67159.t00029 | At4g26210 | T25K17.20 | mitochondrial ATP synthase g subunit family protein | contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit

NAME	START	P-VALUE	SITES
Citrus_sinensis-65435	107	1.01e-14	TCATTGTTTC **TGCAAAATTTTTGAAGCTGAGAAATCAG** TGGGTAACTT
Gossypium_hirsutum-83958	76	8.62e-14	TTGTTGTTTT **CATGAAAATTTTGAAGCTGAGAAATCAG** TGGTTAATAT
Vitis_vinifera-48219	104	2.79e-13	TTTGTATTTC **TGCAAAAAATTTTAAGCTGAGGAATCAG** TAAGTTTGAT
AT4G26210.1	150	1.86e-12	ATAATTTATA **CACAAAAGTTTTGAAGGTGAGGCATCAT** CACTCGTGCT
Glycine_max-410271729	280	4.51e-10	CTGTTATTCT **CATAAAATATTAAAACCAGAATAAAAAG**
Nicotiana_tabacum-90383	160	4.51e-10	GAGCCTTCTG **CTAAAGATTTCAAAGGCTGAGTTAGGAG** TAATATACGT

67168.t00029 | At4g28100 | T13J8.210 | expressed protein

NAME	START	P-VALUE	SITES
Vitis_vinifera-23345	42	5.31e-14	ATTCTGTCGG **GTCACGTGAAGCTACTAGACAA** ACGGGCAAGC
Citrus_sinensis-33723	79	2.41e-12	TTCTGTTGAG **GTCACGTGAAGCTGGGAGACAA** AGTCTTTTTC
AT4G28100.1	38	4.09e-12	GGTAAAGAGA **GTCACGTGAAGCTACAAGACAG** TTATGTGTAT
Nicotiana_tabacum-76627	71	1.79e-10	TTGGGGGATT **CACGTGAGAAGCTAGTTGCCAA** AATGAAGGGA
Gossypium_hirsutum-83101081	38	3.55e-09	AGTTGTTGCA **CACACTGGAATCTAATTCCGGA** TAACCTATAT

51902.t00033 | At1g20190 | T20H2.4 | expansin, putative (EXP11) | similar to GB:U30460 from (Cucumis sativus); alpha-expansin gene family, PMID:11641069

NAME	START	P-VALUE	SITES
Vitis_vinifera-17666265	56	2.21e-15	AGAGGCGTGC **TTACTATTTTAATGAAGCAGCCCGCCCTA** AATTATGAGA
Gossypium_hirsutum-68848	52	2.41e-14	AGAGGTGTGC **TTACTATTTTACAAAAGCTGCCCGCCATA** TCGTATGAGA
Glycine_max-498271731	32	3.23e-14	GAGGCGTGCT **TTTTTATTTTACTGGAGCAGCCCGCCAAA** CCCTTCTTCT
AT1G20190.1	56	4.25e-14	TTTGAGTCTG **TTTCTTTTCTCCCTGAGCGACCCGCCCTC** TTTGTTTTTT
Nicotiana_tabacum-24789	67	3.38e-13	GCGGCGTGCT **TACTCTTTTGCTATAAGCAGCCCGCCCTC** CCCCCTCCCC

51141.t00014 | At2g07687 | T17H1.13 | cytochrome c oxidase subunit 3 | identical to cytochrome c oxidase subunit 3 (GI:15215914) (Arabidopsis thaliana); similar to Cytochrome c oxidase polypeptide III (EC 1.9.3.1) (Swiss-Prot:P92514) (Arabidopsis thaliana)

NAME	START	P-VALUE	SITES

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-231840	24	4.64e-20	GGATTGAGGA **ATGAAAGCTCGAAGACAAAGAGAACCGGGC** TTTTTCTTTA
AT2G07687.1	24	4.64e-20	GGATTACAAA **ATGAAAGCTCGAAGACAAAGAGAACCGGGC** TTTTCCAAAG
Vitis_vinifera-12208	24	4.64e-20	GGATTGAGGA **ATGAAAGCTCGAAGACAAAGAGAACCGGGC** TTTTCCAAAG
Gossypium_hirsutum-112101072	24	1.58e-19	GGATTAAAAA **ATGAAAGCTCGAAGACAAAGAGAATCGGGC** TTTTCCAAAG

12844.t00011 | At2g39700 | F17A14.7 | expansin, putative (EXP4) | similar to alpha-expansin 6 precursor GI:16923359 from (Cucumis sativus); alpha-expansin gene family, PMID:11641069

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-121687	289	7.94e-15	AAGCTAAATG **GAGGCTGAAGCGGCTGCAAAAGCA** CCCAAAAAAA
Vitis_vinifera-1266263	320	4.11e-14	GCAAAGCGTT **GGGGCTGAAGTGGCTGCAAAGCAA** AAACATGTAG
Gossypium_hirsutum-17811	313	6.24e-14	GTAAGGTGGG **GGTGCTGAAGCGGCTGCAAAGCAA** AAGAAAACAT
Citrus_sinensis-78299	326	1.30e-13	TGAAAGTGTA **GTGGCTGAAGTGGCTGCAGGAACA** AACTAAAAAA
AT2G39700.1	257	3.83e-12	GAGAAAGTGA **GTAGCTGAAGTGGCTGTGAGAACA** TTTTGTAACA
Glycine_max-143273	228	2.91e-11	TAGTGTAGGA **AATGCTGAAGCGGCTAAGCAAAGA** GGGTAGCCCG

67321.t00003 | At3g62070 | T17J13.30 | expressed protein | hypothetical protein F14M4.23 - Arabidopsis thaliana, PIR:T02193

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-28444	37	2.45e-21	GCGGGGATGT **GAAGGCACGGCTCAAGGTGTGGGCGCAGGC** TGTGGCACTT
Glycine_max-34312	285	1.30e-20	CACGAGACGT **GAAGGCACGGCTCAAAGTGTGGGCGCAGGC** GGTGGCACTT
Vitis_vinifera-52514	52	2.87e-19	CACGAGACGT **GAAGGCCCGGCTCAAGGTATGGGCACAGGC** GGTGGCGCTG
AT3G62070.1	387	1.11e-13	AATTTCAAAA **AAAGGGACATCTCAAAAGAAGAGTTCATGA** TCGGTTTTTG

60560.t00002 | At3g13460 | MRP15.12 | expressed protein | contains Pfam profile PF04146: YT521-B-like family

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-25935	490	2.57e-15	GTACTAGTCA **AAAAGAGCTAGAAGCAAGGTGGGAA** TGCATTGCAA
Vitis_vinifera-35266257	507	2.84e-15	TTTGAATTGT **AAGAGAGCTAGAGGCAGGGTGGGAA** AAGTATTGCA
Glycine_max-135147	447	1.71e-14	TGTTACTTTC **AACAGGGGTAGAAGCAAGGTGGGAA** ATACTGAAAA
AT3G13460.1	331	1.81e-12	GAATTAGAGA **AAAGGAGATAAAAGCAGGGTGGGAT** TTTGTTTTTT
Citrus_sinensis-75276	478	2.51e-11	GTCAAGAGAG **GGCTGCTAAAGCGCCAAGCTGGGAA** AATTATTTCA

67099.t00028 | At4g10380 | F24G24.180 | major intrinsic family protein / MIP family protein | contains Pfam profile: MIP PF00230

NAME	**START**	**P-VALUE**	**SITES**
AT4G10380.1	95	8.59e-18	TTGTGTGAAG **AATAAAAGGCGATGTGACTATAAGTCCACG** CATGGCATCG
Gossypium_hirsutum-43349	159	1.25e-17	AGCTTTTGGG **AATAATAGGCGATGTGACCTTAAGTCCACG** ACCTACAGTA
Vitis_vinifera-12724	99	6.79e-17	AAAGCTTAAC **AATAAAAGTGGAAGTGACGCAAAGTCCACG** CCCCATCAGT

