTAKEMVALSGSHTI 197

Score = 79.0 bits (193), Expect = 4e-12
Identities = 37/57 (64%), Positives = 46/57 (80%)
Frame = +1

Query: 613 FVLIWGSANAQLSTNFYYHSCPFLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
F+L+ G A+AQL++NFY SCP++ S +KS V SA+S E RMGASLLRL FHDCFVN
Sbjct: 21 FLLLVGVASQAQLASNFYGTSCPSVLSVIKSAVDSAVSNEARMGASLLRLHFHDCFVN 77

>gb|EEC82681.1| hypothetical protein OsI_27325 [Oryza sativa Indica Group]
Length = 313

Score = 155 bits (392), Expect = 4e-35
Identities = 70/124 (56%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFD Y+ NL+
Sbjct: 190 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTTPYSFDTAYYSNLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR +++N FSS F++AM+KM ++ PL GS G+IR +C
Sbjct: 250 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLIGSQGQIRLSC 309

Query: 2167 RRIN 2178
++N
Sbjct: 310 SKVN 313

Score = 129 bits (325), Expect = 2e-27

Identities = 73/167 (43%), Positives = 91/167 (54%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPCGVVSCADILAI AARD 1336
GCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AARD

Sbjct: 65 GCDASVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAARD 124

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR

Sbjct: 125 SV-----VALGGPSWTVGLGRR 141

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS +ANN +P P +L LI F G S D+VALSG I

Sbjct: 142 DSTTASMDSANNDLPPPFDFLENLIKAFGDKGFSVTDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 5e-08
Identities = 30/61 (49%), Positives = 43/61 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774

++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC

Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTA AVNNEPRMGASLLRLHFHDC 63

Query: 775 F 777

F

Sbjct: 64 F 64

>gb|EAZ01280.1| hypothetical protein OsI_23303 [Oryza sativa Indica Group]
Length = 327

Score = 155 bits (392), Expect = 4e-35
Identities = 73/124 (58%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986

+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV

Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNP GTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC

Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RRIN 2178

R++N

Sbjct: 324 RKNV 327

Score = 135 bits (339), Expect = 5e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTPTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANANLPGPASSGASLVAAFAGKGLSAREMTALSG 199

Score = 67.0 bits (162), Expect = 2e-08
Identities = 30/51 (58%), Positives = 39/51 (76%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+A A LST FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSTKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIIRLFFHDCFVN 79

>gb|AAV89058.1| class III peroxidase [Phelipanche ramosa]
Length = 325

Score = 155 bits (392), Expect = 4e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
Q+RC FR+RIY N T+I+ FA TR++ CP+T G DNNLAPLDL TP SFDN YF+NL
Sbjct: 203 QSRCFLFRSRIYSNGTDIDPNFASTRRRRQCPQTGG--DNNLAPLDLVTSPNSFDNNYFRNL 260

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+Q+KGLL SDQ LFNGGST+++V YS NP F++DFA+AM++M +I PL GSNG IR+
Sbjct: 261 IQRKGLLESdqVLFNGGSTNALVTSYNNPRLFATDFASAMVRMSEIQPLLGSNGIIRRV 320

Query: 2164 CRRIN 2178
C IN
Sbjct: 321 CNVIN 325

Score = 124 bits (311), Expect = 9e-26
Identities = 70/169 (41%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD SILLDD+ + EK+A PN NS RG++VI+ K VE +CP VSCADI+A+AA
Sbjct: 76 VQGCASILLDDSPTIQSEKSAGPNVNSVRGYDVIETAKREVESICPRNVSCADIVALAA 135

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGPTW VKLG
Sbjct: 136 RDA-----SVAVGGPTWTVKLG 152

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TA+ + AN +P+P ++L LI+ F GLS D+VALSG+ I
Sbjct: 153 RRDSTTANPNEANTDLPSPFASLQTLITAFDDKGLSETDMVALSGSHTI 201

Score = 61.2 bits (147), Expect = 9e-07
Identities = 31/71 (43%), Positives = 46/71 (64%), Gaps = 3/71 (4%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGS---ANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
S S LT+ ++ +L+ S AQLS FY CPN S++++++ A++ E RM AS
Sbjct: 6 SINSLLTLTISSLILLSLSITPCQAQLSPTFYDSICPNALSTIRTSIRRAVAAERRMAAS 65

Query: 748 LLRLFFHDCFV 780
L+RL FHDCFV
Sbjct: 66 LIRLHFHDCFV 76

>gb|AAW52719.1| peroxidase 5 [Triticum monococcum]
Length = 259

Score = 155 bits (392), Expect = 4e-35
Identities = 72/126 (57%), Positives = 96/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C NFR R+YNETNI + FA + + +CP+ +GSGD NLA LD+ TP SFDN Y+ NL
Sbjct: 134 QAQCLNFRDRLYNETNINSGFATSLKANCPQPTGSGDRNLANLDVLTPTSFDNAYYSNLK 193

Query: 1987 QKKGLLHSDQQLF--NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+KGLLHSDQ LF GG TD+ V +++NP FSS FA+AM+KMG++SPLTGS G++R
Sbjct: 194 SQKGLLHSDQVLFVTGTGGTDNTVNNFASNPAAFSSAFASAMVKMGNLSPLTGSQGGQVRL 253

Query: 2161 NCRRIN 2178
+C ++N

Sbjct: 254 SCSKVN 259

Score = 101 bits (252), Expect = 6e-19
Identities = 64/169 (37%), Positives = 83/169 (49%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGFVID+IK+ +E +C VSCADIL +AA
Sbjct: 12 VQGCDAVLLSGM-----EQNAFPNVMSLRGFVIDSIKAKLETMCKQTVSCADILTVAA 66

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 67 RDSV-----VALGGPSWTVPLG 83

Query: 1511 RRDARTASQSAANNNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P P +L L F G + D+VALSG I
Sbjct: 84 RRDSTNANEAVANSDLPPPFDLVNLTSFGDKGFTVTDMVALSGAHTI 132

>gb|AAC49819.1| peroxidase [Oryza sativa Indica Group]
Length = 315

Score = 155 bits (392), Expect = 4e-35
Identities = 70/124 (56%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986
QA+CTNFR RIYNETNI+ +A + + +CP T+G+GD+NLA LD TP SFD Y+ NL+
Sbjct: 192 QAQCTNFRGRIYNETNIDAGYAASLRANCPPTAGTGDSNLAALDTTPYSFDTAYYSNLL 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
KGLLHSDQ LFNG STD+ VR ++N FSS F++AM+KM ++ PL GS G+IR +C
Sbjct: 252 SNKGLLHSDQVLFNGNSTDNTVRNFASNRAAFSSAFSSAMVKMANLGPLIGSQGQIRLSC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 132 bits (331), Expect = 4e-28
Identities = 74/169 (43%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL DT++FTGE+NA PN+NS RGF V+D+IK+ +E +C VSCADILA+AA
Sbjct: 65 VQGCDAVLLADTATFTGEQNALPNKNSLRGFNVVDSIKTQLEGICSQTVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVGLG 141

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSGTKHI 1657
RRD+ TAS +ANN +P P +L LI F G S D+VALSG I
Sbjct: 142 RRDSTTASMDSANNDLPPPFDLLENLIKAFGDKGFSVTDMVALSGAHTI 190

Score = 67.0 bits (162), Expect = 2e-08
Identities = 31/62 (50%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLLFFHDC 774
++ +A+ + + +A AQLS FY SCP +++KS V +A++ E RMGASLLRL FHDC
Sbjct: 4 SLSVAVLLCLAAAAAQLSPTFYDTSCPRALATIKSAVTA AVNNEPRMGASLLRLHFHDC 63

Query: 775 FV 780
FV
Sbjct: 64 FV 65

>dbj|BAD97435.1| peroxidase [Pisum sativum]
Length = 318

Score = 155 bits (392), Expect = 4e-35
Identities = 80/125 (64%), Positives = 91/125 (72%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q C FR RIYNETNI+T FA R+ +CP S GD NLAPLD TPT+FDN Y+ +L+
Sbjct: 196 QTECQFFRNRIYNETNIDTNFATLRKSNCP--SSGGDTNLAPLDSVTPTTFDNNYYNDLI 253

Query: 1987 QKKGLLHSDQQLFNG--GSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
KGLLHSDQ LFNG GS S+VR YS N F DFAAAMIK+ ISPLTG+NGEIRKN
Sbjct: 254 ANKGLLHSDQALFNGVGSQVSLVRTYSRNTVAFKRDFAAAMIKLSRISPLTGTNGEIRKN 313

Query: 2164 CRRIN 2178
CR +N
Sbjct: 314 CRLVN 318

Score = 141 bits (355), Expect = 7e-31
Identities = 82/169 (48%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCDGSILLDDT++FTGEK+A PN NSARGFEVID IK+ VE C VSCADILA+AA
Sbjct: 69 VNGCDGSILLDDTATFTGEKSAGPNINSARGFEVIDTIKTNVEASCNATVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD + ++ GGPTW V LG
Sbjct: 129 RDGIFLL-----GGPTWMVPLG 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRDARTASQSAAN+ IP P+S+L L + F GL+ DL LSG I
Sbjct: 146 RRDARTASQSAANSQIPGPSSDLATLTMTFRNKGLTLNDLTVLSGAHTI 194

Score = 73.9 bits (180), Expect = 1e-10
Identities = 38/71 (53%), Positives = 52/71 (73%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLSSVKSTVQSAISKETRMGASL 750
MA+F +L + L++ L+ S NAQL NFY +CP+L + V++T+ SAI E R+GAS+
Sbjct: 1 MATFI-KLFVTLSTIIISLLACSTNAQLINNFYATTCPSLQTIVRNTMISAIKTEARIGASI 59

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN
Sbjct: 60 LRLFFHDCFVN 70

>ref|NP_001057821.1| Os06g0547100 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54117.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69329.1| TPA: class III peroxidase 87 precursor [Oryza sativa (japonica
cultivar-group)]
gb|EAZ37289.1| hypothetical protein OsJ_21627 [Oryza sativa Japonica Group]
Length = 327

Score = 155 bits (392), Expect = 4e-35
Identities = 73/124 (58%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV
Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC
Sbjct: 264 AQRGLLHSDQQLFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RRIN 2178
R++N

Sbjct: 324 RKNV 327

Score = 134 bits (338), Expect = 7e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTLTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANLPGPASSGASLVAAFAGKGLSAREMTALSG 199

Score = 64.7 bits (156), Expect = 8e-08
Identities = 29/51 (56%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+A A LS FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSIKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIIRLFFHDCFVN 79

>emb|CBI19220.1| unnamed protein product [Vitis vinifera]
Length = 373

Score = 155 bits (391), Expect = 5e-35
Identities = 85/167 (50%), Positives = 103/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1336
GCD SILLDDT+SFTGEK A PN++S RG+EVID IKS VE +CPGVVSCADI+A+AARD
Sbjct: 70 GCDASILLDDTASFTGEKTAGPNKDSVRGYEVIDTIKSQVESLCPGVVSCADIVAVAARD 129

Query: 1337 SVQIVSGQTTNKNLTN*IIKLYISKLTNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW ++LGR
Sbjct: 130 SV-----VALGGPTWTLQLGR 146

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN+ +P P S+L+ LISRFS G +TK++VALSGT I
Sbjct: 147 DSTTASLSTANSIDLPGPASDLSTLISRFSNKGFTTKEMVALSGTHTI 193

Score = 128 bits (321), Expect = 6e-27
Identities = 64/95 (67%), Positives = 76/95 (80%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARCT+FR+RIYNETNI+ AFA ++Q+ CP T G DNNL+ LD +T T FDN YF+NL
Sbjct: 195 KARCTSFRRSRIYNETNIDAAFATSKQKICPSTGG--DNNLSLDL-ETTTVFDNVYFRNLK 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSD 2091
KKGLLHSDQQL+NGGSTDSIV YSTN TF +D
Sbjct: 252 AKKGLLHSDQQLYNGGSTDSIVETYSTNSATFFTD 286

Score = 75.1 bits (183), Expect = 6e-11
Identities = 38/70 (54%), Positives = 49/70 (70%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+NFY SCP S++++ V +A++KE RMGASL
Sbjct: 1 MASLSLFSLCVFSFLL--GMAHAQLSSNFYASSCPKALSTIRAAVNNAVAKERRMGASL 58

Query: 751 LRLFFHDCFV 780
LRL FHDCFV
Sbjct: 59 LRLHFHDCFV 68

>gb|ACN30737.1| unknown [Zea mays]
Length = 260

Score = 155 bits (391), Expect = 5e-35
Identities = 73/127 (57%), Positives = 97/127 (76%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF NL+
Sbjct: 134 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPDADFNDAYFGNLL 193

Query: 1987 QKKGLLHSDQQLF---NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIR 2157
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GEIR
Sbjct: 194 SQRGLLHSDQALFGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGSISPLTGTGDEIR 253

Query: 2158 KNCRIN 2178
NCRN+N
Sbjct: 254 VNCRRVN 260

Score = 145 bits (365), Expect = 5e-32
Identities = 82/164 (50%), Positives = 96/164 (58%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AAR 1333
QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AAR
Sbjct: 8 QGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAV AAR 67

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV LGGP+W V LGR
Sbjct: 68 DSAQ-----LGGPSWAVPLGR 84

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 85 RDATTASASLANSDLPGPTSSLNGLLNAFSNGLSSTDMMVALSG 128

>gb|ACG40622.1| peroxidase 2 precursor [Zea mays]
Length = 342

Score = 155 bits (391), Expect = 5e-35
Identities = 73/127 (57%), Positives = 97/127 (76%), Gaps = 3/127 (2%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF NL+
Sbjct: 216 RAQCKNCRARIYNDTIDASFAASLRASCPAQAGAGDGALEPLDGSTPDADFNDAYFGNLL 275

Query: 1987 QKKGLLHSDQQLF---NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIR 2157
++GGLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GEIR
Sbjct: 276 SQRGLLHSDQALFGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGSISPLTGTGDEIR 335

Query: 2158 KNCRRIN 2178
NCRR+N
Sbjct: 336 VNCRRVN 342

Score = 145 bits (366), Expect = 4e-32
Identities = 82/165 (49%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI A 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AA
Sbjct: 89 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAV A 148

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV LGGP+W V LG
Sbjct: 149 RDSVAQ-----LGGPSWAVPLG 165

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 166 RRDATTASASLANSDLPGPTSSLNGLLNAFSNKGLSSTDMDVALSG 210

Score = 57.8 bits (138), Expect = 1e-05
Identities = 32/67 (47%), Positives = 41/67 (61%), Gaps = 1/67 (1%)
Frame = +1

Query: 583 CSRLTICLALFVLIWGSANAQLSTNFYYH-SCPNLFSSVKSTVQSAISKETRMGASLLRL 759
C L + LAL +AQLS+ YY SCP ++++ V +A+ E RMGASLLRL
Sbjct: 24 CGLLVLALALATTA-AVGSAQLSSESYYDASCPAALLTIRTAVSTAVLLEPRMGASLLRL 82

Query: 760 FFHDCFV 780
FFHDCFV
Sbjct: 83 HFHDCFV 89

>emb|CAN83972.1| hypothetical protein [Vitis vinifera]
Length = 290

Score = 154 bits (390), Expect = 6e-35
Identities = 76/124 (61%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A+C+ FR RIYNETNI+ FA ++Q CP S GD NL+ LD T T FDN YF NL+
Sbjct: 169 KQCSKFRDRIYNETNIDATFATSKQAICP--SSGGDENLSDLXTT-TXFDNVYFTNLI 225