67260.t00026 | At3g48070 | T17F15.60 | expressed protein

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-47045	107	6.87e-18	GTACTCTTGT **TGGTATGTGAATAGATAAGGTGGTATAGAA** ATTCAATACA
Vitis_vinifera-35460	210	6.87e-18	GGATTCGTGT **TGGTATGTGAATAGATAAGGTGGTATAGAA** ATTGAATACA
Nicotiana_tabacum-46155	212	1.85e-15	TAGAACACTC **TATTATGTGAATAAATAAGGTGGTATAGAA** GTTAAATAAA
AT3G48070.1	221	5.32e-15	TTATGTAGAG **TGGTGTGTGAGTACATAAGGTGGTACACGA** ATTTCAAATA
Citrus_sinensis-33106184	225	7.43e-15	CTCATGGTGG **TATTATGTGAATAGATAAACTGGGATAGAA** ATCCAT

67307.t00014 | At3g58790 | T20N10.140 | glycosyl transferase family 8 protein | contains Pfam profile: PF01501 glycosyl transferase family 8; general stress protein gspA, Bacillus subtilis, PIR:S16423

NAME	**START**	**P-VALUE**	**SITES**
AT3G58790.1	70	7.98e-17	ATACTTGCGG **CTGTGTGAGAGAACAGAGGGAAGAAGGT** TTAAGCCTTC
Citrus_sinensis-66037	52	2.81e-14	CAGAGAAGAC **CTACGTGTGAGACCAAAGGGAAAAAGGT** TGGCTTCAAC
Glycine_max-237958	50	3.30e-14	AACAGTGATA **CTGTATGGGATTTCAGAGGGAAGAAGGT** TCTGCCTTCA
Gossypium_hirsutum-81420	77	1.54e-13	AGGAACACGG **TTCGGAACCAAAGCAGAGGGAAGAAGGT** ATTGGCTTCA

67653.t00019 | At5g22770 | MDJ22.19 | adaptin family protein | similar to SP|P18484 adaptor-related protein complex 2 alpha 2 subunit (Alpha-adaptin C) (Clathrin assembly protein complex 2 alpha-C large chain) {Rattus norvegicus}; contains Pfam profiles PF01602 Adaptin N terminal region, PF02883 Adaptin C-terminal domain

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-71706	104	2.33e-17	CCTAACAACA **TGATGCAAGGGCTGGCGGAAGTGAGGGTG** GCACTGATTT
Glycine_max-5339	101	2.06e-16	GACAAAATCA **TGATGCAAGGGCTGGCGGAATTAAGAGTG** AGCTTGTTTA
Vitis_vinifera-57391	114	5.70e-16	TGGAAAACTA **TGATGCAGGGGCTGGCGGAATTAAAAGGG** TGAGGTCATT
Gossypium_hirsutum-20565	99	1.00e-13	GAAAATTTCA **TGATGCAAGGGCTTGCCGGATCACGGAGG** AGCTTAATTA

NAME	START	P-VALUE	SITES
AT5G22770.3	108	7.22e-12	GAGTAAATGT **AGAGCCAAGGGGGGTGGAGAGGGGAAGGG** TTTAATAGGA
Citrus_sinensis-20741	102	3.01e-11	GGGCCCCCTT **TGAAGCTTAGGAAAGGGCCAGAAGGGGGG** GAACAGGCCA

51101.t00005 | At2g16370 | F16F14.13 | bifunctional dihydrofolate reductase-thymidylate synthase 1 / DHFR-TS (THY-1) | identical to GP:289193:L08593 (SP|Q05762)

NAME	START	P-VALUE	SITES
Citrus_sinensis-37031	197	7.40e-13	AAGAGTCGGT **GGTTCTAAGGTGATTTAGGAT** GTTTGTATTT
Vitis_vinifera-16566259	194	7.40e-13	ACAAAATGTT **GGTTCTAAGGTGATTTAGGAT** ATATATTTAT
AT2G16370.1	167	4.63e-11	AGTTCCACAT **GGTTCTAGAGCGATTTAGGAT** TTTATACTTC
Nicotiana_tabacum-99906	190	5.15e-11	ATGGTTCGTG **GTTGCTAAGGTGATTTAGAAT** ACAAATGACT
Glycine_max-99456	166	7.66e-11	CACCTGTTAT **GCCTCTAAGGTGATTTAGATT** AACTTAATTT

67939.t00022 | At5g67500 | K9I9.6 | porin, putative | similar to SP|P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-45514	82	2.91e-13	ATTGATTAAG **GGTGGCAATAAATAGTTCCACAG** ATGATAAATA
AT5G67500.1	127	1.63e-11	ACGTTTAATT **GGAATCAATAAATAGTTCCGCAG** TGAAATTGAC
Nicotiana_tabacum-99507	57	3.07e-11	TGGAGGACAG **GTGCTCAATAAATAGTTCAACAA** ACTGGTGGTT
Vitis_vinifera-60317	76	4.56e-10	CTGAAAGGGA **GCTCTTAATAAATAATTCCACAA** TATATTCATT
Citrus_sinensis-38692	75	6.39e-10	CTTGAGAAGT **GTCGTCAATAAGGAGTTCCAAGA** TAAATTTGTT
Glycine_max-40271729	74	1.48e-09	CCTTGAAAGG **AGGGAAAATAATTAGCTCCCCAG** ACGAGACCAT

51047.t00057 | At1g65295 | T8F5.7 | expressed protein

NAME	START	P-VALUE	SITES
AT1G65295.1	85	1.32e-12	AGGAAAAAAA **GAAGAATATCTGTTCTTGGTT** TGAGTCTTCT
Citrus_sinensis-4538	76	6.48e-12	TGAAGCAAAA **GAAGAATATCTGTTCTTGATT** TGTTTGTTTA
Glycine_max-18894	96	1.48e-11	GAAGTGAAGT **TAAGAATATCTGTTCTTGGTT** AGTTTTTTTA
Vitis_vinifera-7997	104	3.01e-11	GTGTGAATGG **CAAGAATATCTGTTCTTGTTT** TATTTGTTTA
Nicotiana_tabacum-72532	113	6.95e-11	TGAAAGGGGA **GAGGAATATCTGTTCTTAGAT** TTGATTTGTT

41826.t00046 | At2g38610 | T6A23.19 | KH domain-containing protein

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-57495	270	1.88e-15	CTGTAAACTC **AATACATTCATTGGATTTATTCTTGTG** TTAGCAGAGC
Glycine_max-472271727	303	1.37e-14	TTGCAAACTT **AATACATTCATTGGATTTATTCATGTG** TCAGTTACTT
Nicotiana_tabacum-13987	233	6.08e-12	GTTCTTGTAA **ACTTCTTCCATTGGATTTATTTTTGTG** TTAGTAATTG
AT2G38610.2	386	7.23e-12	ATAAACAAAA **AACACATTTATTGGATTGATTCTTATC** GTTTGATTTG
Vitis_vinifera-600	217	1.39e-11	TTGTAAAAGT **AGAACAATCATTGGATTTATTTCTCTA** ATTAACCTTG

60078.t00034 | At1g72230 | T9N14.17 | plastocyanin-like domain-containing protein | similar to blue copper protein SP:Q41001 from (Pisum sativum)