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KKGLLHSDQQL+NG STDS+V YS + TF +D A+AM+KMG++SPLTG++GEIR NC
Sbjct: 226 EKKGLLHSDQQLYNGNSTDSMVETYSNDSTTFFTDVASAMVKGNSPLTGTGDEIRTNC 285

Query: 2167 RRIN 2178
R IN
Sbjct: 286 RAIN 289

Score = 135 bits (340), Expect = 4e-29
Identities = 81/186 (43%), Positives = 101/186 (54%), Gaps = 18/186 (9%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFE-----VIDNIKSAVE 1279
QGCD SILLDDT++FTGEK A PN NS RG++ + IKS +E

Sbjct: 25 QGCDASILDDDTANFTGEKTAGPNNNSXRGYDSSNCGSDWYPLCIRVVTCTENTIKSQME 84

Query: 1280 KVC PGV VSCADILAI AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC 1459
+CPGVVSCADI+A+AARDSV

Sbjct: 85 SLCPGVVSCADIVAVAARDSV----- 105

Query: 1460 *F*SI*LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVAL 1639
+ LGGPTW V+LGRRD+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V L

Sbjct: 106 ----VALGGPTWTVQLGRRDSTASFSTANS DLPAPTS DLDALISLFSNKGFTTQEMVVL 161

Query: 1640 SGTKHI 1657
SGT I

Sbjct: 162 SGHTTI 167

>ref|XP_002509737.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus communis]
gb|EEF51124.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus communis]
Length = 322

Score = 154 bits (389), Expect = 8e-35
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ +CP+T G+G NLAPLDL TP +FDN Y+ NL

Sbjct: 200 QAQCVTFRDRIYNNASDIDPDFAATRRGNCPQTGGNG--NLAPLDLVTPNNFDNNYYSNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ K+GLL SDQ LF+GGSTDSIV YST+ +F SDFAAAM+KMG+ISPLTG+ GEIR+

Sbjct: 258 IAKRGLLASDQILFSGGSTDSIVNEYSTDSSSFSDFAAAMVKGNI SPLTGTQGEIRRI 317

Query: 2164 CRRIN 2178
C +N

Sbjct: 318 CSAVN 322

Score = 131 bits (330), Expect = 6e-28
Identities = 75/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI A 1330
+QGCDGS+LL DT +FTGEK+A N NS RG VID+ K+ VE +CPG+VSCADILA+AA

Sbjct: 73 VQGCDGSVLLVDTPFTTGEKSARNNANSIRGENVIDDAKAQVESICPGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GGP+W V LG

Sbjct: 133 RDA-----SVAAGGPSWTVNLG 149

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P + LN+LIS FS GL+ +D+VALSG I

Sbjct: 150 RRDSTTASLAQANSDLPGFSDPLNRLISLFSKGLNERDMVALSGAHTI 198

Score = 68.9 bits (167), Expect = 4e-09
Identities = 36/73 (49%), Positives = 49/73 (67%), Gaps = 3/73 (4%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGS---NAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMG 741
MAS S + L +F +I S+ AQLS+NFY ++CPN +++KS + +AI E RM
Sbjct: 1 MASRLSFACMILTIFFIINYSSLPCQAQLSSNFYDNTCPNALTTIKSAIDAAIESEQRMA 60

Query: 742 ASLLRLFFHDCFV 780
ASL+RL FHDCFV
Sbjct: 61 ASLIRLHFHDCFV 73

>ref|XP_002268412.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 318

Score = 154 bits (389), Expect = 8e-35
Identities = 75/123 (60%), Positives = 93/123 (75%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C F+ RIYNE+NI+ AFAR RQ +CP GD LAPLD T FD YF NLV+
Sbjct: 199 AQC�FFKNRIYNESNIDPAFARARQSTCP--PNGGDTKLAPLD-PTAARFDTGYFTNLVK 255

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGSTD++V+ YSTN G FS+DFA +M+KMG+I PLTG G+IR NCR
Sbjct: 256 RRGLLHSDQALFNGGSTDTLVKTYSTNFGAFSADFAKSMVKMGNIKPLTGKKGQIRVNCR 315

Query: 2170 RIN 2178
++N
Sbjct: 316 KVN 318

Score = 136 bits (343), Expect = 2e-29
Identities = 82/166 (49%), Positives = 97/166 (58%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+ EKNA N NSARGF V+D+IKS V+KVC VVSCADILA+A
Sbjct: 70 VNGCDASILLDATSTIDSEKNAGANANSARGFNVVDDIKSQVDKVCGRPVVSCADILAVA 129

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 130 ARDSV-----VALGGPSWTVQL 146

Query: 1508 GRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TAS++ ANN IP+P +L LI+RFS GL TKDLVALSG
Sbjct: 147 GRRDSTTASRTDANNIPSPFMDLPALITRFSNQGLDTKDLVALSG 192

Score = 66.6 bits (161), Expect = 2e-08
Identities = 35/69 (50%), Positives = 42/69 (60%), Gaps = 3/69 (4%)
Frame = +1

Query: 586 SRLTICLALFVLI---WGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASLLR 756
SR +CL FVL +A LS FY CP ++K V++A+ KE RMGASLLR
Sbjct: 3 SRSLLCLYAFVLFLATADFSAAALSPYFYNKVCPKALPTIKRVVEAAVQKEKRMGASLLR 62

Query: 757 LFFHDCFVN 783
L FHDCFVN
Sbjct: 63 LHFHDCFVN 71

>dbj|BAD36900.1| peroxidase [Lotus japonicus]
Length = 143

Score = 154 bits (389), Expect = 8e-35
Identities = 73/124 (58%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC+ FR+RIY+E NI+ A+AR+ Q CPRTSG GD+NL+P+D TP FD+ Y++NL+
Sbjct: 21 QSRCSLFRSRIYSEQNIDPAYARSLQGQCPRTSVGVDNSLSPIDT-TPNFFDSTYYRNL 79

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
K+GL HSDQQLFNGGSTDS V Y++NP F DFA AM+KMG++ LTG+ G+IRK C
Sbjct: 80 NKRGLFHSDQQLFNGGSTDSKVSQYASNPLLFRIDFANAMVKMGNLGTLTGTGQGIKVC 139

Query: 2167 RRIN 2178
+N
Sbjct: 140 SSVN 143

>gb|ACN26131.1| unknown [Zea mays]
Length = 323

Score = 154 bits (388), Expect = 1e-34
Identities = 71/124 (57%), Positives = 93/124 (75%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR RIYN+ NI FA RQQ+CP G D LAP+D+QTP +FDN Y+KNL+

Sbjct: 202 QARCATFRNRIYNDGNINATFASLRQQTCPLAGG--DAALAPIDVQTPEAFDNAYYKNLM 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ+LFNGGS D++V+ YS N F++DFA AM++MG ISPLT + GE+R +C

Sbjct: 260 ARQGLFHSDQELFNGGSQDALVKKYSGNAAMFTADFAKAMVRMGASPLTATQGEVRLDC 319

Query: 2167 RRIN 2178

R++N

Sbjct: 320 RKNV 323

Score = 140 bits (353), Expect = 1e-30

Identities = 79/165 (47%), Positives = 94/165 (56%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA

Sbjct: 75 VNGCDASILLDDTATFTGEKNAGPNANSVRGYEVIDAIKARVEASCNATVSCADILALAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + LGGP+W V LG

Sbjct: 135 RDAVNL-----LGGPSWTVYLG 151

Query: 1511 RRDARTASQSAANN GIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645

RRDARTASQS AN +P P S+L L++ F GLS +D+ ALSG

Sbjct: 152 RRDARTASQSDANANLP GPGSSLATLVMTFGNKGLSARDMTALSG 196

Score = 67.8 bits (164), Expect = 1e-08

Identities = 36/73 (49%), Positives = 47/73 (64%), Gaps = 4/73 (5%)

Frame = +1

Query: 577 SFCSRLTICLALF----VLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGA 744
S S + CL L VL +A LST+FY CP++ S V++ V SA++ E RMGA

Sbjct: 4 SAASSVVRCLQLLTVA AVLAGAAAGGLSTSFYSKKCPDVQSIVRAGVASAVAAE KRMGA 63

Query: 745 SLLRLLFFHDCFVN 783

S+LR+FFHDCFVN

Sbjct: 64 SILRMFFHDCFVN 76

>gb|ACF08094.1| class III peroxidase [Triticum aestivum]

Length = 321

Score = 153 bits (387), Expect = 1e-34
Identities = 70/124 (56%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR+R+YNETNI+ AFA + + +CPRT+ SG+++LAPLD TP FDN Y+ NL+
Sbjct: 198 QSQCRFFRSRLYNETNIDAAFATSLKANCPRRTSSGNSSLAPLDTTTPNGFDNAYYSNLM 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DFAAAM++MG+ISPLTG+ G+IR +C
Sbjct: 258 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRFDAAMVRMGNISPLTGAQGGIRLSC 317

Query: 2167 RRIN 2178
R+N
Sbjct: 318 SRVN 321

Score = 132 bits (332), Expect = 3e-28
Identities = 76/165 (46%), Positives = 93/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 71 VQGCDAVLLSDTATFTGEQGAAPNARSIRGMNVIDNIKAQVEAVCRQTVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 131 RDSV-----VALGGPSWTVPPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RRD+ TAS S AN+ +PAP+ +L L + F+A GLS D+VALSG
Sbjct: 148 RRDSTTASLSLANS DLPAPSF DLANLTANFAAKGLSVTDMVALSG 192

Score = 65.5 bits (158), Expect = 5e-08
Identities = 32/63 (50%), Positives = 41/63 (65%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L++ L L + SA+ LS FY SCP +++KS V +A+ E RMGASLLRL FHD
Sbjct: 9 LSVLLLLCLAAAASAPPLSPQFYAKSCPRALATIKSAVTA AVRSEPRMGASLLRLHFHD 68

Query: 772 CFV 780
CFV
Sbjct: 69 CFV 71

>ref|XP_002509733.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
gb|EEF51120.1| Lignin-forming anionic peroxidase precursor, putative [Ricinus
communis]
Length = 321

Score = 153 bits (387), Expect = 1e-34
Identities = 77/125 (61%), Positives = 97/125 (77%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYNE-TNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C FR RIYN ++I+ FA TR+ +CP+T G+G NLAPLDL TP +FDN Y+ NL
Sbjct: 199 QAQCVTFRDRIYNNASDIDPDFAATRRGNCPQTGGNG--NLAPLDLVTPNNFDNNYYSNL 256

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ K+GLL SDQ LF+GGSTDSIV YST+ +F SDFAAAM+KMG+ISPLTG+ GEIR+
Sbjct: 257 MAKRGLLASDQILFSGGSTDSIVNEYSTDSSSFSDFAAAMVKGNIPLTGTQGEIRRL 316

Query: 2164 CRRIN 2178
C +N
Sbjct: 317 CSAVN 321

Score = 131 bits (330), Expect = 6e-28
Identities = 75/169 (44%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCDGS+LL DT +FTGEK+A N NS RG VID+ K+ VE +CPG+VSCADILA+AA
Sbjct: 72 VQGCDGSVLLVDTPFTFTGEKSARNNANSIRGENVIDDAKAQVESICPGIVSCADILAVAA 131

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ GGP+W V LG
Sbjct: 132 RDA-----SVAAGGPSWTNVLG 148

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + AN+ +P + LN+LIS FS GL+ +D+VALSG I
Sbjct: 149 RRDSTTASLAQANSIDLPGFSDPLNRLISLFSKGLNERDMVALSGAHTI 197

Score = 67.4 bits (163), Expect = 1e-08
Identities = 35/72 (48%), Positives = 48/72 (66%), Gaps = 2/72 (2%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGA--NAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGA 744
MAS S + L +F + S+ AQLS+NFY ++CPN +++KS + +AI E RM A

Sbjct: 1 MASHLSFACMILTIFIPNYSSLCAQLSSNFYDNTCPNALTTIKSAIDAAIESEQRMAA 60

Query: 745 SLLRLFFHDCFV 780
SL+RL FHDCFV

Sbjct: 61 SLIRLHFHDCFV 72

>ref|XP_002319407.1| predicted protein [Populus trichocarpa]
gb|EEE95330.1| predicted protein [Populus trichocarpa]
Length = 302

Score = 153 bits (387), Expect = 1e-34
Identities = 72/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR R+YNET++++ A + + +CP T D++L+ LD TP +FDN YFKNL
Sbjct: 181 QARCLLFRNRVYNETSLSLSTLTKSNCPNTGS--DDSLSSLDATTPVTFDNSYFKNLA 238

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQQLF+GG+TDS V+ YS N TF +DFA+AM+KMG ISPLTGS+G+IR NC
Sbjct: 239 NNKGLLHSDQQLFSGGTTDSQVKTYINSATFYADFASAMVKMGISPLTGSQGIRTNC 298

Query: 2167 RRIN 2178
++N
Sbjct: 299 AKVN 302

Score = 147 bits (372), Expect = 8e-33
Identities = 83/180 (46%), Positives = 105/180 (58%)
Frame = +2

Query: 1118 AS*ILSKH*QMCGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGV 1297
AS + + H QGCD S+LLDDTSSFTGEK A PN NS RG++VID IKS +E +CPGV
Sbjct: 43 ASLLRLHFHDCFQGCDA SVLLDDTSSFTGEKTAGPNANSLRGYDVIDTIKSQLESICPGV 102

Query: 1298 VSCADILAI AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI* 1477
VSCADILA+AARDSV +
Sbjct: 103 VSCADILAVAARDSV-----VA 119

Query: 1478 LGGPTWNVKLGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
L GP+W V+LGRRD+ TAS AAN+ +P+P +L+ LI+ FS G + K++VALSG+ I
Sbjct: 120 LSGPSWTVQLGRRDSTASLGAANS DLP SPLMDLSDLITSFSNKGFTAKEMVALSGSHTI 179

Score = 65.5 bits (158), Expect = 5e-08
Identities = 30/54 (55%), Positives = 39/54 (72%)

Frame = +1

Query: 616 VLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRRLFHDCF 777
+L+ G +AQLST FY +CP S++++ V A+ KE RMGASLLRL FHDCF
Sbjct: 1 MLLGLVHAQLSTTFYATTCPKALSTIRTAVLKAVVKEHRMGASLLRLHFHDCF 54

>dbj|BAA77388.1| peroxidase 2 [Scutellaria baicalensis]
Length = 325

Score = 153 bits (387), Expect = 1e-34
Identities = 78/126 (61%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
Q++C NFRARIY N ++IE FA TR++ CP+ GSGD+NLAPLDL TP SFDN Y++NL
Sbjct: 201 QSQCGNFRARIYSNGSDIEANFASTRRRQCPQ-DGSGDSNLAPLDLVTPNSFDNYYRNL 259

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPL-TGSNGEIRK 2160
V ++GLL SDQ L +GG TD+IV YS+NP TF+SDFA AMIKMG+I PL G NG IR+
Sbjct: 260 VARRGLLQSDQVLLSGGETDAIVTSYSSNPATFASDFANAMIKMGEIQPLQLGQNGIIRR 319

Query: 2161 NCRRIN 2178
C +N
Sbjct: 320 TCGAVN 325

Score = 140 bits (353), Expect = 1e-30
Identities = 75/165 (45%), Positives = 98/165 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD SILLD+TS+ EK A PN S RGF+VID K+AVE++CPGVVSCADIL +AA
Sbjct: 74 VQGC DASILLDETSTIQSEKTAGPNAGSVRGFQVIDAAKTAVERLCPGVVSCADILTAA 133

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+ S+ +GGP+W V+LG
Sbjct: 134 RDA-----SVAVGGPSWTVRLG 150

Query: 1511 RRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRD+ TA+++ AN +P PTS L QLI+RF A GL+ +++VALSG
Sbjct: 151 RRDSTTANRAQANTDLPGPTSTLTQLITRFDAKGLNAREMVALSG 195

Score = 63.9 bits (154), Expect = 1e-07
Identities = 30/68 (44%), Positives = 44/68 (64%)
Frame = +1

Query: 577 SFC SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLR 756
SF +I + +L + AQLS FY +CPN S++++++ A+S E RM ASL+R
Sbjct: 7 SFRPIFSIAALVLLLTLPSEAQLSATFYDSTCPNAVSTIRTSIRQAVSAERRMAASLIR 66

Query: 757 LFFHDCFV 780
L FHDCFV
Sbjct: 67 LHFHDCFV 74

>gb|ACF08095.1| class III peroxidase [Triticum aestivum]
Length = 321

Score = 153 bits (386), Expect = 2e-34
Identities = 69/124 (55%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR+R+YNETNI+ AFA + + +CPR++GSG+++LAPLD TP FDN Y+ NL+
Sbjct: 198 QSQCRFFRSRLYNETNIDAAFAASLKANCPRSTGSGNSSLAPLDTNTPNGFDNAYYSNLM 257

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ L N G T +VR YS+ F+ DFA AM++MG+ISPLTG+ G+IR +C
Sbjct: 258 SQKGLLHSDQVLINDGRTAGLVRTYSSASAQFNRFDAVAMVRMGNISPLTGAQGGIRLSC 317

Query: 2167 RRIN 2178
R+N
Sbjct: 318 SRVN 321

Score = 132 bits (332), Expect = 3e-28
Identities = 76/165 (46%), Positives = 93/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL DT++FTGE+ A PN S RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 71 VQGCDASVLLSDTATFTGEQGAAPNARSIRGMNVIDNIKAQVEAVCRQTVSCADILAVAA 130

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 131 RDSV-----VALGGPSWTVPLG 147

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRD+ TAS S AN+ +PAP+ +L L + F+A GLS D+VALSG
Sbjct: 148 RRDSTTASLSLANS DLPAPSFDLANLTANFAAKGLSVTDMVALSG 192

Score = 67.8 bits (164), Expect = 1e-08
Identities = 33/63 (52%), Positives = 42/63 (66%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L++ L L + SA+ QLS FY SCP +++KS V +A+ E RMGASLLRL FHD
Sbjct: 9 LSVLLLLCLAAAASAPQLSPQFYAKSCPRALATIKSAVTA AVRSEPRMGASLLRLHFHD 68

Query: 772 CFV 780
CFV
Sbjct: 69 CFV 71

>gb|EAZ01279.1| hypothetical protein OsI_23302 [Oryza sativa Indica Group]
Length = 318

Score = 153 bits (386), Expect = 2e-34
Identities = 68/124 (54%), Positives = 96/124 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D+ LAP+D+QTP +FDN Y+ NLV
Sbjct: 197 QARCATFRSRIFGDGNVDAFAALRQQACPSGG--DSTLAPIDVQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 255 KKQLFLHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 140 bits (354), Expect = 9e-31
Identities = 78/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW ++LG
Sbjct: 130 RDAVNLL-----GGPTWTMQLG 146

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 147 RRDALTASQAANGNLPGPSDLATLVTMFGNKGLSPRDMTALSG 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>ref|NP_001046392.1| Os02g0236600 [Oryza sativa (japonica cultivar-group)]
dbj|BAD27598.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69269.1| TPA: class III peroxidase 27 precursor [Oryza sativa (japonica cultivar-group)]
gb|EAY85140.1| hypothetical protein OsI_06495 [Oryza sativa Indica Group]
gb|EAZ22363.1| hypothetical protein OsJ_06021 [Oryza sativa Japonica Group]
dbj|BAH01530.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 321

Score = 152 bits (385), Expect = 2e-34
Identities = 82/169 (48%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD S+LLDD+S+ TGEKNA PN NS RGFEVID+IKS VE CPG VSCADILA+AA
Sbjct: 73 VNGCDASVLLDDSSSTITGEKNAGPNANSLRGFEVIDSIKSQVEAACPGTVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW V+LG
Sbjct: 133 RDGVNLL-----GGPTWAVQLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD RTASQSAAN+ +P+P+S+ L+S F++ GL ++D+VALSG I
Sbjct: 150 RRDTRTASQSAANSNLPSPSSAAALVSAFASKGLDSRDMVALSGAHTI 198

Score = 151 bits (382), Expect = 5e-34
Identities = 72/123 (58%), Positives = 89/123 (72%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989

ARC FRAR+YN+TNI FA R+Q CP + GD NLAPLD + FDN YF+NL+
Sbjct: 201 ARCATFRARVYNDTNISPGFAVRRRQVCP--ASGGDGNLAPLDALSSVRFDNGYFRNLGM 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+ GLLHSDQ+LFNGG DSI + Y+ N FS DF A++KMG+ISPLTGS+GE+R NCR

Sbjct: 259 RFGLLHSDQELFNGGPVDSIAQQYAANGAASFSDVFTAVVKMGNISPLTGSSGEVRSNCR 318

Query: 2170 RIN 2178
+ N

Sbjct: 319 KPN 321

Score = 68.2 bits (165), Expect = 8e-09
Identities = 33/66 (50%), Positives = 47/66 (71%), Gaps = 1/66 (1%)
Frame = +1

Query: 589 RLTICLALFVLIW-GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFF 765
R+ + +A+ L+ G AQL+ +Y SCP+L S V+S + +A+ +E RMGAS+LRLFF
Sbjct: 9 RMVVVVAIAALVAPGEVAAQLTPTYDGCPSLQSIVRSAMAAVQQEPRMGASILRLFF 68

Query: 766 HDCFVN 783
HDCFVN
Sbjct: 69 HDCFVN 74

>gb|EAZ37287.1| hypothetical protein OsJ_21626 [Oryza sativa Japonica Group]
Length = 309

Score = 152 bits (385), Expect = 2e-34
Identities = 68/124 (54%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D LAP+D+QTP +FDN Y+ NLV
Sbjct: 188 QARCATFRSRIFGDGNVDAAFALRQQACPQSGG--DTLAPIDVQTPDAFDNAYYANLV 245

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 246 KKQGLFHSQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 305

Query: 2167 RRIN 2178
R++N
Sbjct: 306 RKNV 309

Score = 122 bits (307), Expect = 3e-25
Identities = 73/165 (44%), Positives = 87/165 (52%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LG GPTWNVKLG 1510
RD+V + LG
Sbjct: 130 RDAVNL-----LG 137

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 138 RRDAL TASQSAANGNLPGPSDLATLVMTFGNKGLSPRDMTALSG 182

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>gb|ABD47726.1| peroxidase [Eucalyptus globulus subsp. globulus]
Length = 258

Score = 152 bits (385), Expect = 2e-34
Identities = 73/123 (59%), Positives = 92/123 (74%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT+FR RIYN++NI+T+FA Q CP+ D+ L LD+QTPT FDN Y+ NL+Q
Sbjct: 138 ARCTSFRGRIYND SNIDTSFAHKLQNICPKIGN--DSVLQRLDIQTPTFFDNLYYHNLLQ 195

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
KKGLLHSDQ+LFNG S DS+V+ Y+ + G F DFA AMIKM I P GS+G+IRKNCR
Sbjct: 196 KKGLLHSDQELFNGSSVDSL VKKYACDTGKFFRDFAKAMIKMSKIKPPKGSSGQIRKNCR 255

Query: 2170 RIN 2178
++N
Sbjct: 256 KVN 258

Score = 152 bits (383), Expect = 4e-34
Identities = 85/169 (50%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDT SF GEK A PN NS RGFEVID IK+++EK CPGVVSCADI+A+AA
Sbjct: 10 VNGCDASILLDDTPSFVGEKTAAPNNNSVRGFEVIDRIKASLEKECPGVVSCADIVALAA 69

Query: 1331 RDSVQIVSGQTNTKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 70 RDSV-----VHLGGPSWTVSLG 86

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
R+D+ TAS+S AN IP PTSNL+ LI+ F+A GLS K++VALSG+ I
Sbjct: 87 RKDSITASRSLANTSIPPPTSNSALITSFAAQGLSVKNMVALSGSHTI 135

>ref|NP_001057820.1| Os06g0546500 [Oryza sativa (japonica cultivar-group)]
dbj|BAD54114.1| putative bacterial-induced peroxidase precursor [Oryza sativa
Japonica Group]
tpe|CAH69330.1| TPA: class III peroxidase 88 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF19734.1| Os06g0546500 [Oryza sativa Japonica Group]
dbj|BAG93666.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 318

Score = 152 bits (385), Expect = 2e-34
Identities = 68/124 (54%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARC FR+RI+ + N++ AFA RQQ+CP++ G D LAP+D+QTP +FDN Y+ NLV
Sbjct: 197 QARCATFRSRIFGDGNVDAFAALRQQACPSGG--DTTLAPIDVQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+K+GL HSDQ+LFNGGS D++VR Y+ N G F++DFA AM++MG + P G+ E+R NC
Sbjct: 255 KKQGLFHSDQELFNGGSQDALVRKYAGNAGMFAADFAKAMVRMGALLPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 142 bits (357), Expect = 4e-31
Identities = 79/165 (47%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCD SILLDDT++FTGEKNA PN NS RG+EVID IK+ VE C VSCADILA+AA
Sbjct: 70 VNGCDASILLDDTANFTGEKNAGPNANSVRGYEVIDAIKTQVEASCNATVSCADILALAA 129

Query: 1331 RDSVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ GGPTW V+LG
Sbjct: 130 RDAVNLL-----GGPTWTVQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
RRDA TASQSAAN +P P S+L L++ F GLS +D+ ALSG
Sbjct: 147 RRDALTASQSAANGNLPGPSDLATLVMTFGNKGLSPRDMTALSG 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 31/71 (43%), Positives = 46/71 (64%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MA+ + + + + G+A QLST +Y CPN+ S V++ + A++ E RMGAS+
Sbjct: 1 MATQWVLVVAVMAVLFAGGAAGGQLSTRYYDGKCPNVQSIVRAGMAQAVAAEPRMGASI 60

Query: 751 LRLFFHDCFVN 783
LR+FFHDCFVN
Sbjct: 61 LRMFFHDCFVN 71

>ref|XP_002438534.1| hypothetical protein SORBIDRAFT_10g021650 [Sorghum bicolor]
gb|EER89901.1| hypothetical protein SORBIDRAFT_10g021650 [Sorghum bicolor]
Length = 325

Score = 152 bits (384), Expect = 3e-34
Identities = 71/124 (57%), Positives = 95/124 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+++C FR+RIY E+NI +FA RQ++CPR+ G D LAP D+QTP FDN Y++NLV
Sbjct: 204 RSQCQFFRSRIYTESNINASFAALRQKTCPRSGG--DATLAPFDVQTPDGF DNAYYQNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFNGGS D++VR YSTN FS+DF +AMIKMG++ P +G+ E+R NC
Sbjct: 262 AQKGLLHSDQELFNGGSQDALVRQYSTNANQFSADFVSAMIKMGNLMPSSGTPTEVRLNC 321

Query: 2167 RRIN 2178
R+ N
Sbjct: 322 RKTN 325

Score = 143 bits (360), Expect = 2e-31
Identities = 81/169 (47%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDTS+FTGEK A PN NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 77 VNGCDGSILLDDTSTFTGEKGAGPNANSVRGFEVIDAIKTKVEASCKATVSCADILALAA 136

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++ GGPTW+V LG
Sbjct: 137 RDGVNLL-----GGPTWSVPLG 153

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
R+D+RTASQS AN+ +P P S+L LI F GLS +D+ ALSG I
Sbjct: 154 RKDSRTASQSLANSNLPGPGSSLATLIRMFGNQLSARDMTALSGAHTI 202

Score = 68.9 bits (167), Expect = 4e-09
Identities = 39/78 (50%), Positives = 54/78 (69%), Gaps = 7/78 (8%)
Frame = +1

Query: 571 MASFCSR----LTICLALFV--LIWGSANAQ-LSTNFYHSCPNLFSSVKSTVQSAISKE 729
MA+F R L++ A+ V L G+A+AQ LS NFY +CPN+ + V+ + SA++ E
Sbjct: 1 MATFTCRSMAFLSLAAAVLVALLTAGAADAQKLSPNFYSKTCPNVATIVRQQMASAVAAE 60

Query: 730 TRMGASLLRLFFHDCFVN 783
RMGAS+LR+FFHDCFVN
Sbjct: 61 KRMGASILRMFFHDCFVN 78

>ref|NP_001140437.1| hypothetical protein LOC100272496 [Zea mays]
gb|ACF83840.1| unknown [Zea mays]
Length = 263

Score = 152 bits (384), Expect = 3e-34
Identities = 72/129 (55%), Positives = 97/129 (75%), Gaps = 5/129 (3%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF +L+
Sbjct: 135 RAQCKNCRARIYNDTIDASFAASLRASCPAQAGAGDGALEPLDGSTPDADFNDAYFGDLL 194

Query: 1987 QKKGLLHSDQQLF-----NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GE
Sbjct: 195 SQRGLLHSDQALFGGGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGISPLTGTGDGE 254

Query: 2152 IRKNCRRIN 2178
IR NCRR+N

Sbjct: 255 IRVNCRRVN 263

Score = 145 bits (366), Expect = 4e-32
Identities = 83/164 (50%), Positives = 96/164 (58%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AAR 1333
QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILAI AAR
Sbjct: 9 QGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAI AAR 68

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV LGGP+W V LGR
Sbjct: 69 DSV AQ-----LGGPSWAVPLGR 85

Query: 1514 RDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 86 RDATTASASLANS DLP GPTSSLNGLLNAFSNKGLSSTD MVALSG 129

>gb|ACF82414.1| unknown [Zea mays]
Length = 349

Score = 152 bits (384), Expect = 3e-34
Identities = 72/129 (55%), Positives = 97/129 (75%), Gaps = 5/129 (3%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPR TSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
+A+C N RARIYN+T+I+ +FA + + SCP +G+GD L PLD TP +FDN YF +L+
Sbjct: 221 RAQCKNCRARIYNDTDIDASFAASLRASCPAQAGAGDGALEPLDGSTPD AFDNAYFGDLL 280

Query: 1987 QKKGLLHSDQQLF-----NGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
++GLLHSDQ LF GG+TD +V Y++N G + +DFAAAM+KMG ISPLTG++GE
Sbjct: 281 SQRGLLHSDQALFGGGGGGGGATDGLVSAYASNAGQWGADFAAAMVKMGSI SPLTGT DGE 340

Query: 2152 IRKNCRRIN 2178
IR NCRR+N
Sbjct: 341 IRVNCRRVN 349

Score = 145 bits (367), Expect = 3e-32
Identities = 83/165 (50%), Positives = 97/165 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI A 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILAI A
Sbjct: 94 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAI A 153