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-81729	16	3.78e-14	CCTTGCTGAT **GACCAGGATAGAGGCAGTGCT** TTTTCTCCTT
Vitis_vinifera-14966260	26	5.16e-14	TGCCTTTTCA **GGCCAGGATGGAGGCAGTGCT** CCCTTTCTAT
AT1G72230.1	44	7.33e-14	TCGTTTGAAG **GACCAGGCTAGAGGCAGTGCT** GTTATATGCT
Gossypium_hirsutum-182101076	5	5.44e-13	CCATC **GTTCAGGATAGAGGCAGTGCT** GATTTTATTG
Glycine_max-80540	12	9.76e-13	TTCCCCACTC **AGTCAGGACAGAGGCAGTGCT** TTCTTTCTTT

45986.t00006 | At2g07733 | T5E7.6 | pseudogene, similar to NADH dehydrogenase subunit 2 | blastp match of 94% identity and 2.0e-77 P-value to GP|1667390|gb|AAB18755.1||M81726 NADH dehydrogenase subunit 2 {Oenothera berteriana}

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-73549	21	8.74e-22	GTCCTAGAAA **CGGCGGCAGCGGCGCGAGGAGTTAACGACC** GGACGTGCTG
Vitis_vinifera-19103	21	8.74e-22	GTCCTAGAAA **CGGCGGCAGCGGCGCGAGGAGTTAACGACC** GGACGTGCTG
AT2G07733.1	205	2.32e-21	GTCCTAGAAA **CGGCGGCAACGGCGCGAGGAGTTAACGACC** GGACGTGCTG

67173.t00032 | At4g28950 | F25O24.70 | Rac-like GTP-binding protein (ARAC7) | identical to rac GTP binding protein Arac7 GI:3702962 from (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-28935	174	2.85e-13	GACAAGAATG **GAGGGAATTGTTCATTCTCTC** CAGCGCTTTT
Gossypium_hirsutum-94663	148	2.85e-13	AAGAATGATA **GAGGGAATTGTTCATTCTCTC** ATGTATTTAT
Vitis_vinifera-4658	177	1.33e-12	GGAAGAGCAA **GTGGGAATTGTTCATTCTCTC** GTGCACTCTT
AT4G28950.1	93	7.67e-11	CTGTGAAGAT **AAGGAAACTGTTGGTTCTCTT** ATTTGTATGT

51718.t00072 | At1g76160 | T23E18.10 | multi-copper oxidase type I family protein | similar to pollen-specific BP10 protein (SP|Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-95470	140	7.39e-18	AAAATTACTA GACCTCAACTCGAGGTCGCATTCTTTCTTA CTATACATTT
Citrus_sinensis-94600	143	5.51e-17	ACTTGAAATT GACCCCAGCTCGAGGTCTCATTCTTTTCTA TTGAAGGTTG
Nicotiana_tabacum-122753	126	9.27e-16	TAATTTGAAT GACCTTAACTCAAGGTCTCATTCTTTCTTC CACGGAACTT
AT1G76160.1	148	1.00e-15	AGTTTGTAAC GATCTCAGCTCGAGGTCTCATTCTTGATTC TTATATTCTT
Vitis_vinifera-10566261	21	1.21e-14	TACTTTAAAT GGCTCCAACTCGGGGCCAGATTCTTTGTTA TACAACTCAT

68082.t00037 | At5g20160 | F5O24.50 | ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein | Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628.

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-24972	17	2.87e-17	ACGTAACTCG TATTCGGTGTGATGGGCCTCTTGGAATGTG GTGGTCGCTC
Citrus_sinensis-103791	15	3.41e-15	ATGGGATTCA TATTCGGTGTGATGGGCCTCTTTGATGGTG GTTAGAGGGC
Glycine_max-258858	8	6.58e-14	AAATTTGA TATTCGGTATGACGGGCTTCTTGAGAGGCT TTGACTGGAC
AT5G20160.1	18	3.19e-13	CTGAATTGAT TGCTCGGTATGATGGGTCTCCGCGAATGGG AAGGCTTTGA
Nicotiana_tabacum-103369	10	8.80e-12	ATCTTGAGCC TTTTCAGCATGAGGGGCCTCATGATTTCTG AAGTGGATTG
Vitis_vinifera-64783	5	8.14e-11	ACCTG TGGCCTCTGCCACGTGCTCCCTGCCAGCTT CCCCCCTGAG

51344.t00028 | At1g11700 | F25C20.15 | expressed protein | contains Pfam profile PF04520: Protein of unknown function, DUF584

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-3012	98	7.80e-19	TATTTTTTAC TTGGGCAATGACTCGGCCGAGTTGACTCAG TACAGAAACC
Gossypium_hirsutum-37802	72	2.53e-17	TTATTTTTAA TTGGGCAATGATTCGGCTGAGTCGACACAG GTGAGTCAAC
Glycine_max-742271731	385	1.51e-16	TGGTTTTGTT CTGGGCGATGATTCGGCTGAGTGGACTCGG CCGAAGAGAG
Nicotiana_tabacum-27015	68	8.78e-12	TTTTTGGTCC TTGGGCAATGATTCAGTTTGAATGAATACA AACTCAGTGA
AT1G11700.1	108	1.57e-10	TTTTGCAACT TTCTTGAATCCCAAGCTTGAGATGTATAAG ATTTATATAT

51205.t00021 | At1g03060 | F10O3.12 | WD-40 repeat family protein / beige-related | similar to BEIGE (GI:3928547) (Rattus norvegicus); Similar to gb|U70015 lysosomal trafficking regulator from Mus musculus and contains 2 Pfam PF00400 WD-40, G-beta repeats. ESTs gb|T43386 and gb|AA395236 come from this gene

NAME	START	P-VALUE	SITES
Citrus_sinensis-38106187	147	1.24e-13	ATCCCAGAAA **ACTGGGCTGGCCTGGGATTATAAGA** CAAGGTTAAG
Gossypium_hirsutum-858101078	143	1.93e-13	AAGCAAGACA **ACAGGGCTGGCCAGGTATCGTAACA** GGACAAACTG
Vitis_vinifera-44888	149	6.54e-13	AAGCAAGACA **GCAGGGCTGGCCTGGGAATTGGAAG** AGGTAAAAGA
AT1G03060.1	52	7.32e-13	ACTAGAATCG **AAAGAGCTGGCCAGGGAACTTAAGG** ACAGGACCAC
Nicotiana_tabacum-111852	4	1.91e-10	AGTC **GACGGCATGCCCTGCTTTAATGAGA** TATGCGAGAC

60517.t00008 | At3g13870 | MCP4.11 | root hair defective 3 (RHD3) | identical to root hair defective 3 (RHD3) GI:1839188 from (Arabidopsis thaliana) (Genes Dev (1997) 11(6), 799-811)

NAME	START	P-VALUE	SITES
Vitis_vinifera-19596	167	1.91e-15	TTTTTGCATA **GGTGCCACATACTGGGGGCTGTGGTTTGT** TGTGAAAAAG
Citrus_sinensis-87226	159	3.61e-15	TTGTGCAAGT **GCCGGCGCATACAGGGGGCTGAGATTTGT** TATGAAAAAG
Gossypium_hirsutum-40683	164	1.27e-14	TTTTTTGTGC **AGTGCCGCATACAGGGGGCCCCACGTTCG** GGGGATCCCC
Glycine_max-221019	138	1.73e-14	TTTTGTTGCA **AGTGCCATATACAGGGGGCAATGATTTGT** TGATGTAGTC
AT3G13870.1	151	1.88e-11	GATGGCATTG **GTTCCCTCTTGCAGGTGTCAAAGTGATCT** TGTATGTTCC

49301.t00014 | At2g07717 | T18C6.21 | pseudogene, similar to NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3). (Field mustard) | blastp match of 99% identity and 2.0e-226 P-value to SP|Q04050|NU4M_BRACM NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3). (Field mustard) {Brassica campestris}