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV LGGP+W V LG
Sbjct: 154 RDSVAQ-----LGGPSWAVPLG 170

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTS+LN L++ FS GLS+ D+VALSG
Sbjct: 171 RRDATTASASLANS DLPGPTSSLNGLLNAFSNKLSSTDMVALSG 215

Score = 57.4 bits (137), Expect = 1e-05
Identities = 36/92 (39%), Positives = 51/92 (55%), Gaps = 1/92 (1%)
Frame = +1

Query: 508 TPFQSNTNT*STKLVLCLSKLTMA SFCSRLTICLALFVLIWGSANAQLSTNFYYH-SCPNL 684
TP + + +++ LS+ C L + LAL +AQLS+ YY SCP
Sbjct: 4 TPLECDMAPAASRNKHLRSWPLPRCGLLV LVLALAATA-AVGSAQLSSEDYYDASCPAA 62

Query: 685 FSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
++++ V +A+ E RMGASLLRL FHDCFV
Sbjct: 63 LLTIRTAVSTAVLLEPRMGASLLRLHFHDCFV 94

>dbj|BAF19735.2| Os06g0547100 [Oryza sativa Japonica Group]
Length = 353

Score = 152 bits (383), Expect = 4e-34
Identities = 72/122 (59%), Positives = 89/122 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA +Q+CP+ SG GD NLAP D QTP +FDN YFKNLV
Sbjct: 205 RARCLMFRGRIYGEANINATFAAALRQTCPQ-SGGGDGNLAPFDDQTPDAFDNAYFKNLV 263

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGGS D++VR Y+ N G F+ DFA AM+KMG + P G+ E+R NC
Sbjct: 264 AQRGLLHSDQELFNGGSQDALVRKYAGNAGMFAGDFAKAMVKMGGLMPAAGTPTEVRLNC 323

Query: 2167 RR 2172
R+
Sbjct: 324 RK 325

Score = 134 bits (338), Expect = 7e-29
Identities = 74/165 (44%), Positives = 95/165 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IKS VE C GVVSCADI+A+A+
Sbjct: 78 VNGCDASILLDDTLTFTGEKNAGANINSVRGYEVIDAIKSQVEAACKGVVSCADIVALAS 137

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 138 RDAVNLLGG-----PTWNVQLG 154

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R+D+RTAS +AAN +P P S+ L++ F+ GLS +++ ALSG
Sbjct: 155 RKDSRTASGTAANANLPGPASSGASLVAAFAGKLSAREMTALSG 199

Score = 64.7 bits (156), Expect = 8e-08
Identities = 29/51 (56%), Positives = 38/51 (74%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+A A LS FY +CP + + V+S V A++KE RMGAS++RLFFHDCFVN
Sbjct: 29 AAKAGLSIKFYAKTCPGVDTIVRSVVAQAVAKEPRMGASIIRLFFHDCFVN 79

>ref|XP_002438533.1| hypothetical protein SORBIDRAFT_10g021640 [Sorghum bicolor]
gb|EER89900.1| hypothetical protein SORBIDRAFT_10g021640 [Sorghum bicolor]
Length = 318

Score = 151 bits (382), Expect = 5e-34
Identities = 71/124 (57%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+ARC FR RIY E NI FA RQQ+CP+T G G NLAP D QTP +FDN Y+ NLV
Sbjct: 197 RARC VF FR GRIYGE PNINATFAAVRQQTCPQTGGDG--NLAPFDDQTPDAFDNAYYANLV 254

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFNGG+ D++VR YS N F++DFA AM+KMG ++P G+ E+R NC
Sbjct: 255 ARRGLLHSDQELFNGGTQDALVRKYSGNGRMFANDFAKAMVKMGLAPAAGTPTEVRLNC 314

Query: 2167 RRIN 2178
R++N
Sbjct: 315 RKNV 318

Score = 136 bits (342), Expect = 2e-29
Identities = 75/165 (45%), Positives = 94/165 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT +FTGEKNA N NS RG+EVID IK+ VE C VSCADI+A+A+
Sbjct: 70 VNGCDASILLDDTPTFTGEKNAGANVNSVRGYEVIDAIKTQVEAACKATVSCADIVALAS 129

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V ++ G PTWNV+LG
Sbjct: 130 RDAVNLLGG-----PTWNVQLG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSG 1645
R D+RTASQSAAN +P P S+ L++ F+A GLS +D+ ALSG
Sbjct: 147 RTDSRTASQSAANANLPGPGSSAASLVAAFAAKGLSARDMTALSG 191

Score = 66.2 bits (160), Expect = 3e-08
Identities = 29/63 (46%), Positives = 43/63 (68%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
++ L + + + +LST FY SCP + + V+S A++KE RMGAS++RLFFHDC
Sbjct: 9 SVALLTLLCLLTCHGKLSTKIFYAKSCPGVAAIIVRSVTAQAVAKEPRMGASIIRLFFHDC 68

Query: 775 FVN 783
FVN
Sbjct: 69 FVN 71

>gb|ACE00594.1| lignin biosynthetic peroxidase [Leucaena leucocephala]
Length = 316

Score = 151 bits (382), Expect = 5e-34
Identities = 76/124 (61%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSF DNYYFKNLV 1986
Q +C FR RIYNE NI+ +FA TR+ +CPRT G NLAPLD TP FDN Y+K+LV
Sbjct: 196 QGQCNNFFRNRIYENNIDPSFAATRRATCPRTGGG--INLAPLDF--TPNRFDNYYKDLV 252

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GL HSDQ FNGGS D+IVR YSTN F DFA AM+KM I+PLTGS GEIRK+C
Sbjct: 253 NRRGLFHSDQVFFNGGSQDAIVRAYSTNSVLFFGDFAFAMVKMSSITPLTGSQGEIRKDC 312

Query: 2167 RRIN 2178
R +N
Sbjct: 313 RVVN 316

Score = 126 bits (317), Expect = 2e-26

Identities = 77/169 (45%), Positives = 93/169 (55%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD ILLDDT+SFTGEKNA PN+ SARG+EVID IK+ VE C G VSCADILA+AA

Sbjct: 70 VNGCDAGILLDDTASFTGEKNAGPNQ-SARGYEVIDAIKTNVEAACRGTVSCADILALAA 128

Query: 1331 RDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
++ V LGGP L

Sbjct: 129 QEGVTQ-----LGGPHGQYHLA 145

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRDARTASQS AN+ IP P+S L+ LIS F+A GL+ +++ LSG I
Sbjct: 146 RRDARTASQSKANSEIPGPSELSTLISMFAAKGLNAREMTVLSGAHSI 194

Score = 80.1 bits (196), Expect = 2e-12
Identities = 37/71 (52%), Positives = 52/71 (73%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISKETRMGASL 750
MAS + L++ L S+NAQLS NFY SCPN+ + V++T++ A+++E R+GAS+

Sbjct: 1 MASLTHFFLLALSVLSLFASSNAQLSPNFYARSCPNVRAIVRNTMRQALAREARLGASI 60

Query: 751 LRLFFHDCFVN 783
LRLFFHDCFVN

Sbjct: 61 LRLFFHDCFVN 71

>emb|CBI19221.1| unnamed protein product [Vitis vinifera]
Length = 441

Score = 151 bits (381), Expect = 7e-34
Identities = 83/167 (49%), Positives = 102/167 (61%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD

Sbjct: 68 GCDASILLDDTANFTGEKTAGPNNNSVRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 127

Query: 1337 SVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V+LGRR

Sbjct: 128 SV-----VALGGPTWTVQLGR 144

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

D+ TAS S AN+ +PAPTS+L+ LIS FS G +T+++V LSGT I
Sbjct: 145 DSTTASFSTANS DLPAPTS DLDALISLFSNKGFTTQEMVVLSGHTI 191

Score = 83.2 bits (204), Expect = 2e-13
Identities = 45/84 (53%), Positives = 55/84 (65%)
Frame = +1

Query: 1867 FARTRQQSCPRTS GSGDNNLAPLDLQTPTSF DNYYFKNLVQKKGLLHSDQQLFNGGSTDS 2046
F RT+ + R GD+NL+PLD +T T F YF++L +KKGLLHSDQQL+N GSTDS
Sbjct: 357 FFRTKGITVIRIESGGDDNLSPLD-KTTTVFYAYFRDLKEKKGLLHSDQQLYNDGSTDS 415

Query: 2047 IVRGYSTNPGTFSSDFAAAMIKMG 2118
IV YS N TF D AM+ G
Sbjct: 416 IVESYSINSATFFRDVTNAMVLDG 439

Score = 69.3 bits (168), Expect = 3e-09
Identities = 34/69 (49%), Positives = 49/69 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASL 750
MAS C+ F+L G A+AQLS+++Y SCP+ S++++ V +A++ E+RMGASL
Sbjct: 1 MASLSLFSLFCMFSFLL--GMAHAQLSSDYSSSCPSALSTIQTAVNNAVADES RMGASL 58

Query: 751 LRLFFHDCF 777
LRL FHDCF
Sbjct: 59 LRLHFHDCF 67

Score = 42.7 bits (99), Expect = 0.35
Identities = 17/30 (56%), Positives = 23/30 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCP 1896
+A+C+ FR RIYNETNI+ FA ++Q CP
Sbjct: 193 KAQCSKFRDRIYNETNIDATFATSKQAICP 222

Score = 38.1 bits (87), Expect = 8.5
Identities = 17/30 (56%), Positives = 22/30 (73%)
Frame = +2

Query: 1556 IPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
+P PT NL+QL+S FS G +TK+ V LSG
Sbjct: 302 LPGPTLNLSQLVSAFSNKGFTTKETVVLSG 331

>ref|XP_002451846.1| hypothetical protein SORBIDRAFT_04g008590 [Sorghum bicolor]
gb|EES04822.1| hypothetical protein SORBIDRAFT_04g008590 [Sorghum bicolor]
Length = 325

Score = 151 bits (381), Expect = 7e-34
Identities = 83/169 (49%), Positives = 102/169 (60%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+QGCD S+LLDD+++ TGEKNA PN NS RGFEVID IKS VE CPG VSCADILA+AA
Sbjct: 75 VQGCDASVLLDDSATLTGEKNAAPNANSLRGFEVIDAIKSQVEAACPGTVSCADILALAA 134

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V ++S GPTW V+LG
Sbjct: 135 RDGVNLLS-----GPTWAVQLG 151

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD RTASQSAAN+ +P+P+S+ L+S F++ GL ++DLVALSG I
Sbjct: 152 RRDTRTASQSAANSNLPSPSSAAALVSAFASKGLDSRDLVALSGAHTI 200

Score = 147 bits (372), Expect = 8e-33
Identities = 70/123 (56%), Positives = 87/123 (70%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARC +FR+RIYN++NI FA R+Q C SG D NLAPLD + FDN YF++LV
Sbjct: 203 ARCASFRRSRIYNDNINAGFAAKRKQICGPGSGGTDGNLAPLDAMSSVKFDNGYFRDLVS 262

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
+ GLLHSDQ+LF G DS+ Y+ N FSSDF A++KMG+ISPLTGS+GEIR NCR
Sbjct: 263 QFGLLHSDQELFGAGVVDVTARYARNGAAFSSDFVTAIVKMGNISPLTGSSGEIRANCR 322

Query: 2170 RIN 2178
+ N
Sbjct: 323 KPN 325

Score = 66.6 bits (161), Expect = 2e-08
Identities = 34/62 (54%), Positives = 44/62 (70%)
Frame = +1

Query: 595 TICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
T+ +A V + G+ QLS FY SCPNL S V+S + +A+ +E RMGAS+LRLFFHDC
Sbjct: 15 TVAVACVVAL-GAMAQQLSPTFYDASCPNLQSIVRSGMAAAVQQEPRMGASILRLFFHDC 73

Query: 775 FV 780

FV
Sbjct: 74 FV 75

>emb|CAL25299.1| properoxidase [Picea abies]
Length = 341

Score = 151 bits (381), Expect = 7e-34
Identities = 86/169 (50%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
++GCDGSILLDDTSSFTGEK ANPNRNS RGF V+D IKS +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNRNSVRGFGVVDQIKSELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGNSTHTLETKFKRQGLNVVDLVALSGAHTI 208

Score = 122 bits (305), Expect = 4e-25
Identities = 65/132 (49%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGKSDPTLDTTYLKHLRAVCPQT-GTDDNQTTPLDPVTPIKFDID 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SDQ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDQILYSTKGSRTVGLVESYSTSMHAFFKQFAASMIKMGNINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 4e-07
Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYYHSCPRLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS

Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780

LLRL FHDCFV

Sbjct: 73 LLRLHFHDCFV 83

>emb|CBI15847.1| unnamed protein product [Vitis vinifera]

Length = 263

Score = 150 bits (380), Expect = 9e-34

Identities = 73/124 (58%), Positives = 94/124 (75%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYFKNLV 1986

Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV

Sbjct: 142 QSRCLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166

KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC

Sbjct: 200 DNKGLLHSDQELFNNGSTDSQVSSYASSATSFYKDFTAAMVKMGNISPLTGTKGQIRVNC 259

Query: 2167 RRIN 2178

R+IN

Sbjct: 260 RKIN 263

Score = 150 bits (378), Expect = 2e-33

Identities = 85/169 (50%), Positives = 101/169 (59%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330

+ GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AA

Sbjct: 15 VNGCDGSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGPTW V+LG

Sbjct: 75 RDSV-----VALGGPTWTVQLG 91

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I

Sbjct: 92 RRDSTTASISDAETDIPSPALDLDLISAFSDKGFSAKEMVALSGSHTI 140

>ref|XP_002451850.1| hypothetical protein SORBIDRAFT_04g008650 [Sorghum bicolor]

gb|EES04826.1| hypothetical protein SORBIDRAFT_04g008650 [Sorghum bicolor]

Length = 323

Score = 150 bits (380), Expect = 9e-34
Identities = 73/124 (58%), Positives = 92/124 (74%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSG-SGDNNLAPLDLQTPTSFDNYYFKNLV 1986
A+C +R+RIY++ NI FA T + +C T G S D NLA LD+QT FDN YF NL+
Sbjct: 200 AQCKTYRSRIYSDANINKQFANTLKGNC SATQGGSTDTNLAGLDVQTQVVF DNAYFGNLM 259

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGISPLTGSNGEIRKNC 2166
+KKGLLHSDQ+LFNGGS D++V+ Y +PG F+S F AMIKMG+ISPLTGS G+IR NC
Sbjct: 260 KKKGLLHSDQELFNGGSQDALVQQYDADPGLFASHFVTAMIKMGNISPLTGSQGGIRANC 319

Query: 2167 RRIN 2178
R+N
Sbjct: 320 GRVN 323

Score = 139 bits (350), Expect = 3e-30
Identities = 77/166 (46%), Positives = 99/166 (59%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDT-SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD SILLDD +F GEKNA PN NS G++VI+NIK+AVE CPGVVSCADI+A+A
Sbjct: 71 VQGC DASILLDDVPGTFVGEKNAGPNANSVLGYDV INNIKTAVEANCPGVVSCADIVALA 130

Query: 1328 ARDSVQIVSGQTTNKNLTN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V ++ GGPTW+V L
Sbjct: 131 ARDGVNLL-----GGPTWSVSL 147

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TASQS AN+ +P+P S+L+ LI+ F++ GL+ D+ ALSG
Sbjct: 148 GRRDSTTASQSQANS DLPSPASSLSTLIAAFASKGLNATDMTALSG 193

Score = 64.3 bits (155), Expect = 1e-07
Identities = 33/56 (58%), Positives = 41/56 (73%), Gaps = 1/56 (1%)
Frame = +1

Query: 616 VLIWGSANAQLSTNFYHSCPNLFSSVKSTVQSAISK-ETRMGASLLRLFFHDCFV 780
+L+ +A QLST+FY SCP+L S+V+S V I+ RMGASLLRLFFHDCFV
Sbjct: 16 ILLSSAAYGQLSTSFYDTSCPSLESTVRSVVG VINNGNRRMGASLLRLFFHDCFV 71

>ref|XP_002276796.1| PREDICTED: hypothetical protein [Vitis vinifera]
Length = 1225

Score = 150 bits (380), Expect = 9e-34

Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV

Sbjct: 1104 QSRCLVFRDRIYNDNIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 1161

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGBISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC

Sbjct: 1162 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFTAAMVKMGNISPLTGTKGQIRVNC 1221

Query: 2167 RRIN 2178

R+IN

Sbjct: 1222 RKIN 1225

Score = 150 bits (378), Expect = 2e-33
Identities = 85/169 (50%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AA

Sbjct: 977 VNGCDGSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAA 1036

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V+LG

Sbjct: 1037 RDSV-----VALGGPTWTVQLG 1053

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RRD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I

Sbjct: 1054 RRDSTTASISDAETDIPSPALDLDLISAFSDKGFSKEMVALSGSHTI 1102

Score = 62.8 bits (151), Expect = 3e-07
Identities = 27/52 (51%), Positives = 37/52 (71%)
Frame = +1

Query: 628 GSANAQLSTNFYYHSCPNIFFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
G ++ LS+ FY CP S++++ V +A++ E RMGASLLRL FHDCFVN

Sbjct: 927 GVVSSGLSSTFYSAKCPKALSTIRTAVNTAVANENRMGASLLRLHFHDCFVN 978

>gb|EAZ22364.1| hypothetical protein OsJ_06022 [Oryza sativa Japonica Group]
Length = 282

Score = 150 bits (380), Expect = 9e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV

Sbjct: 160 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 217

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC

Sbjct: 218 AGAGLLHSDQELFNNGPVDVSVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 277

Query: 2167 RRIN 2178

R++N

Sbjct: 278 RKNV 281

Score = 78.6 bits (192), Expect = 6e-12

Identities = 38/65 (58%), Positives = 46/65 (70%), Gaps = 1/65 (1%)

Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR

Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAVGSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQI 1348

DSV +

Sbjct: 138 DSVNL 142

Score = 61.2 bits (147), Expect = 9e-07

Identities = 28/63 (44%), Positives = 40/63 (63%)

Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD

Sbjct: 14 LLLLLAVALALAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRLFYHD 73

Query: 772 CFV 780

CFV

Sbjct: 74 CFV 76

>gb|EAY85141.1| hypothetical protein OsI_06496 [Oryza sativa Indica Group]
Length = 326

Score = 150 bits (380), Expect = 9e-34

Identities = 71/124 (57%), Positives = 92/124 (74%)

Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDSVQLYSSNAAAFSSDFAASMIRLGNIPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 119 bits (298), Expect = 3e-24
Identities = 68/164 (41%), Positives = 89/164 (54%), Gaps = 1/164 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR
Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAIGSTTVFDLVDTIKAQVEAVCPATVSCADVLAI AAR 137

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W V LGR
Sbjct: 138 DSVNL-----LGGPSWAVPLGR 154

Query: 1514 RDARTASQSAANNGIPAPTSNLNLISRF SALGLSTKDLVALSG 1645
RDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 155 RDALSPSRSAVSTDLPGP EADISALVS AFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 9e-07
Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALALAAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>tpe|CAH69268.1| TPA: class III peroxidase 26 precursor [Oryza sativa (japonica
cultivar-group)]
Length = 326

Score = 150 bits (380), Expect = 9e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDSVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 112 bits (281), Expect = 3e-22
Identities = 65/166 (39%), Positives = 88/166 (53%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNR--NSARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAIA
Sbjct: 76 VQGCDASVLLDDTPAAPGEKGVGPNAVSTTVFDLVDTIKAQVEAVCPATVSCADVLAIA 135

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
R + + LGGP+W V L
Sbjct: 136 GRR-----RVQLGGPSWAVPL 152

Query: 1508 GRRDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 153 GRRDALSPSRSAVSTDLPGPEDISALVSAFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 9e-07
Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCP NFLSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLLAVALAARARAQLSPGFYSASCTVHGVVRQVMSQAVMNDTRAGAAVLRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>ref|NP_001046393.1| Os02g0236800 [Oryza sativa (japonica cultivar-group)]
dbj|BAD27599.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
dbj|BAD29072.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
dbj|BAF08307.1| Os02g0236800 [Oryza sativa Japonica Group]
dbj|BAG91008.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG94336.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96877.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 326

Score = 150 bits (380), Expect = 9e-34
Identities = 71/124 (57%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
+A C NFR R+Y + N+ AFA ++QSCP + GD LAPLD TP +FDN Y++NLV
Sbjct: 204 RASCVNFRTRVYCDANVSPAFASHQRQSCP--ASGGDAALAPLDSLTPDAFDNGYYRNLV 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGLDISPLTGSNGEIRKNC 2166
GLLHSDQ+LFN G DS+V+ YS+N FSSDFAA+MI++G+I PLTGS GE+R NC
Sbjct: 262 AGAGLLHSDQELFNNGPVDVVQLYSSNAAAFSSDFAASMIRLGNIGPLTGSTGEVRLNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 119 bits (298), Expect = 3e-24
Identities = 68/164 (41%), Positives = 89/164 (54%), Gaps = 1/164 (0%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNR-NSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
GCD S+LLDDT + GEK PN S F+++D IK+ VE VCP VSCAD+LAI AAR
Sbjct: 78 GCDASVLLDDTPAAPGEKGVGPNAVSTTVFDLVDTIKAQVEAVCPATVSCADVLAIAAR 137

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGP+W V LGR
Sbjct: 138 DSVNL-----LGGPSWAVPLGR 154

Query: 1514 RDARTASQSAANNIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RDA + S+SA + +P P ++++ L+S F+A GLS++DL ALSG
Sbjct: 155 RDALSPSRSAVSTDLPGEADISALVSAFAAKGLSSRDLAALSG 198

Score = 61.2 bits (147), Expect = 9e-07

Identities = 28/63 (44%), Positives = 40/63 (63%)
Frame = +1

Query: 592 LTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRRLFHD 771
L + LA+ + + A AQLS FY SCP + V+ + A+ +TR GA++LRLF+HD
Sbjct: 14 LLLLAVALALAARARAQLSPGFYSASCPTVHGVVRQVMSQAVMNDTRAGAAVLRLFYHD 73

Query: 772 CFV 780
CFV
Sbjct: 74 CFV 76

>gb|ABK22680.1| unknown [Picea sitchensis]
Length = 341

Score = 150 bits (379), Expect = 1e-33
Identities = 85/169 (50%), Positives = 97/169 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
++GCDGSILLDDTSSFTGEK ANPN+NS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNKNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F LGL+ DLVALSG I
Sbjct: 160 RRDERSASKSGANNDIPGPNSTHQTLTKFKRLGLNVVDLVALSGAHTI 208

Score = 122 bits (305), Expect = 4e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGNHDPTLDTTYLKQLRAVCPQT-GTDDNQTTPLDPVTPIKFDIN 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 4e-07
Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ---LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPQAIIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>emb|CAN61440.1| hypothetical protein [Vitis vinifera]
Length = 262

Score = 150 bits (379), Expect = 1e-33
Identities = 73/124 (58%), Positives = 94/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q+RC FR RIYN+ NI+++FA + + +CP T G D+NL+ LD +P FDN YFKNLV
Sbjct: 141 QSRCLVFRDRIYNDNDIDSSFAESLKSNCPTDG--DDNLSALDDTSPVIFDNGYFKNLV 198

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KGLLHSDQ+LFN GSTDS V Y+++ +F DF AAM+KMG+ISPLTG+ G+IR NC
Sbjct: 199 DNKGLLHSDQELFNGGSTDSQVSSYASSATSFYKDFXAAMVKMGNISPLTGTKGQIRVNC 258

Query: 2167 RRIN 2178
R+IN
Sbjct: 259 RKIN 262

Score = 150 bits (378), Expect = 2e-33
Identities = 85/168 (50%), Positives = 101/168 (60%)
Frame = +2

Query: 1154 QGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AAR 1333
+GCDGSILLDDT++FTGEK A PN +S RGFEVID+IKS VE VCPGVV+CADILA+AAR
Sbjct: 15 KGCDSILLDDTANFTGEKTAGPNADSVRGFEVIDDIKSRVESVCPGVVTCADILAVAAR 74

Query: 1334 DSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1513
DSV + LGGPTW V+LGR
Sbjct: 75 DSV-----VALGGPTWTVQLGR 91

Query: 1514 RDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

RD+ TAS S A IP+P +L+ LIS FS G S K++VALSG+ I
Sbjct: 92 RDSTTASISDAETDIPSPALDLDLISAFSDKGFSKEMVALSGSHTI 139

>gb|AAC31550.1| peroxidase PXC2 precursor [Avena sativa]
Length = 313

Score = 150 bits (379), Expect = 1e-33
Identities = 71/126 (56%), Positives = 97/126 (76%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKN 1980
QA+C NFR+RIY +TNI AFA + Q +CP+ T GSGD++LAPLD +TP +FDN Y+ N
Sbjct: 187 QAQCKNFRSRIYGGDTNINAAFATSLQANCPQATGGSGDSSLAPLDTKTPNAFDNSYYNN 246

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
L+ +KGLLHSDQ LFN G+TD+ VR +++++ F+ F AMIKMG+ISPLTG+ G+IR
Sbjct: 247 LLSQKGLLHSDQVLFNNGTTDNTVRNFASSASAFTGAFTTAMIKMGNISPLTGTQGQIRL 306

Query: 2161 NCRRIN 2178
+C ++N
Sbjct: 307 SCSKVN 312

Score = 105 bits (261), Expect = 6e-20
Identities = 69/167 (41%), Positives = 84/167 (50%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCD S+LL E+NA PN S RGF VIDNIK+ VE VC VSC DILA+AARD
Sbjct: 69 GCDASVLLSGN-----EQNAAPNAGSLRGFSVIDNIKTQVEAVCKQTVSCDDILAVAARD 123

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGP+W V LGRR
Sbjct: 124 SV-----VALGGPSWTVPLGRR 140

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ +A+ + + +PAPTS+L QL + FS L T D+VALSG I
Sbjct: 141 DSTSATGNTGD--LPAPTSSLAQLQAASFKNLDTTDMVALSGAHTI 185

Score = 65.5 bits (158), Expect = 5e-08
Identities = 32/64 (50%), Positives = 45/64 (70%)
Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
S +++ + L L +A+AQLS+ FY SCP +++KS V +A+S + RMGASLLRL F

Sbjct: 5 SCISLRVMLVALAATAASAQLSSTFYDTSCPKALATIKSGVAAVSSDRRMGASLLRLHF 64

Query: 766 HDCF 777

HDCF

Sbjct: 65 HDCF 68

>gb|AAC31551.1| peroxidase PXC6 precursor [Avena sativa]

Length = 314

Score = 150 bits (379), Expect = 1e-33

Identities = 71/126 (56%), Positives = 97/126 (76%), Gaps = 2/126 (1%)

Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPR-TSGSGDNNLAPLDLQTPTSFDNYYFKN 1980

QA+C NFR+RIY +TNI AFA + Q +CP+ T GSGD++LAPLD +TP +FDN Y+ N

Sbjct: 188 QAQCKNFRSRIYGGDTNINAAFATSLQANCPQATGGSGDSSLAPLDTKTPNAFDNSYNN 247

Query: 1981 LVQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160

L+ +KGLLHSDQ LFN G+TD+ VR ++++ F+ F AMIKMG+ISPLTG+ G+IR

Sbjct: 248 LLSQKGLLHSDQVLFNNGTTDNTVRNFASSASAFTGAFTAMIKMGNISPLTGTQGGIRL 307

Query: 2161 NCRRIN 2178

+C ++N

Sbjct: 308 SCSKVN 313

Score = 94.0 bits (232), Expect = 1e-16

Identities = 68/168 (40%), Positives = 82/168 (48%), Gaps = 1/168 (0%)

Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336

GCD S+LL E+NA PN S RGF VIDNIK+ VE VC VSCADILA+AARD

Sbjct: 69 GCDASVLLSGN-----EQNAAPNAGSLRGFSVIDNIKTQVEAVCKQTVSCADILAVAARD 123

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGP-TWNVKLGR 1513

SV + LGGP V LGR

Sbjct: 124 SV-----VALGGPFLEQVPLGR 140

Query: 1514 RDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657

RD+ +A+ + + +PAPTS+L QL + FS L T +VALSG I

Sbjct: 141 RDSTSATGNTGD--LPAPTSSLAQLQAAFSKKNLDTTGMVALSGAHTI 186

Score = 65.5 bits (158), Expect = 5e-08

Identities = 32/64 (50%), Positives = 45/64 (70%)

Frame = +1

Query: 586 SRLTICLALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFF 765
S +++ + L L +A+AQLS+ FY SCP +++KS V +A+S + RMGASLLRL F
Sbjct: 5 SCISLRVMLVALAATAASAQLSSTFYDTSCP KALATIKSGVAAVSSDRRMGASLLRLHF 64

Query: 766 HDCF 777
HDCF
Sbjct: 65 HDCF 68

>emb|CAA71492.1| peroxidase [Spinacia oleracea]
Length = 315

Score = 149 bits (375), Expect = 3e-33
Identities = 81/165 (49%), Positives = 101/165 (61%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAIAA 1330
+ GCDGSILLDDTS+F GEK A PN+NS RGF+ +D+IK+++EK CPGVVSCADILAIA+
Sbjct: 66 VNGCDGSILLDDTSTFRGEKTAIPKNNSVRGFKAVDSIKASLEKACPGVVSCADILAIA 125

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD+V + GGPTW V+LG
Sbjct: 126 RDAV-----VQYGGPTWQVRLG 142

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSA LGLSTKDLVALSG 1645
RRD+ TA++SAAN IPAP+ NL L S F+ +GLS KD+V LSG
Sbjct: 143 RRDSLTANRSAANAFIPAPSFNLRNLTSFTTVGLSFKDMVVLSG 187

Score = 133 bits (335), Expect = 1e-28
Identities = 66/124 (53%), Positives = 93/124 (75%), Gaps = 1/124 (0%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
ARCT+FR I+N+TNI AFA++ Q+ CP+ SG+G L PLD QT FD+ Y++NL+
Sbjct: 194 ARCTSFRPHIHNDTNINAFAKSLQKKCPQ-SGNG-KVLQPLDYQTKFRFDDKYYQNLLV 251

Query: 1990 KKGLLHSDQQLFNGGST-DSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQQL++G + D+ VR Y++ G F +F +MI+MG+I PLTG++G+IR+NC
Sbjct: 252 KKGLLHSDQQLYSGNNNADAYVRKYASKQGEFFQEFGNSMIRMGNIKPLTGTHGQIRRNC 311