NAME	START	P-VALUE	SITES
Glycine_max-253936	0	4.05e-18	**ACCCCCTACGGGCGGTCGTCCGTCG** TAAAGTAGTC
AT2G07717.1	0	4.05e-18	**ACCCCCTACGGGCGGTCGTCCGTCG** TCGTAAAGTA
Gossypium_hirsutum-15970	0	6.50e-13	**ACCCCCTACTTGTCTCGTCCTCTGC** CTGAT

67846.t00009 | At5g53480 | MYN8.11 | importin beta-2, putative | similar to importin-beta2 (Oryza sativa (japonica cultivar-group)) GI:3983665; contains Pfam profile PF03810: Importin-beta N-terminal domain

NAME	START	P-VALUE	SITES
Glycine_max-191117	1395	2.92e-16	TGAAGGTCTT **CTAGTTGTCACTAACTCTTGCATCATCACC** AATGCATCAC
Gossypium_hirsutum-66756	132	2.92e-16	TGTCCGTCTT **CAAGTTGTCACTAACTCTTGCATCATCATC** ATCATCATCA
Nicotiana_tabacum-14959	138	2.38e-14	AATTTACCAT **CATGTTGTCATTAACTCATGCGCCAGCACC** ATGGGGTCGA
AT5G53480.1	104	6.15e-12	GGTAGAGCTG **CAACATCCGAGTCACATCAGCATCATCAGC** ATCAGTTTCA
Citrus_sinensis-87895	62	3.34e-11	TCAATGCAGT **AAGGGTGACGAAGAGCTGTGCCCCTCCAGC** GGTGAGTTTG

60557.t00007 | At3g14200 | MAG2.19 | DNAJ heat shock N-terminal domain-containing protein | low similarity to SP|O75190|DJB6_HUMAN DnaJ homolog subfamily B member 6 (Heat shock protein J2) {Homo sapiens}; contains Pfam profile PF00226 DnaJ domain

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-744101078	6	1.80e-17	TAGACG **GAGAAATGGCAGGAAACAAAAGGTTTCATC** CGGCCACGAT
Citrus_sinensis-17782	3	4.57e-14	TCG **AAGGGAAGGCAGGAAACAAAAACTTTCACC** CAGTCATGAT
Vitis_vinifera-56752	6	6.39e-14	ACGAAG **AAGAACGGGTAGAAAGCAAAAGGTTTCATC** TGGCCATGAT
Nicotiana_tabacum-110873	3	1.27e-12	TAC **GAGGGACGCCAAAAGGCAAAGGGTTGTATC** AAGGGAGAGC
Glycine_max-53167	9	6.33e-12	AAGTAGACA **CAGAAGTGGCAGAAAGCAAAAAATGTTCTA** TGGCCATGAT
AT3G14200.1	88	5.09e-11	TCTTCTCAAT **GAGGAATACATCGAAACTCAAAGGGTCGTC** GTTTTGTAAA

51944.t00031 | At1g75380 | F1B16.9 | wound-responsive protein-related | similar to wound inducive gene GI:8096273 from (Nicotiana tabacum)

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-11592	32	4.65e-17	TTGTAAATAG **AAATCATTGTTGGAAGCCGATGAGCTCGAC** CACTTACAGC
Nicotiana_tabacum-36812	48	3.46e-14	TGTATATAGG **GAGTTATTCATCGGAGCCAATGTGGTCAGC** ATCGTCAAAG
Gossypium_hirsutum-307101075	34	2.19e-13	TTGTAAATAG **GAATTATTGTTGGAAGCCGATAGACTCAGC** TGGGCAGTGG
Vitis_vinifera-15326	30	3.48e-13	GTAAATAGAT **AAAACATTGTTCAAGGCTGATGAGGTCCAC** TTCTGTAGTT
AT1G75380.3	46	1.02e-11	ACTAAGAAGA **AAGTCATTGGTCGGAATCAAAGTGGAGGAA** GAAGCCTGAA

67305.t00043 | At3g58170 | F9D24.80 | Bet1-like SNARE 1-1 / Bet1 / Sft1-like SNARE 14a / BS14a (BET11) | identical to SP|Q9M2J9 Bet1-like SNARE 1-1 (AtBET11) (Bet1/Sft1-like SNARE 14a) (AtBS14a) (Mouse-ear cress) {Arabidopsis thaliana}; supporting cDNA gi|14030602|gb|AF368175.1|AF368175

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-3575	17	6.32e-16	ATGGTGGATG **TGATACAGCTGCTAGCTTTCTGTTAGAACT** GGGGAGACTT
Glycine_max-18744	9	7.40e-13	TTTGATCTT **TCATTCAACTGCCAGCTTTATGTTAGGTCC** AAGAGGACGC
Citrus_sinensis-138106186	17	3.18e-12	ATGATGTATT **TGATAACGCCAGCAGCTTTGTGTTAGTATT** GGGATGACCC
Gossypium_hirsutum-94420	22	4.14e-12	GTATGTGATG **TGATACAACTGCAAGCTTTATATAAGAATT** TGGAAGACCC
AT3G58170.1	45	5.23e-11	CATGATCTCA **TGATATTCCCAGTCTCTCTCTGTTGGCTCC** TACGATCTAA

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-22285	66	9.68e-11	TTACTCAAAA **TTCTGCTGCCAATTGCTCAATGTAAGAATC** TTGTGACTTG

51305.t00070 | At1g59750 | F23H11.7 | auxin-responsive factor (ARF1) | identical to auxin response factor 1 GI:2245378 from (Arabidopsis thaliana)

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-121308	20	3.48e-17	TGATGAGGAT **GACATGATGATGGTTGGAGATGATCCATGG** CATGAGTTCT
Citrus_sinensis-30967	11	8.87e-16	GATGGAAAAT **GACATAATGATGGTTGGAAATGATCCCTGG** GATGAACTCT
Glycine_max-77824	247	1.17e-15	TAATGAAAAT **GAAATGAAGATAGATGGAGACCATCCGTGG** CATGAA
AT1G59750.2	43	4.85e-12	CCACGTAGGA **AATATGAAAGCAGAAGCAAGAGATCGTTAG** ACAATATGAA

67791.t00004 | At5g45600 | K2N11.8 | YEATS family protein | contains Pfam domain PF03366: YEATS family

NAME	START	P-VALUE	SITES
Citrus_sinensis-24904	9	2.73e-17	ATATGATGA **ACGGGCTGCCGCCACCACCAAACCCGGCC** TCCGGGCATG
Vitis_vinifera-43701	199	1.19e-16	AGCGTGATCG **ATGGACTGCCTCGGCCATTGAAACCAGCC** TTTGATGAGT
Nicotiana_tabacum-22813	200	3.39e-15	AGCTTGATAG **AGGGCCAGCATCAACAATTGAAACCGGCC** TCTGATCTGT
AT5G45600.1	151	8.22e-13	TTCCAGTTTC **ATAGACTGCAACTGCAAAATAACTCTTCC** AGATTAGATA

67299.t00002 | At3g56370 | T5P19.20 | leucine-rich repeat transmembrane protein kinase, putative | leucine-rich receptor-like protein kinase - Malus domestica, EMBL:AF053127

NAME	START	P-VALUE	SITES
AT3G56370.1	38	1.10e-13	TCACCAAGTT **CCGGCGAAGAGGAATCCGGT** TTGTTCATTT
Glycine_max-229156	45	6.76e-13	AATGGGATGT **CCGGGGAAGAAGAATCCGGC** TTTATTTATT
Nicotiana_tabacum-80801	56	2.59e-11	ATGTGTTATC **CTGGCGAAGAAGAATCCGGT** TGATTTATTC
Gossypium_hirsutum-62901	61	4.39e-09	TTGGAAGAAG **GCACGGTGGAGGAATGCGTT** GACGGAAGGC
Citrus_sinensis-31143	174	8.42e-09	TTGNCTTTGC **CCCTGGCGCATGACGCAGCT** AGTGAGGGTT