Query: 2167 RRIN 2178
R+ N
Sbjct: 312 RKS N 315

Score = 64.3 bits (155), Expect = 1e-07
Identities = 29/51 (56%), Positives = 34/51 (66%)
Frame = +1

Query: 631 SANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLLFFHDCFVN 783
+ N QLS NFY +CPN VK + I KE R+GAS+LRL FHDCFVN
Sbjct: 17 TVNGQLSPNFYSSTCPNALRIVKQGIKRIKKEARVGASILRLHFHDCFVN 67

>ref|NP_001054096.1| Os04g0651000 [Oryza sativa (japonica cultivar-group)]
emb|CAE04507.2| OSJNBb0059K02.17 [Oryza sativa (japonica cultivar-group)]
tpe|CAH69299.1| TPA: class III peroxidase 57 precursor [Oryza sativa (japonica
cultivar-group)]
dbj|BAF16010.1| Os04g0651000 [Oryza sativa Japonica Group]
dbj|BAG98582.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 319

Score = 149 bits (375), Expect = 3e-33
Identities = 82/169 (48%), Positives = 99/169 (58%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AA
Sbjct: 70 VNGCDGSVLLDDTAAITGEKNAKPNKNSLRGFEVVDDIKSQLEDACEQVSCADILAVAA 129

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW+V+LG
Sbjct: 130 RDSV-----VALGGPTWDVELG 146

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 147 RRDGTTASLDAANNLPPPTSDLADLIKSFSKGLTASDMIALSGAHTI 195

Score = 148 bits (373), Expect = 6e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 197 QARCTNFRGRLYNETNLATLATS LKPSCPNPTG-GDDNTAPLDPATSYVFDNFYRNLL 255

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 256 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 315

Query: 2167 RRIN 2178
R++N

Sbjct: 316 RKNV 319

Score = 74.7 bits (182), Expect = 8e-11
Identities = 34/70 (48%), Positives = 52/70 (74%), Gaps = 1/70 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSNAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLL 753
++ ++ +C A+ L++ + +AQLST+FY +CP+ ++S V+ A+SKE+RMGASLL
Sbjct: 2 AYSRQIFVCSAMAALLFSAVVSAQLSTDFYDETCPDALDIIESAVRDAVSKESRMGASLL 61

Query: 754 RLFFHDCFVN 783
RL FHDCFVN
Sbjct: 62 RLHFHDCFVN 71

>ref|XP_002308244.1| predicted protein [Populus trichocarpa]
gb|EEE91767.1| predicted protein [Populus trichocarpa]
Length = 321

Score = 149 bits (375), Expect = 3e-33
Identities = 71/123 (57%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
A+C F+ RIYNETNI+ FAR R+ +CPRT G D+NLAPL+ TP+ FD Y+ +L++
Sbjct: 202 AQCFTFKDRIYNETNIDPKFARERKLTCPRTGG--DSNLAPLN-PTPSYFDARYYNDLLK 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
K+GL HSDQ LFNGGSTDS+V+ YS+N F +DFA +M+KMG+I+PLTG G+ R NCR
Sbjct: 259 KRGLFHSDQALFNGGSTDSLKAYSSNAKAFWTFANSMVKMGNIPLTGKQGQTRLNCR 318

Query: 2170 RIN 2178
++N
Sbjct: 319 KVN 321

Score = 135 bits (339), Expect = 5e-29
Identities = 82/166 (49%), Positives = 93/166 (56%), Gaps = 1/166 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+F EKNANPN NS RGFEVID IK V+K C VVSCADILA+A
Sbjct: 73 VNGCDASILLDSTSAFDSEKNANPNINSIRGFEVIDRIKLEVDKACGRPVVSCADILAVA 132

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGPTW V+L

Sbjct: 133 ARDSV-----VALGGPTWAVQL 149

Query: 1508 GRRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
GRRD+ TAS++ ANN IPAP +L LI F GL+ KDLV LSG

Sbjct: 150 GRRDSTTASKTTANNDIPAPFMDLPDLIINFKKHGLNKKDLVVLSG 195

Score = 64.3 bits (155), Expect = 1e-07
Identities = 34/76 (44%), Positives = 47/76 (61%)
Frame = +1

Query: 556 LSKLTMAFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPFLSSVKSTVQSAISKETR 735
++ L + S S L + LAL S++ LS N+Y + CP ++K V++A+ E R

Sbjct: 1 MASLGIFSLISTLFLVLALATT--ASSSKGLSPNYYDYVCPKALPTIKRVVEAAVYNERR 58

Query: 736 MGASLLRLFFHDCFVN 783
MGASLLRL FHDCFVN

Sbjct: 59 MGASLLRLHFHDCFVN 74

>emb|CBI19222.1| unnamed protein product [Vitis vinifera]
Length = 255

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 101/167 (60%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCD SILLDDT++FTGEK A PN NS RG++VID IKS +E +CPGVVSCADI+A+AARD

Sbjct: 17 GCDASILLDDTANFTGEKTAGPNNNSLRGYDVIDTIKSMESLCPGVVSCADIVAVAARD 76

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGR 1516
SV + LGGPTW V++GRR

Sbjct: 77 SV-----VALGGPTWTVMGR 93

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D+ TAS S AN +PAPTS+L+ L S FS G +T+++VALSGT I

Sbjct: 94 DSTTASLSTANADLPAPTSDDLVLTSLSFKGFTTQEMVALSGTHTI 140

Score = 126 bits (317), Expect = 2e-26
Identities = 62/106 (58%), Positives = 82/106 (77%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPSFNYYFKNLV 1986
+A+C FR RIYNETN++ AFA+++Q+ CP T G D NL+ LD +T T FD YFK+L+

Sbjct: 142 KAQCIKFRYRIYNETNVDAFAKSKQKICPWTGG--DENLSDLD-ETTTVFDTVYFKDLI 198

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDI 2124
+KKGLLHSDQQL+NG STDS+V YST+ TF +D A AM+KMG++
Sbjct: 199 EKKGLLHSDQQLYNGNSTDSMVETYSTDSTTFFTDVANAMVKMGNL 244

>ref|XP_002467656.1| hypothetical protein SORBIDRAFT_01g031740 [Sorghum bicolor]
gb|EER94654.1| hypothetical protein SORBIDRAFT_01g031740 [Sorghum bicolor]
Length = 344

Score = 148 bits (374), Expect = 4e-33
Identities = 83/165 (50%), Positives = 98/165 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILATAA 1330
+QGCD S+LLDDT+SFTGEK A PN S RGF+VIDNIK +E +CP VSCADILA+AA
Sbjct: 92 VQGCDASVLLDDTASFTGEKGAGPNAGSLRGFDVIDNIKMLLELLCPQTVSCADILAVAA 151

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV LGGP+W+V LG
Sbjct: 152 RDSVAQ-----LGGPSWSVPLG 168

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSG 1645
RRDA TAS S AN+ +P PTSNLN L++ FS GLS+ D+VALSG
Sbjct: 169 RRDATTASASLANSDLPGPTSNLNGLLNAFSNKGLSSTDMVALSG 213

Score = 143 bits (361), Expect = 1e-31
Identities = 69/126 (54%), Positives = 95/126 (75%), Gaps = 2/126 (1%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCP-RTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
+A+C N R+RIYN+T+I+ +A + + SCP + G+ D L PLD TP +FDN YF NL
Sbjct: 219 RAQCKNIRSRIYNDTDIDATYAASLRASCPAQAGGASDGALEPLDDATPDADFNDAYFGNL 278

Query: 1984 VQKKGLLHSDQQLFNGG-STDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRK 2160
+ ++GLLHSDQ LF GG +TD +V Y+++ + SDFAAAM+KMG+ISPLTG++GEIR
Sbjct: 279 LSQRGLLHSDQALFGGGGATDGLVSTYASSADQWGSDFAAAMVKMGNISPLTGTGGEIRV 338

Query: 2161 NCRRIN 2178
NCRR+N
Sbjct: 339 NCRRVN 344

Score = 55.5 bits (132), Expect = 5e-05
Identities = 29/65 (44%), Positives = 42/65 (64%), Gaps = 5/65 (7%)
Frame = +1

Query: 601 CLALFVLIWGSA----NAQLSTNFYYH-SCPNLFSSVKSTVQSAISKETRMGASLLRLFF 765
CL + ++ +A +AQLS+ YY SCP +++++ V +A+ + RMGASLLRL F
Sbjct: 28 CLLILIVALAAAAVASAQLSSEDYYDASCPAALFTIRTAVSTAVLLDRRMGASLLRLHF 87

Query: 766 HDCFV 780
HDCFV
Sbjct: 88 HDCFV 92

>gb|EEE61812.1| hypothetical protein OsJ_16433 [Oryza sativa Japonica Group]
Length = 1129

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGF EV+D+IKS +E C VVSCADILA+AARD
Sbjct: 78 GCDGSVLLDDTAAITGEKNAKPNKNSLRGF EVVDDIKS QLEDACEQV VSCADILAVAARD 137

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISK LITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 138 SV-----VALGGPTWDVELGRR 154

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 155 DGTASLDAANNDLPPTS D LADLIKSFSDKGLTASDMIALSGAHTI 201

Score = 134 bits (336), Expect = 1e-28
Identities = 63/115 (54%), Positives = 82/115 (71%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 203 QARCTNFRGRLYNETNLDATLATS LKPSCPNPTG-GDDNTAPLDPATSYVFDNFY YRNLL 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGE 2151
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G+
Sbjct: 262 RNKGLLHSDQQLFSGGSADAQT TAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQ 316

Score = 69.7 bits (169), Expect = 3e-09
Identities = 31/49 (63%), Positives = 40/49 (81%)
Frame = +1

Query: 637 NAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783
+AQLST+FY +CP+ ++S V+ A+SKE+RMGASLLRL FHDCFVN
Sbjct: 11 SAQLSTDFYDETCPDALDIIESAVRDAVSKE SRMGASLLRLHFHDCFVN 59

>gb|EEC78144.1| hypothetical protein OsI_17703 [Oryza sativa Indica Group]
Length = 325

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AARD
Sbjct: 78 GCDGSVLLDDTAAITGEKNAKPNKNSLRGFEVVDDIKSQLEDACEQVVSCADILAVAARD 137

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 138 SV-----VALGGPTWDVELGRR 154

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 155 DGTASLDAANNDLPPTS DLA DLIKSFS DKGLTASDMIALSGAHTI 201

Score = 148 bits (373), Expect = 6e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 203 QARCTNFRGRLYNETNL DATLATS LKPSCPNPTG-GDDNTAPLDPATSYVFDNFYYRNLL 261

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GG S D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 262 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGGIGVVTGSGGQVRVNC 321

Query: 2167 RRIN 2178
R++N
Sbjct: 322 RKNV 325

Score = 70.1 bits (170), Expect = 2e-09
Identities = 31/49 (63%), Positives = 41/49 (83%)
Frame = +1

Query: 637 NAQLSTNFYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFVN 783

+AQLST+FY +CP+ ++S V++A+SKE+RMGASLLRL FHDCFVN
Sbjct: 11 SAQLSTDFYDETCPDALDIIESAVRAAVSKESRMGASLLRLHFHDCFVN 59

>emb|CAJ86184.1| H0212B02.16 [Oryza sativa (indica cultivar-group)]
emb|CAJ86323.1| OSIGBa0113E10.6 [Oryza sativa (indica cultivar-group)]
Length = 337

Score = 148 bits (374), Expect = 4e-33
Identities = 82/167 (49%), Positives = 98/167 (58%)
Frame = +2

Query: 1157 GCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI AARD 1336
GCDGS+LLDDT++ TGEKNA PN+NS RGFEV+D+IKS +E C VVSCADILA+AARD
Sbjct: 90 GCDGSVLLDDTAAITGEKNAKPNKNSLRGFVVDDIKSQLEDACEQV VSCADILAVAARD 149

Query: 1337 SVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLGRR 1516
SV + LGGPTW+V+LGRR
Sbjct: 150 SV-----VALGGPTWDVELGRR 166

Query: 1517 DARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
D TAS AANN +P PTS+L LI FS GL+ D++ALSG I
Sbjct: 167 DGTASLDAANNDLPPTSDLADLIKSFSKGLTASDMIALSGAHTI 213

Score = 148 bits (373), Expect = 6e-33
Identities = 68/124 (54%), Positives = 90/124 (72%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNAPLDLQTPTSFDNYYFKNLV 1986
QARCTNFR R+YNETN++ A + + SCP +G GD+N APLD T FDN+Y++NL+
Sbjct: 215 QARCTNFRGRLYNETNLATLATS LKPSCPNPTG-GDDNTAPLDPATSYVFDNFYYRNLL 273

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+ KGLLHSDQQLF+GGS D+ Y+T+ F DF AM+KMG I +TGS G++R NC
Sbjct: 274 RNKGLLHSDQQLFSGGSADAQTAYATDMAGFFDDFRGAMVKMGIGVVTGSGGQVRVNC 333

Query: 2167 RRIN 2178
R++N
Sbjct: 334 RKNV 337

Score = 75.1 bits (183), Expect = 6e-11
Identities = 34/70 (48%), Positives = 53/70 (75%), Gaps = 1/70 (1%)
Frame = +1

Query: 577 SFCSRLTICLALFVLIWGSA-NAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLL 753

++ ++ +C A+ L++ + +AQLST+FY +CP+ ++S V++A+SKE+RMGASLL
Sbjct: 2 AYSRQIFVCSAMAALLFSAVVSAQLSTDFYDETCPDALDIIESAVRAAVSKESRMGASLL 61

Query: 754 RLFFHDCFVN 783

RL FHDCFVN

Sbjct: 62 RLHFHDCFVN 71

>gb|EAZ22372.1| hypothetical protein OsJ_06030 [Oryza sativa Japonica Group]
Length = 257

Score = 148 bits (374), Expect = 4e-33
Identities = 69/123 (56%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLVQ 1989

A CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT +FDN Y+ NL+

Sbjct: 135 ALCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNAFDNAYYGNNLV 194

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169

++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR

Sbjct: 195 RRGLLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 252

Query: 2170 RIN 2178

+N

Sbjct: 253 VVN 255

Score = 93.6 bits (231), Expect = 2e-16
Identities = 46/68 (67%), Positives = 53/68 (77%), Gaps = 2/68 (2%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324

+QGCD SILLDD + F GEK A PN NS RG+EVID IK+ VE VCPGVVSCADI+A+

Sbjct: 69 VQGCDASILLDDVPATGFVGEKTAAPNNNSVRGYEVIDQIKANVEDVCPGVVSCADIVAL 128

Query: 1325 AARDSVQI 1348

AARDS +

Sbjct: 129 AARDSTAL 136

Score = 70.1 bits (170), Expect = 2e-09
Identities = 34/59 (57%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPNISSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780

L +F L+ A+ QLST++Y SCP++ V +TV SAI E RMGASL+RLFFHDCFV

Sbjct: 11 LLVFLLSDDASGQLSTSYADSCPSVEKVVHATVASAIQAERRMGASLIRLFFHDCFV 69

>ref|NP_001046401.1| Os02g0240300 [Oryza sativa (japonica cultivar-group)]
dbj|BAD28871.1| putative bacterial-induced peroxidase precursor [Oryza sativa Japonica Group]
tpe|CAH69271.1| TPA: class III peroxidase 29 precursor [Oryza sativa (japonica cultivar-group)]
dbj|BAF08315.1| Os02g0240300 [Oryza sativa Japonica Group]
dbj|BAG90221.1| unnamed protein product [Oryza sativa Japonica Group]
dbj|BAG96858.1| unnamed protein product [Oryza sativa Japonica Group]
Length = 321