49202.t00007 | At2g25490 | F13B15.15 | F-box family protein (FBL6) | contains similarity to grr1 GI:2407790 from (Glycine max)

NAME	START	P-VALUE	SITES
Vitis_vinifera-50899	280	1.27e-17	GCCACCTCTT **TCATGGCCATGGTTCCCTGAGAATACAG** TCACCAAGTC
Gossypium_hirsutum-26598	246	1.11e-14	GTTTGTTTCT **TCATGGCCGGAGTTCCCTGAGAATATAG** TCGCTGCTGG

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-724271733	248	1.50e-14	GCTACTTCTT **TCATGGCTAGGGTCCCCTGAGAATACAG** TTACTAAGTC
Nicotiana_tabacum-122859	430	1.36e-11	TTTCCGGTTC **TTCCAGCCATACTTCTCTGAGATTTCAG** ATGCTGAGTT
AT2G25490.1	429	1.85e-11	TCAGGTTTGG **TTCAGGCCTTGGTTCTCTCAGAGGTTTG** CTCTGGCTTT
Citrus_sinensis-31017	232	3.54e-10	CCCCCTCCCC **AGAGGGCCTTCCTACCCTTCAAGGGACG** GGGGTTTTTT

67117.t00039 | At4g13710 | F18A5.100 | pectate lyase family protein

NAME	**START**	**P-VALUE**	**SITES**
AT4G13710.1	196	4.04e-15	GAATATAGAG **AGGAGCAAGCACAGAAGCGTTGTTCA** AAAAGTTTTC
Vitis_vinifera-16354	289	1.02e-14	GTGCCATTGT **CGGAGCAGGTGCGGTAGCGTTGTTCA** TTTCTATTTC
Citrus_sinensis-89077	261	1.17e-14	TTGCATTCCC **AGAAGCAGGTGCGGAAGTGTTGTTCA** TTTTATTTTC
Gossypium_hirsutum-135101080	269	1.12e-13	AATCCATCTT **AGGCGCAGGTACACGAGCGTTGTCCT** TGGTTCCCTT
Glycine_max-129518	292	4.90e-12	ATGCAATTGT **AGAAACGAGTACAGAAGTATCATCCA** TTATTGTCTT

67623.t00029 | At5g14060 | MUA22.6 | aspartate kinase, lysine-sensitive | nearly identical to gi:2257743

NAME	**START**	**P-VALUE**	**SITES**
AT5G14060.1	2	7.51e-15	TG **CAACACAGAGCACCCATCTCTC** TCCTTCAACT
Nicotiana_tabacum-33385	32	2.32e-13	GAATCTACTT **CAACACAGATCAATCATCTCTC** TGATTGGGAA
Gossypium_hirsutum-19197	147	8.41e-12	TCAATCTCTT **CAGCACAGATCTATCATTTCTC** TCATTGGCAA
Citrus_sinensis-10262	130	6.27e-11	TGCGGCCAAC **CAAAGCAACTTACCCCTTTCTC** GAACGTTGGA

68129.t00048 | At1g45688 | F2G19.25 | expressed protein

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-15009	117	1.11e-13	GAACGAGAGA **TACAGCTAAGCGGGCAGGTTTGGAGAT** TATTGGGCAG
AT1G45688.1	73	2.09e-13	AACGTGATTT **TACAGCTCAACGGGCAGCATTTTGGGT** TGTTGGGGCA
Glycine_max-34164	121	4.73e-13	GTAATGTGTA **TACAGCTCATAGGGCAGGATTGGAAGG** ACGCGTGCGT
Citrus_sinensis-51332	152	4.73e-13	GTAGTTGAGT **TACAGCTAAGCGGGAGAGCTTTTGAGT** TGTTTGGGCA
Vitis_vinifera-2643	82	1.05e-11	AGATCAAAGG **GACAGCTATGACGGGCAGCTTTTGAGT** TGTTTGGGCA
Nicotiana_tabacum-27263	71	7.27e-10	TACGTACATT **GATAGCTATTGGAGCAGTTTGTGGTCT** CTATCTTTAC

50716.t00125 | At1g23750 | F5O8.30 | DNA-binding protein-related | contains weak similarity to G-quartet DNA binding protein 3 (Tetrahymena thermophila) gi|4583503|gb|AAD25098

NAME	START	P-VALUE	SITES
Citrus_sinensis-98121	109	1.62e-16	AAAACTGTGT **TGCCTTTAGGAAGAAGAAATCTGGAAGC** TATTACTACC
Gossypium_hirsutum-60637	116	3.92e-16	TTGTGAAGTT **CGCTTTTAGGAAGAAGAAATCTGGAAGC** TAGTGTGTAG
Vitis_vinifera-38468	119	5.92e-13	CATGAAAGTT **CGCTTTTAGGAAGAAGAGATATGGCTAC** AGTAACAATC
AT1G23750.1	33	1.68e-10	CTAGGAGAAA **CGCCCTCAAGAATAAACAAGTCAAATCC** GTAACCGTTT
Nicotiana_tabacum-11045	25	2.27e-10	ACAACGGTAA **TGCCGTTAGAGAGAAGCAATATAAGTAA** GTTTCGTTCT
Glycine_max-12931	63	4.70e-10	ACAGTTCACC **TGAGTTTAGGAATAGAGATTTGAGAAGC** CAGTAGTACC

50723.t00079 | At1g51200 | F11M15.7 | zinc finger (AN1-like) family protein | contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger

NAME	START	P-VALUE	SITES
Citrus_sinensis-41685	137	1.12e-14	CAGTTATAGG **ACATCTCTGCAGTATGAAGAACTCT** ATGTCGTGTG
Vitis_vinifera-4698	130	5.20e-14	GACAGTCCCG **ACATCTCTGCAGTTTGAAGAACTTT** ATATTCCATG
Glycine_max-71391	135	3.57e-13	GAGTTATTGG **ACATCTCTGCAATTTGAAGGACTCT** TTCATGTGAT
Nicotiana_tabacum-32427	84	7.84e-12	GAAATTTGAA **AAACATCTCCAGGCGGAAGAACTCC** TATTCATTGT
AT1G51200.1	136	8.21e-11	TTAGCGTCTT **CCATCTCTCTGTGGTGTGGAACTTT** CTATTATCTG

67938.t00021 | At5g67420 | K8K14.16 | LOB domain protein 37 / lateral organ boundaries domain protein 37 (LBD37) | identical to LOB DOMAIN 37 (Arabidopsis thaliana) GI:17227170

NAME	START	P-VALUE	SITES
Vitis_vinifera-49949	74	2.13e-18	TCTTTTATTG **GGGGAGGGTTTTTCCCGGAATTGAATTCGG** GAATTTTTGT
Gossypium_hirsutum-33236	98	7.75e-15	GGATACTTCT **GGGGAGGGGTTTCCCCGGAAATGAATTTTC** CGGCGAGTTT
Nicotiana_tabacum-9913	67	9.61e-15	TTTTCTATGG **GGGGAGGATTTTTCCCGGAAGTAAATTCCG** GGAGAGTTTT
Glycine_max-157039	83	9.56e-14	CTTTATTTTG **AGAAAGAGGTTTTCCCGGAATTGAATCCGG** TGAGATTTTG
Citrus_sinensis-62844	16	9.28e-13	AAGGTGTACC **GGGCAAGGTTCCGCCCGGAAAACAAGCGGC** GAACTGGTTA
AT5G67420.1	7	3.60e-11	TGCAAAA **CGGCGGCGGTTTTCTCAGAGTTAGTCTAGG** GTTTTAAATG

60082.t00004 | At1g29350 | F15D2.27 | expressed protein

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-98677	128	1.94e-16	GAGACTTTGG **CTGGCTACTGCCCTGTGCCATGAGG** TTGTATTCTA
Nicotiana_tabacum-38497	107	6.98e-16	AGGGACTTGA **CCGGCTACTGCCCTGTGCTATGAGG** CTGCACTTTA

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-15236	127	5.34e-13	GGAGACTCGA **CTTGCAACTGCTCTTTGCCTTGGGG** ATGTATTCTA
Glycine_max-111421	128	5.27e-12	ACCATATATG **GCCGCAGCTGCCCTGTGCGAAGTTG** TATTCTATAT
AT1G29350.1	201	2.37e-10	ACTCTTGCCT **CTTCTTACTTCTCTTGTCTAAGGGC** TCAACGTGAT

51066.t00024 | At2g36830 | T1J8.1 | major intrinsic family protein / MIP family protein | contains Pfam profile: MIP PF00230

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-83401	44	6.22e-14	AGCTTTCTTT **TGTGCTTAATTTGTGGCCGTTGATCT** TGTTTACTTT
Glycine_max-74271726	97	1.22e-13	TGTTTTCTTT **CCTGTTGAATCGGTGGCCGTTGATCT** TTGGTTGGAT
Citrus_sinensis-10194	85	2.02e-13	ATTTTTAATT **TGTGTTTAATTTATGGCCGTTGATCT** GTTTCCATCG
Vitis_vinifera-3638	67	8.64e-11	GGCTTGTTCA **TGTGTTTATTTCGTGATCGCTGATCT** TTCCATCATC
AT2G36830.1	121	2.99e-10	GTTCGATCTT **TTAGATGAATCCTTGTCCGTTGGTTT** CAAGAGTGGC
Nicotiana_tabacum-74734	62	2.60e-09	TTATTCTCTG **TTTGATTTCACAATTGCCCTTGATTT** GGGATGAACT

51786.t00032 | At1g01720 | T1N6.12 | no apical meristem (NAM) family protein | contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC domain protein NAM GB:AAD17313 GI:4325282 from (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-18155	147	1.17e-15	CGAGACTCAA **GGTCCATGAGTGTGCCTGTGCGACC** ACACACATAC
Vitis_vinifera-6366259	90	3.39e-14	TGAAGACTCA **GGTCCATGAGTGTGCACGTGCGAGA** GGTTTGGCGG
Citrus_sinensis-61432	81	8.29e-14	ACGAGACGAA **AGTCAATGAGTGTGCCTGTGCGGTG** CGGGGCCCAG
AT1G01720.1	84	7.06e-13	CGTTTTATAT **GGTCAATGAGTGTGCCGATTCGGCC** ATTAGATTTC
Nicotiana_tabacum-59576	47	8.48e-12	GCAAAGAGAC **GAGTCATGACTGGGCACGTGCGATG** TTTTGTTTGT
Gossypium_hirsutum-73156	75	8.48e-12	AAAAAACGGA **AATCCATGAATGTACCGGGGGGGGG** GGCGCGTAAA

35227.t00037 | At2g03090 | T17M13.26 | expansin, putative (EXP15) | identical to SWISS-PROT:O80622 alpha-expansin 15 precursor (At-EXP15)(Arabidopsis thaliana); alpha-expansin gene family, PMID:11641069

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-49361	280	5.36e-17	CCTTTTTCAT **GGCAGAGGTGGTCTTTTACCACCCGCC** ACTAGTATCT
AT2G03090.1	355	2.00e-16	AGTGGGTAGG **GGCAGAGGAGGAATTTCACCACCCGCC** TATGTGTTTT
Gossypium_hirsutum-141101076	314	2.00e-13	GGAGGAGATG **GCAGAGGTGGGACTTTTACCACCCGCC** AGCAGTGTTA

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-102257	376	3.58e-13	AGAAGAGGAA **AGCAGTGGTGGAAATTTATCACCCGCA** CTTGGTTTAG
Glycine_max-113009	414	1.09e-11	AAATTGGAAG **AGGTGGACTTTGTTGTTACCACCCGCC** AATTAGTATT

67612.t00022 | At5g11330 | F2I11.220 | monooxygenase family protein | low similarity to 2,6-dihydroxypyridine 3-hydroxylase (DHPH) (GI:14495302) (Arthrobacter nicotinovorans); contains Pfam profile PF01360: Monooxygenase

NAME	START	P-VALUE	SITES
Glycine_max-149644	138	1.08e-17	AGCTCAATTG **GATTTGGTATGTGAATCAGCCTGAGCCTGA** AGT
Citrus_sinensis-42528	29	1.38e-17	GAAGTCAATT **GGGTTGGTATGTCAATCAACCTGAGCCCGA** ACTCCAGGGA
Gossypium_hirsutum-22020	4	3.17e-17	ATTG **GATTTTCTATGTCAATCAACCTGAGCCTGA** GATAAAGAGA
AT5G11330.1	21	3.14e-12	TGATGTGAGA **GATGTTGTATGTTAATAATTGTGTGTTTAA** TAGACTTGAA

60522.t00016 | At3g14440 | MOA2.4 | 9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative | similar to 9-cis-epoxycarotenoid dioxygenase GB:AAF26356 (GI:6715257)(Phaseolus vulgaris)

NAME	START	P-VALUE	SITES
Citrus_sinensis-59235	59	1.62e-18	CCAGAGGGAT **GCTTGCATACACGTCCCCGGAATCTGCTCC** TCTGTTTTTA
AT3G14440.1	89	3.36e-18	CAGTGGGATG **CTCTGCATATACGTCCCCGGAATCTGCTCC** TCTGTTTTTT
Glycine_max-49853	59	9.51e-18	ACTGTGGGAT **GCTTGCAGATACGCCCCCGGAATCTACTCC** TCTTCAGTTT
Vitis_vinifera-22502	107	1.74e-15	CAGAGGGATG **GTCCGCATATGCGTCCCCGGAATCTCCAGA** CTCTCTACAG
Gossypium_hirsutum-70154	95	4.39e-12	AGGTTCATTT **GGCTTCCTCTACAAAGACTGAATCGAATGC** AATGTAACC

67161.t00003 | At4g26580 | T15N24.30 | zinc finger (C3HC4-type RING finger) family protein | contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)

NAME	START	P-VALUE	SITES
Vitis_vinifera-34650	135	1.53e-17	GTTCATTCAT **TGTACAGTGGAGCTCACCAGTAACCAAGA** TTTTATGTTG
Glycine_max-137583	102	7.06e-16	AGTTTGTACA **TGTACAGAAGAGGTCACCAGTAACCAAAA** CTACATTGAA
AT4G26580.1	133	4.53e-15	TTTTTTCTTG **TGTACAAAGTAGCTCACCAGTAACTGTAA** TTTTACCTAA
Citrus_sinensis-70756	124	1.35e-13	AGTTTATTGC **TTGTACATGGAACTCACCAGTAACTCGAA** AATTATACCA

51171.t00026 | At2g20570 | T13C7.1 | golden2-like transcription factor (GLK1) | identical to golden2-like transcription factor GI:13311003 from (Arabidopsis thaliana); contains Pfam profile: PF00249 Myb-like DNA-binding domain