Score = 148 bits (374), Expect = 4e-33
Identities = 68/123 (55%), Positives = 95/123 (77%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT +FDN Y+ NL+
Sbjct: 199 SQCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNAFDNAYYGNNLV 258

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR
Sbjct: 259 RRGLLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 316

Query: 2170 RIN 2178
+N
Sbjct: 317 VVN 319

Score = 137 bits (344), Expect = 1e-29
Identities = 79/168 (47%), Positives = 95/168 (56%), Gaps = 2/168 (1%)
Frame = +2

Query: 1151 MQGCDGSILLDDT--SSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1324
+QGCD SILLDD + F GEK A PN NS RG+EVID IK+ VE VCPGVVSCADI+A+
Sbjct: 69 VQGCDASILLDDVPATGFVGEKTAAPNNNSVRGYEVIDQIKANVEDVCPGVVSCADIVAL 128

Query: 1325 AARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVK 1504
AARDS + LGGP+W V
Sbjct: 129 AARDSTAL-----LGGPSWAVP 145

Query: 1505 LGRRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGT 1648
LGR D+ TAS+S AN+ +P P SNL LI+RF GLS +D+ ALSG+
Sbjct: 146 LGRCDSTTASRSEANSDLPGPGSNLTMLIARFGNKGLSPRDMTALSGS 193

Score = 70.1 bits (170), Expect = 2e-09
Identities = 34/59 (57%), Positives = 43/59 (72%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
L +F L+ A+ QLST++Y SCP++ V +TV SAI E RMGASL+RLFFHDCFV
Sbjct: 11 LLVFLLSDDASGQLSTSYADSCPSVEKVHATVASAIQAERRMGASLIRLFFHDCFV 69

>gb|ABK21983.1| unknown [Picea sitchensis]
Length = 341

Score = 148 bits (373), Expect = 6e-33
Identities = 84/169 (49%), Positives = 96/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
++GCDGSILLDDTSSFTGEK ANPN+NS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTGEKTANPNKNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGNSTHTLETKFQRQLNVVDLVALSGAHTI 208

Score = 121 bits (304), Expect = 6e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFARLYNQTVNGKPDPTLDTTYLKQLRAVCPQT-GTDDNQTPDPVTPIKFDID 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142
Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N
Sbjct: 330 HGEIRKNCRRMN 341

Score = 62.4 bits (150), Expect = 4e-07

Identities = 37/71 (52%), Positives = 45/71 (63%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYYHSCP NLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE RM AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYYKSCPKAQAIKSVVEDAVRKEARMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>ref|XP_002461210.1| hypothetical protein SORBIDRAFT_02g042860 [Sorghum bicolor]
gb|EER97731.1| hypothetical protein SORBIDRAFT_02g042860 [Sorghum bicolor]
Length = 313

Score = 148 bits (373), Expect = 6e-33
Identities = 70/124 (56%), Positives = 93/124 (75%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C+NF IYN+TNI+ AFA + Q +CP SG +LAPLD TPT+FDN Y+ NL+
Sbjct: 191 QAQCSNFNDHIYNDTNIDAAFATSLQANCP---ASGSTSLAPLDTMTPTTFDNDYYTNLM 247

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ+LFN GSTDS V ++++ F+S F AAM+KMG++SPLTG++GEIR C
Sbjct: 248 SQKGLLHSDQQLFNGGSTDSTVSNFASSASAFTSAFTAAMVKMGNLSPLTGTGEIRLAC 307

Query: 2167 RRIN 2178
+N
Sbjct: 308 GIVN 311

Score = 123 bits (309), Expect = 2e-25
Identities = 76/169 (44%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LL+DTS GE+++ PN+ S R F+VID+IK+ VE VCPGVVSCADILA+AA
Sbjct: 68 VHGCDGSVLLNDTS---GEQSSPPNKGSLRRFDVIDSIKAQVEAVCPGVVSCADILAVAA 124

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 125 RDSV-----VALGGPSWTVLLG 141

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS + +PAPTS+L QL+S FS L D+VALSG I
Sbjct: 142 RRDS-TASFPSETTDLPAPTSSLQQLLSLFSNKNLDATDMVALSGAHTI 189

Score = 68.2 bits (165), Expect = 8e-09
Identities = 34/63 (53%), Positives = 44/63 (69%), Gaps = 2/63 (3%)
Frame = +1

Query: 601 CLALFVL--IWGSANAQLSTNFYYHSCPNI FSSVKSTVQSAISKETRMGASLLRLFFHDC 774
CLA V + A+AQLS+ FY SCPN S++KS V +A+ +E R GASLLR+ FHDC
Sbjct: 7 CLAFLVAAAVASVASAQLSSTFYDTSCPINALSTIKSGVDAAVMQEARTGASLLRMHFHDC 66

Query: 775 FVN 783
FV+
Sbjct: 67 FVH 69

>emb|CBI18065.1| unnamed protein product [Vitis vinifera]
Length = 413

Score = 147 bits (372), Expect = 8e-33
Identities = 83/169 (49%), Positives = 101/169 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+ GCD SILLDDTS+FTGEK A PN NS RG+EV+D IKS +E CPGVVSCADILA+AA
Sbjct: 15 VNGCDASILLDDTSNFTGEKTAGPNANSVRGYEVVDTIKSQLEASCPGVVSCADILAVAA 74

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + L GP+W V+LG
Sbjct: 75 RDSV-----VALRGPSWMVRLG 91

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS SAAN+ IPAPT NL+ LIS F+ G + +++VALSG+ I
Sbjct: 92 RRDSTTASLSAANSNIPAPTLNLSGLISAFTNKGFNAREMVALSGSHTI 140

Score = 136 bits (343), Expect = 2e-29
Identities = 66/101 (65%), Positives = 77/101 (76%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFNYYFKNLV 1986
QARCT FR RIYNE NI+ +F + Q +CP S GDN L+PLD QTPT+FDN Y+ NLV
Sbjct: 142 QARCTTFRTRIYNEANIDASFKTSLQANCP--SSGGDNTLSPLDTQTPTTFDNAYYTNLV 199

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMI 2109
KKGLLHSDQQLFNGGST++V YST TF +DFA AM+
Sbjct: 200 NKKGLLHSDQQLFNGGSTDAVVNTYSTRSTTFFTFDFANAMM 240

Score = 106 bits (265), Expect = 2e-20
Identities = 64/139 (46%), Positives = 77/139 (55%), Gaps = 1/139 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC-PGVVSCADILAIA 1327
+ GCD SILLD TS+ EKNA N NSARGF V+D+IKS V+KVC VVSCADILA+A
Sbjct: 309 VNGCDASILLDATSTIDSEKNAGANANSARGFNVVDDIKSQVDKVCGRPVVSCADILAVA 368

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARDSV + LGGP+W V+L
Sbjct: 369 ARDSV-----VALGGPSWTVQL 385

Query: 1508 GRRDARTASQSAANNGIPA 1564
GRRD+ TAS++ ANN IP+
Sbjct: 386 GRRDSTTASRTDANNIPS 404

Score = 68.2 bits (165), Expect = 8e-09
Identities = 40/89 (44%), Positives = 49/89 (55%), Gaps = 4/89 (4%)
Frame = +1

Query: 529 NT*STKLVL-SKLTMASFCSRLTICLALFVLI---WGSANAQLSTNFYYHSCPRLFSSV 696
NT ST+ + A SR +CL FVL +A LS FY CP ++
Sbjct: 222 NTYSTRSTTFFTFDFANAMMASRLLCLYAFVLFLSLATADFSAAALSPYFYNKVC PKALPTI 281

Query: 697 KSTVQSAISKETRMGASLLRLFFHDCFVN 783
K V++A+ KE RMGASLLRL FHDCFVN
Sbjct: 282 KRVVEAAVQKEKRMGASLLRLHFHDCFVN 310

>gb|ACF08091.1| class III peroxidase [Triticum aestivum]
Length = 316

Score = 147 bits (372), Expect = 8e-33
Identities = 69/125 (55%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTS GSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL
Sbjct: 191 QACSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTGGQIRLS 310

Query: 2164 CRRIN 2178

C R+N
Sbjct: 311 CSRVN 315

Score = 94.4 bits (233), Expect = 1e-16
Identities = 63/170 (37%), Positives = 85/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 68 VQGCDA SVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VA SG I
Sbjct: 140 RRDSIDANEAEANS DLPGFNSSRSELEAAFLRKGLNTVDMVAPSGAHTI 189

Score = 66.6 bits (161), Expect = 2e-08
Identities = 33/62 (53%), Positives = 44/62 (70%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L VL+ +A+ QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAASGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|EAY85149.1| hypothetical protein OsI_06504 [Oryza sativa Indica Group]
Length = 135

Score = 147 bits (372), Expect = 8e-33
Identities = 69/123 (56%), Positives = 94/123 (76%)
Frame = +1

Query: 1810 ARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLVQ 1989
++CTNFRA IYN+ NI+ +FA R+++CP + +GD NLAPLD+QT FDN Y+ NL+
Sbjct: 13 SQCTNFRAHIYNDANIDPSFAALRRRACPAAPNGDTNLAPLDVQTQNLFDNAYYGNLLV 72

Query: 1990 KKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNCR 2169
++GLLHSDQ LFNGGS D++VR Y+ NP F++DFA AM+KMG+I S+GE+R +CR

Sbjct: 73 RRGLHSDQVLFNGGSQDALVRQYAANPALFAADFAKAMVKMGNIG--QPSDGEVRCDCR 130

Query: 2170 RIN 2178

IN

Sbjct: 131 FIN 133

>gb|AAW52716.1| peroxidase 2 [Triticum monococcum]

Length = 316

Score = 147 bits (372), Expect = 8e-33

Identities = 69/125 (55%), Positives = 94/125 (75%), Gaps = 1/125 (0%)

Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983

QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL

Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163

+ ++GLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +

Sbjct: 251 MSQRGLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTQQQIRLS 310

Query: 2164 CRRIN 2178

C R+N

Sbjct: 311 CSRVN 315

Score = 97.1 bits (240), Expect = 2e-17

Identities = 64/170 (37%), Positives = 86/170 (50%), Gaps = 1/170 (0%)

Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330

+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA

Sbjct: 68 VQGCDA SVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQTVSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510

RDSV + LGGP+W V LG

Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNIGIPAPTSNLNLISRFSAL-GLSTKDLVALSGTKHI 1657

RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VALSG I

Sbjct: 140 RRDSIDANEAEANS DLPGFNSSRSELEAAFLRKGLNTVDMVALSGAHTI 189

Score = 66.6 bits (161), Expect = 2e-08

Identities = 33/62 (53%), Positives = 44/62 (70%), Gaps = 2/62 (3%)

Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L VL+ +A+ QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAASGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|AAA32972.1| peroxidase [Hordeum vulgare]
Length = 315

Score = 147 bits (372), Expect = 8e-33
Identities = 70/125 (56%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI TA+A + + +CP+T GSGD +LA LD T +FDN Y+ NL
Sbjct: 190 QAQCSTFRARIYGGDTNINTAYAASLRANCPQTVGSGDGLANLDTTANTFDNAYYTNL 249

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ +KGLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 250 MSQKGLLHSDQVLFNNDTTDNTVRNFASNPAAFSSAFTTAMIKMGNIAPKTGTQQGIRLS 309

Query: 2164 CRRIN 2178
C R+N
Sbjct: 310 CSRVN 314

Score = 95.9 bits (237), Expect = 3e-17
Identities = 64/170 (37%), Positives = 84/170 (49%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAIAA 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 67 VQGCDAVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQT TNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 122 RDSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRF-SALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN +P S+ +L + F GL+T D+VALSG I
Sbjct: 139 RRDSIDANENEANTDLPGFNSSRAEEAAFLKKGGLNTVDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 5e-08
Identities = 31/59 (52%), Positives = 42/59 (71%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
L + V + +A+AQLS FY SCP +++KS V +A++ + RMGASLLRL FHDCFV
Sbjct: 9 LLVLVALVTAASAQLSPTFYDTSCP RALATIKSGVMAAVTSDPRMGASLLRLHFHDCFV 67

>emb|CBI22008.1| unnamed protein product [*Vitis vinifera*]
Length = 154

Score = 147 bits (371), Expect = 1e-32
Identities = 82/163 (50%), Positives = 97/163 (59%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCD SILLDDT++FTGEKNA PN+NS RGFEVID IK+ VE C VSCADILA+AA
Sbjct: 25 VNGCDASILLDDTATFTGEKNALPNQNSVRGFEVIDTIKTRVEAACKATVSCADILALAA 84

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RD V + LGGP+W V LG
Sbjct: 85 RDGVVL-----LGGPSWTVPLG 101

Query: 1511 RRDARTASQSAANN GIPAPTSNLNLISRFSALGLSTKDLVAL 1639
RRDARTA+QSAANN +PAP +NL+ LIS F+A GL+ D+ AL
Sbjct: 102 RRDARTANQSAANN DLPAPFANLSALISGFAAKGLNADDMTAL 144

Score = 43.5 bits (101), Expect = 0.20
Identities = 18/23 (78%), Positives = 21/23 (91%)
Frame = +1

Query: 715 AISKETRMGASLLRLFFHDCFVN 783
A+ +E RMGAS+LRLFFHDCFVN
Sbjct: 4 AVIREPRMGASILRLFFHDCFVN 26

>gb|ACD70388.1| class III peroxidase [*Triticum aestivum*]
Length = 316

Score = 147 bits (371), Expect = 1e-32
Identities = 70/124 (56%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR RIYNETNI+TAF + + +CPR+ G DN+LAPLD TP FDN Y+ NL+
Sbjct: 194 QSQCRFFRDRIYNETNIDTAFATSLRANCPRSGG--DNSLAPLDTGTPNGFDNAYYT NLM 251

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
+KGLLHSDQ LFNGG D+ VR +S++ TF+S F AMI MG+I+P TG+ G+IR C
Sbjct: 252 SQKGLLHSDQVLFNGGGADNTVRSFSSSAATFNSAFTTAMINMGNIAPKTGTQGQIRLVC 311

Query: 2167 RRIN 2178
++N
Sbjct: 312 SKVN 315

Score = 127 bits (320), Expect = 8e-27
Identities = 76/169 (44%), Positives = 89/169 (52%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI AA 1330
+ GCDGS+LL DT SF GE+ A PN NS RG VIDNIK+ VE VC VSCADILA+AA
Sbjct: 67 VDGCDGSVLLADTGSFIGEQGAAPNNNSIRGMNVIDNIKTQVEAVCKQTVSCADILAVAA 126

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGPTW V LG
Sbjct: 127 RDSV-----VALGGPTWTVLLG 143

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657
RRD+ TAS++ A N +P PT +L L + F LS D+VALSG I
Sbjct: 144 RRDSTTASKTNAENDLPPPTFDLQNLTTLFGNKQLSMTDMVALSGAHTI 192

Score = 70.1 bits (170), Expect = 2e-09
Identities = 34/63 (53%), Positives = 46/63 (73%), Gaps = 2/63 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCPNLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
CL L VL+ +A+AQLS+ FY SCPN +++K+ V +A+ E RMGASL+RL FHDC
Sbjct: 6 CLGLVVLVAMASAASAQLSSTFYDTSCPNALATIKAGVTAAVQNEARMGASLVRHLFHDC 65