NAME	START	P-VALUE	SITES
Vitis_vinifera-57152	46	1.08e-12	ACGAAGACAA **AAACCCAAAATTCGACGACAT** TCCTGCACTT
Glycine_max-11753	54	5.08e-12	TGATGGCCAT **AAAACCCTAATTCGACGACTT** CTCATCTCTC
Gossypium_hirsutum-46388	67	5.08e-12	CGCCATTTTC **AACACCTTAATTCGACGACAT** TAACCATATG
AT2G20570.1	30	9.13e-12	AAGCGAGAAC **CAAACAAAAATTCGACGACAT** GTCTTTCAAT

67036.t00003 | At4g00730 | F15P23.4 | anthocyaninless2 (ANL2) | nearly identical to Anthocyaninless2 (Arabidopsis thaliana) GI:5702094 67035.t00035 | At4g00730 | F6N23.10 | anthocyaninless2 (ANL2) | nearly identical to Anthocyaninless2 (Arabidopsis thaliana) GI:5702094

NAME	START	P-VALUE	SITES
Glycine_max-231357	169	6.90e-17	TTGGTTGGTT **GAGTCAAGAACGAACCGCGCGTGG** GGAAAAAAAG
Citrus_sinensis-34906	189	6.90e-17	CGGGGGTGTT **GAGTCAAGAACGAACCGCGCGTGG** AAACTCCTTG
Vitis_vinifera-58802	185	6.90e-17	ACTCGGGTGT **GAGTCAAGAACGAACCGCGCGTGG** AGAATCCTTG
Gossypium_hirsutum-29929	93	6.90e-17	TGGGGGTATT **GAGTCAAGAACGAACCGCGCGTGG** AGAATTATTG
AT4G00730.1	105	1.20e-15	AGGGGGTGTC **GAGTCAAGAACGAACCGCGCGAGT** GGGCGAGATC
Nicotiana_tabacum-109408	330	1.02e-12	TTAAAAGAGG **GAGTCAAGAACGCACCATACTTTT** CTTTCTCTCA

52277.t00039 | At1g55840 | F14J16.8 | SEC14 cytosolic factor (SEC14) / phosphoglyceride transfer protein | similar to polyphosphoinositide binding protein SEC14 homolog Ssh1p (GB:AAB94598) (Glycine max); identified in Eur J Biochem 1998 Dec 1;258(2):402-10 as AtSEC14, characterized by functional complementation in S. cerevisiae.

NAME	START	P-VALUE	SITES
AT1G55840.1	113	4.24e-15	TACTAGTTTC **GCTTGCATCAGCTCGATGCAGG** TTTTGTTTAA
Citrus_sinensis-42867	136	4.95e-14	AAAAGTGCTT **GCTTGCATCAGATCGATGCAGG** TGAATGTAAT
Gossypium_hirsutum-24867	116	1.61e-13	AGCAGAGCTT **TCTTGCATCAGCTCGATGCAGA** CTTGGTAGAC
Nicotiana_tabacum-30361	116	1.89e-13	AATACTAATG **GCTTGCATCATCTCGATCCAGG** ATTTAGATAG
Glycine_max-103569	151	5.63e-12	ATATTGTAAT **GTTTACATCAACTCCATGCAGA** ATTCTTCCCA

60024.t00003 | At1g79930 | F19K16.11 | heat shock protein, putative | contains Pfam profile: PF00012 Heat shock hsp70 proteins; similar to heat-shock proteins GB:CAA94389, GB:AAD55461 (Arabidopsis thaliana)

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-91008	369	1.49e-14	GGAATTTTTG **GGTGGTGGGGGGGATTTGGGGCGGG** AGAAATTTTT

NAME	START	P-VALUE	SITES
Citrus_sinensis-50122	83	5.58e-13	GAGACACGAA **CTTGGTGGGATGGCTTTGGAAGGGG** TGGACTGTTC
Vitis_vinifera-51183	57	3.51e-11	ACAAGTCTTT **GGTGGGGGGCTGCCAGTGAGAGAGG** CTATGAGATG
Nicotiana_tabacum-47	29	7.96e-11	TGACAGAAAT **CTTGGTGGGAGGGATTTTGATGAGC** TTTTTTCCAA
Glycine_max-1086271730	63	5.22e-10	CTGGAAAAAT **CGTCGTGGGTGAGAGTTGATGCTGG** GATTCTTTGC
AT1G79930.2	47	7.69e-10	ACAAGCCAAG **GGAGGTGAGCAGGCGGATGAGGGCA** AGAGTGAGCC

60730.t00015 | At1g33470 | F10C21.14 | RNA recognition motif (RRM)-containing protein | similar to RRM-containing protein SEB-4 (Xenopus laevis) GI:8895698; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)

NAME	START	P-VALUE	SITES
AT1G33470.1	123	2.50e-15	CAAGACCTGT **GGCCTAACCATGGTTGCCCTTTTCCC** TTTATGCTTC
Glycine_max-179809	118	9.60e-13	ATCAACCTTT **GCCCTAACCATGGTGCTCTCTCTCTC** TCACACACCC
Gossypium_hirsutum-28394	88	5.75e-12	TTCAACCTTG **GGCCTAACCATGGTTCTTTTTTCTCC** CTCTATCTCT
Nicotiana_tabacum-20749	120	7.82e-12	GGTTATCCAG **CACAGCACTATGGTACCCCATTTCCC** CCCCTCCTCA
Citrus_sinensis-86824	6	7.06e-11	CCAATA **TGGCTCTGCATGCTCCACCATTTCAC** ATCGCTAGAG

67288.t00031 | At3g54180 | F24B22.140 | cell division control protein 2 homolog B (CDC2B) | identical to cell division control protein 2 homolog B (Arabidopsis thaliana) SWISS-PROT:P25859

NAME	START	P-VALUE	SITES
Citrus_sinensis-46815	168	5.15e-13	TCATGTTAGT **TGTCATCATCTTGGTGATTTCAC** CATCTGAAGT
Glycine_max-170133	128	3.59e-12	TGTAATATTT **CGTCATCATCTTGGTGATATGAA** CAGGTCACTC
AT3G54180.1	19	8.63e-12	CTGTATCTGT **TGTCATCGTCTTGGTGAATTTAA** ACATTTGATC
Nicotiana_tabacum-12487	72	2.66e-11	TCCTGAAGAA **TATCATCTTCTTGGTGATTTGAA** GTCTGCATTG
Gossypium_hirsutum-96573	138	2.60e-10	GGAAATAAGT **TGTCTTCAACTTAGGGGATCCAA** AAAGGTTTTC

52154.t00044 | At1g78430 | F3F9.6 | tropomyosin-related | similar to Tropomyosin 1 (Baker's yeast)(SP:P17536) {Saccharomyces cerevisiae}; similar to enterophilin-2L (GI:12718845) (Cavia porcellus); similar to latent nuclear antigen (GI:5669894) (Human herpesvirus 8); similar to multiple ligand-binding protein 1 (GI:1403575) (Streptococcus sp.)