Query: 775 FVN 783
FV+
Sbjct: 66 FVD 68

>gb|ABF48527.1| cell wall peroxidase [Capsicum annuum]
gb|ABG73021.1| cell wall peroxidase [Capsicum annuum]
Length = 322

Score = 147 bits (370), Expect = 1e-32
Identities = 79/125 (63%), Positives = 91/125 (72%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIY-NETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
 QA+C FR RIY N T+I+ FA TR++ CP+ +G NLAPLDL TP DN YFKNL
 Sbjct: 200 QACFLFRDRIYSNGTDIDAGFASTRRRRCQEDQNG--NLAPLDLVTPNQLDNNYFKNL 257

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
 Q+KGLL SDQ L +GGSTD IV YS +P F+SDFAAAMI+MGDISPLTGSNG IR
 Sbjct: 258 RQRKGLLQSDQVLLSGGSTDDIVLEYSNSPRAFASDFAAAMIRMGDISPLTGSNGIIRTV 317

Query: 2164 CRRIN 2178
 C IN
 Sbjct: 318 CGAIN 322

Score = 127 bits (320), Expect = 8e-27
 Identities = 71/169 (42%), Positives = 92/169 (54%)
 Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVSCADILAI AA 1330
 +QGCD SILLD+T + EK A PN S RG+ +I++ K +EK CPG+VSCADILA+AA
 Sbjct: 73 VQGCDASILLDETPTIVSEKTALPNLGSVRGYIIEDAKRELEKTC PGIVSCADILAVAA 132

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
 RD+ +V GGP+W VKLG
 Sbjct: 133 RDASTLV-----GGPSWTVKLG 149

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
 RRD+ TAS + A +P P L +LIS F+ GLST+D+VALSG+ I
 Sbjct: 150 RRDSTTASHTLAETDLP GPFDP LTRLISGFAKKGLSTRDMVALSGSHSI 198

Score = 62.8 bits (151), Expect = 3e-07
 Identities = 28/58 (48%), Positives = 41/58 (70%)
 Frame = +1

Query: 607 ALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
 +L +L +AQLS+ FY +CPN ++++ +V+ A+S E RM ASL+RL FHDCFV
 Sbjct: 16 SLVLLCSMQCHAQLSSTFYDRACPNALNTIRKSVRQAVSAERRMAASLIRLHFHDCFV 73

>gb|ACF08092.1| class III peroxidase [Triticum aestivum]
 Length = 316

Score = 146 bits (369), Expect = 2e-32
 Identities = 68/125 (54%), Positives = 94/125 (75%), Gaps = 1/125 (0%)
 Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD TP +FDN Y+ NL
Sbjct: 191 QAQCSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGLANLDTTTPNAFDNAYYTNL 250

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ ++GLLHSDQ LFN +TD+ VR +++NP FS+ F AMIKMG+I+P TG+ G+IR +
Sbjct: 251 MSQRGLLHSDQVLFNNDTTDNTVRNFASNPAAFSNAFTTAMIKMGNIAPKTGTQGQIRLS 310

Query: 2164 CRRIN 2178
C R+N
Sbjct: 311 CSRVN 315

Score = 97.1 bits (240), Expect = 2e-17
Identities = 64/170 (37%), Positives = 86/170 (50%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVC PGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 68 VQGCDA SVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICNQT VSCADILTVAA 122

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 123 RDSV-----VALGGPSWTVPLG 139

Query: 1511 RRDARTASQSAANNGIPAPTSNLNQLISRFSAL-GLSTKDLVALSGTKHI 1657
RRD+ A+++ AN+ +P S+ ++L + F GL+T D+VALSG I
Sbjct: 140 RRDSIDANEAEANS DLPGFNSSRSELEAAFLRKGLNTVDMVALSGAHTI 189

Score = 65.5 bits (158), Expect = 5e-08
Identities = 33/62 (53%), Positives = 43/62 (69%), Gaps = 2/62 (3%)
Frame = +1

Query: 601 CLALFVLIW--GSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDC 774
C++L VL+ +A QLS FY SCP +++KS V +A+S + RMGASLLRL FHDC
Sbjct: 7 CISLVVLVALATAAAGQLSPTFYDTSCPRALATIKSGVMAAVSSDPRMGASLLRLHFHDC 66

Query: 775 FV 780
FV
Sbjct: 67 FV 68

>gb|ACN37032.1| unknown [Zea mays]
Length = 314

Score = 146 bits (369), Expect = 2e-32

Identities = 68/124 (54%), Positives = 91/124 (73%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
QA+C +F IYN+TNI AFA + + +CP SG ++LAPLD TPT+FDN Y+ NL+

Sbjct: 193 QAQCLSFNDHIYNDTNINPAFAMSLRTNCP---ASGSSSLAPLDAMTPTAFDNAYYTLL 249

Query: 1987 QKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
++GLLHSDQ+LFN GS DS V ++ N F+S FA AM+KMG++SPLTGS G++R NC

Sbjct: 250 SQRGLLHSDQELFNNGSADSTVSSFAANAAFTSAFATAMVKMGNLSPLTGSQGGVRINC 309

Query: 2167 RRIN 2178

R+N

Sbjct: 310 WRVN 313

Score = 115 bits (287), Expect = 5e-23
Identities = 72/170 (42%), Positives = 93/170 (54%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRN-SARGFEVIDNIKSAVEKVCPGVVSCADILAIA 1327
+QGCD S+LL+DTS GE+N PN+ + RGF+V D+IK+ VE VCPG+VSCADILA+A

Sbjct: 69 VQGCDAVLLNDTS---GEQNQIPNQTNLNPRGFDVFDSIKAQVEAVCPGIVSCADILAVA 125

Query: 1328 ARDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKL 1507
ARD V + LGGP+W V L

Sbjct: 126 ARDGV-----VALGGPSWTVAL 142

Query: 1508 GRRDARTASQAANNIGIPAPTSNLNQLISRFSALGLSTKDLVALSGTKHI 1657

GRRD+ TAS A + +P PTS+L QL+ +S L+ D+VALSG I

Sbjct: 143 GRRDS-TASFPAQTSDLPPPTSSLQQLLRAYSCKNLNQDTMVALSGAHTI 191

Score = 66.6 bits (161), Expect = 2e-08
Identities = 35/70 (50%), Positives = 50/70 (71%)
Frame = +1

Query: 571 MASFCSRLTICLALFVLIWGSANAQLSTNFYYHSCPRLFSSVKSTVQSAISKETRMGASL 750
MA+ S L + L + V++ A+AQLS+ FY SCP+ S++ S V +A+++E R+GASL

Sbjct: 1 MAASASCL-LSLLVVVLAALASAQLSSTFYDTSCPSALSTISSGVTAAVAQEARVGASL 59

Query: 751 LRLFFHDCFV 780

LRL FHDCFV

Sbjct: 60 LRLHFHDCFV 69

>sp|P27337.1|PER1_HORVU RecName: Full=Peroxidase 1; Flags: Precursor

emb|CAA41294.1| peroxidase [Hordeum vulgare]
Length = 315

Score = 146 bits (369), Expect = 2e-32
Identities = 69/125 (55%), Positives = 93/125 (74%), Gaps = 1/125 (0%)
Frame = +1

Query: 1807 QARCTNFRARIYN-ETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNL 1983
QA+C+ FRARIY +TNI A+A + + +CP+T GSGD +LA LD T +FDN Y+ NL
Sbjct: 190 QACSTFRARIYGGDTNINAAYAASLRANCPQTVGSGDGSANLDTTANTFDNAYYTNL 249

Query: 1984 VQKKGLLHSDQQLFNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKN 2163
+ +KGLLHSDQ LFN +TD+ VR +++NP FSS F AMIKMG+I+P TG+ G+IR +
Sbjct: 250 MSQKGLLHSDQVLFNDDTTNVRNFASNPAAFSSSFTTAMIKMGNIAPKTGTQQGIRLS 309

Query: 2164 CRRIN 2178
C R+N
Sbjct: 310 CSRVN 314

Score = 95.9 bits (237), Expect = 3e-17
Identities = 64/170 (37%), Positives = 84/170 (49%), Gaps = 1/170 (0%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+QGCD S+LL E+NA PN S RGF VID+IK+ +E +C VSCADIL +AA
Sbjct: 67 VQGCDAVLLSGM-----EQNAIPNAGSLRGFGVIDSIKTQIEAICKQTVSCADILTVAA 121

Query: 1331 RDSVQIVSGQTTNKNTLN*I IKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP+W V LG
Sbjct: 122 RDSV-----VALGGPSWTVPLG 138

Query: 1511 RRDARTASQSAANNIPAPTSNLNLISRF-SALGLSTKDLVALSGTKHI 1657
RRD+ A+++ AN +P S+ +L + F GL+T D+VALSG I
Sbjct: 139 RRDSIDANENEANTDLPGFNSSRAELEAAFLKKGGLNTVDMVALSGAHTI 188

Score = 65.5 bits (158), Expect = 5e-08
Identities = 31/59 (52%), Positives = 42/59 (71%)
Frame = +1

Query: 604 LALFVLIWGSANAQLSTNFYYHSCP NLFSSVKSTVQSAISKETRMGASLLRLFFHDCFV 780
L + V + +A+AQLS FY SCP +++KS V +A++ + RMGASLLRL FHDCFV
Sbjct: 9 LLVLVALVTAASAQLSPTFYDTSCPRLATIKSGVMAAVTSDPRMGASLLRLHFHDCFV 67

>gb|ABV24961.1| peroxidase [Catharanthus roseus]

Length = 135

Score = 146 bits (368), Expect = 2e-32
Identities = 82/170 (48%), Positives = 98/170 (57%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
+ GCDGS+LLDDTSSFTGEKNA PN+ S RGFEVID IKS +E +CPGVVSCADILA+AA
Sbjct: 8 VNGCDGSVLLDDTSSFTGEKNARPNKGLRGFEVIDTIKSQLETICPGVVSCADILAVAA 67

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV + LGGP W V+LG
Sbjct: 68 RDSV-----VALGGPAWIVELG 84

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHIS 1660
RRD+ TAS S A IP P +L +++ FS G S K++VALSG I+
Sbjct: 85 RRDSTTASLSDAEANIPFPRMDLTDILTAFSNKGFSKEMVALSGAHTIT 134

>emb|CAL25298.1| properoxidase [Picea abies]
Length = 341

Score = 146 bits (368), Expect = 2e-32
Identities = 84/169 (49%), Positives = 95/169 (56%)
Frame = +2

Query: 1151 MQGCDGSILLDDTSSFTGEKNANPNRNSARGFEVIDNIKSAVEKVCPGVVSCADILAI 1330
++GCDGSILLDDTSSFT EK ANPNRNS RGF V+D IK +EK CPGVVSCADILA+AA
Sbjct: 83 VKGCDGSILLDDTSSFTREKTANPNRNSVRGFGVVDQIKCELEKACPGVVSCADILAVAA 142

Query: 1331 RDSVQIVSGQTTNKNTLN*IIKLYISKLITNLVPHMQLKRTFC*F*SI*LGGPTWNVKLG 1510
RDSV GGP W V LG
Sbjct: 143 RDSVGF-----SGGPFWKVLLG 159

Query: 1511 RRDARTASQSAANNGIPAPTSNLNLISRFSALGLSTKDLVALSGTKHI 1657
RRD+R+AS+S ANN IP P S L ++F GL+ DLVALSG I
Sbjct: 160 RRDSRSASKSGANNDIPGPNSTHTLETKFQRQLNVVDLVALSGAHTI 208

Score = 121 bits (303), Expect = 8e-25
Identities = 64/132 (48%), Positives = 88/132 (66%), Gaps = 9/132 (6%)
Frame = +1

Query: 1810 ARCTNFRARIYNET-----NIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNY 1968
ARC++F+AR+YN+T ++T + + + CP+T G+ DN PLD TP FD
Sbjct: 211 ARCSSFKARLYNQTVNGKPDPTLDTTYLKLHRAVCPQT-GTDDNQTTPLDPVTPIRFDIN 269

Query: 1969 YFKNLVQKKGLLHSDQQLFN--GGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGS 2142

Y+ N+V KGLL SD+ L++ G T +V YST+ F FAA+MIKMG+I+PLTGS
Sbjct: 270 YYDNVVAGKGLLASDEILYSTKGSRTVGLVESYSTSTHAFFKQFAASMIKMGNNINPLTGS 329

Query: 2143 NGEIRKNCRRIN 2178
+GEIRKNCRR+N

Sbjct: 330 HGEIRKNCRRMN 341

Score = 59.7 bits (143), Expect = 3e-06
Identities = 36/71 (50%), Positives = 44/71 (61%), Gaps = 4/71 (5%)
Frame = +1

Query: 580 FCSRLTICLALFVLIWGSANAQ----LSTNFYYHSCPRLFSSVKSTVQSAISKETRMGAS 747
F S L LAL + I + +AQ LS +FYY SCP + +KS V+ A+ KE M AS
Sbjct: 14 FLSVLITGLALMLWIQ-TVDAQSCNGLSHHFYKSCPKAQAIKSVVEDAVRKEAGMAAS 72

Query: 748 LLRLFFHDCFV 780
LLRL FHDCFV
Sbjct: 73 LLRLHFHDCFV 83

>gb|ACF08089.1| class III peroxidase [Triticum aestivum]
Length = 149

Score = 146 bits (368), Expect = 2e-32
Identities = 70/124 (56%), Positives = 92/124 (74%)
Frame = +1

Query: 1807 QARCTNFRARIYNETNIETAFARTRQQSCPRTSGSGDNNLAPLDLQTPTSFDNYYFKNLV 1986
Q++C FR RIYNETNI TAFa + + +CPR+ G DN+LAPLD TPT+FDN Y+ NL+
Sbjct: 27 QSQCRFFRDRIYNETNIGTAFATSLRANCPRSGG--DNSLAPLDGTPTAFDNAYYTNLN 84

Query: 1987 QKKGLLHSDQQLFNNGGSTDSIVRGYSTNPGTFSSDFAAAMIKMGDISPLTGSNGEIRKNC 2166
KKGLLHSDQ LFNGG D+ V ++++ TF+S F AMI MG+I+P TG+ G+IR C
Sbjct: 85 SKKGLLHSDQVLFNNGGADNTVMSFASSAATFNSAFTTAMINMGNIAPKTGTQGGIRLVC 144

Query: 2167 RRIN 2178
++N
Sbjct: 145 SKVN 148

Database: /usr/local/blast/db/blastlibs/nr
Posted date: Feb 13, 2010 7:16 AM
Number of letters in database: 3,559,509,877
Number of sequences in database: 10,432,217

Lambda K H
0.318 0.134 0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 10432217

Number of Hits to DB: 20,370,324,626

Number of extensions: 397276250

Number of successful extensions: 861113

Number of sequences better than 10.0: 1949

Number of HSP's gapped: 858181

Number of HSP's successfully gapped: 6554

Length of query: 1289

Length of database: 3,559,509,877

Length adjustment: 149

Effective length of query: 1140

Effective length of database: 2,005,109,544

Effective search space: 2285824880160

Effective search space used: 2285824880160

Neighboring words threshold: 12

Window for multiple hits: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 33 (17.3 bits)