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-198101077	33	3.26e-13	ATATTATTGT **GAAATGGTTACTCACCATTTCA** GTTTTGGTTG

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-54236	56	1.42e-12	TTTGCCAGCA **AAAATGGTTCCTCACCATTTCA** ACTTTCTTGG
Citrus_sinensis-31257	48	8.80e-12	AATGTTCGGA **GAAATGGTTGCTTACTATTTCA** CGTTCTGTTG
AT1G78430.1	85	1.22e-11	GTGTGTCGAC **GAAATGATGGCTCATCATTTCC** ATAGATTCTT

6547.t00023 | At2g40610 | T2P4.4 | expansin, putative (EXP8) | similar to expansin 2 GI:7025493 from (Zinnia elegans); alpha-expansin gene family, PMID:11641069

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-20467	109	4.26e-18	GGAGATCTAT **TGCTGTGGTGGCTAATTGGCACCCGCATGG** GCTAGTATAT
Nicotiana_tabacum-108202	165	4.26e-18	TTGGCTCTAT **TGCTGTGGTGGCTAGTTAGCACCCGCTTAG** GCCTATAGTA
Citrus_sinensis-63672	119	7.51e-18	CCTGTCTTGT **TGCTGTGGTGGTCTGTTGGCACCCGCTAGG** CCTCTATAAA
Glycine_max-107175	140	1.04e-17	TGGCCCCTAA **TGCTGTGGTGGCTATATGGCACCCGCTAGG** ACTAATATAA
Gossypium_hirsutum-263101077	131	1.19e-16	GGCTGTCAAT **TGCTGAGGTGATTTATTGGCACCCGCTAGG** CCTATACATA
AT2G40610.1	52	2.94e-16	GGCTGCATAT **TGCTGAGGTGGCTCGTAAGCACCCGCTTAA** TTAGCTTAGC

51739.t00011 | At1g08420 | T27G7.10 | kelch repeat-containing protein / serine/threonine phosphoesterase family protein | contains Pfam profiles: PF00149 calcineurin-like phosphoesterase, PF01344 kelch motif

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-39580	71	3.95e-16	TTTCTGGTGT **TCTGTATAGAGCATGATGCCATATACGGG** AATTCTTGAA
Gossypium_hirsutum-62346	71	5.18e-15	ATCTCGGTGT **TCTGTATAGACCATACAGCCACATACAGG** TGTTCCCAAA
Glycine_max-593271730	66	8.23e-13	GTTTTAGTGT **TAGGTATATAGCATAATGCCATTTACGGG** AGTCTCTTCG
AT1G08420.1	77	9.12e-12	GTGTTCCTCA **TGTGTACAGAAAAAGATGAGCCATAGACG** AGAAACGATG
Nicotiana_tabacum-53664	440	1.58e-11	GTGGTTACTT **TGTGTAATTGTATTGCTGCCCCTTCCACG** CGAACAAGAA

67174.t00023 | At4g29160 | F19B15.190 | SNF7 family protein | contains Pfam domain, PF03357: SNF7 family

NAME	**START**	**P-VALUE**	**SITES**
AT4G29160.1	47	1.52e-10	GATAGACACG **AACAGACGATGTATATA** AGGATCTGAA
Vitis_vinifera-10089	271	6.95e-10	TTTACCGGTA **AACAGACAATGTATATA** AAGGTGGCAT
Gossypium_hirsutum-39884	81	2.84e-09	TTTAAGGTTT **AACAGACAATGTACAAA** TTTATCTGTA
Glycine_max-1535271731	113	7.11e-09	TATTGAGCTG **ACCAGAGGATGTATATA** AAAGTGGAAA
Nicotiana_tabacum-2284	19	3.27e-08	GTTGCCTACC **ACGAGACAGTGTAAAGA** TGTGATGTAT

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-3158	106	3.84e-08	GCATTCAATG **AACAGACTGTATATAAA** GTTTGCGTAA

51945.t00047 | At1g07470 | F22G5.18 | transcription factor IIA large subunit, putative / TFIIA large subunit, putative | nearly identical to transcription factor IIA large subunit GI:2826884 from (Arabidopsis thaliana); contains Pfam profile: PF03153 transcription factor IIA, alpha/beta subunit

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-198849	139	5.24e-14	ACTATTGTGA **TGTTGGCCTCTTGTACATAGAGAATGAG** CAATTTTTTG
Vitis_vinifera-14660	163	5.24e-14	TGGGTTGGAT **GATTGGCCAGTTGTACATAAGGGAAGAG** CTTTTTTTGG
Gossypium_hirsutum-769101073	178	7.34e-14	TGGGTTCGAT **GGTTGTCGTATTGTACATAAAGGAAGAG** AGCATTTTCG
AT1G07470.1	126	8.23e-13	TATGTACTCT **GGTTGGCTTGTTGTACAAAAAGAACAGA** TTTTTCCGGC
Nicotiana_tabacum-50387	150	1.98e-11	GAAGTTTTTT **GGTTGGCCGAGTGTATATATATAGTAAA** AGAGCTGCTG

67995.t00026 | At5g16000 | F1N13.140 | leucine-rich repeat family protein / protein kinase family protein | contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-39630	97	3.11e-15	AGCTATGTAA **TGCTCGTATTCATCTGTAAAAAGAAAAAAA** AAAAAGAGGA
Gossypium_hirsutum-8318	89	3.11e-15	AGTTGTTGAA **TGCTTGTATTCATCTGTAAAAATTAAAAAA** AGAAAATCAT
Vitis_vinifera-43347	112	1.45e-14	GCTGTTGAGT **TGCATGTATTCAACTGTAAAGAAAAGGAAA** GTCATATGTA
Citrus_sinensis-36257	95	8.21e-13	ATGCCAACAC **GCCATGTATTCATCTGTAAAAAAGTTAAAA** GAGGAAATTC
AT5G16000.1	220	5.28e-11	GGGAACACTT **TGGGAGATTTCATGTGTGAAATTTGGGAAT** TCATGTTTGA

51140.t00033 | At2g42670 | F14N22.6 | expressed protein

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-6196	69	1.08e-15	GTAGAAGTTA **GGCATTTGGCGTTGTACATATTACTACAC** CAATGTAATC
Vitis_vinifera-6191	96	1.06e-12	AACTGTGCTA **GGCATTTGGCTTTGTACATATTTATATAT** ATTGATGAGA
Citrus_sinensis-90861	134	3.61e-12	TATGTAATTT **AGGCATTGGGCGTGTACATATTATTATAC** ACCATTGTAG
Glycine_max-75408	114	1.54e-11	ATGTCCTTTA **GGCATTGGAATATGTACATAATAATGCAC** TAGTGTAATC
Nicotiana_tabacum-21090	123	2.58e-11	CTATAGAATA **GGGCACTTCTGATGTACATATCAATATAC** CGTAACATT
AT2G42670.2	100	1.48e-10	CTTTTTATAT **TGCAAACGGGATTGTACATACTAATTTGT** GATACACCGT

51571.t00057 | At1g53910 | T18A20.14 | AP2 domain-containing protein RAP2.12 (RAP2.12) | identical to AP2 domain containing protein GI:2281649 from (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-16926	29	5.63e-11	GCTGGTCTTC **TGTAAATAAAGCTACATG** AATGGTTGTT
AT1G53910.3	15	1.45e-10	TCCAGTTTCA **TGTAAATAAGGCTGCATG** TTTGTGAGTT
Glycine_max-1748271730	26	3.13e-10	TCTCCCTGTG **TGTAAATAAAGCTACAAG** TTGTTTTTCT
Gossypium_hirsutum-833101075	26	3.13e-10	AACTAGTGTT **TGTAAATAAAGCAACATG** AATTTGGTCA
Citrus_sinensis-61262	26	3.56e-09	TTGCTAGTTT **TGTAAATAAGGCTATATC** TTAGAGGACT
Nicotiana_tabacum-57511	28	8.89e-09	TGCTAAGTTT **TGTAATTAAAGCTTCATT** TGAGTGAAGT

67258.t00024 | At3g47470 | F1P2.20 | chlorophyll A-B binding protein 4, chloroplast / LHCI type III CAB-4 (CAB4) | identical to SP|P27521 Chlorophyll A-B binding protein 4, chloroplast precursor (LHCI type III CAB-4) (LHCP) {Arabidopsis thaliana}

NAME	**START**	**P-VALUE**	**SITES**
AT3G47470.1	145	6.19e-13	AATTTGGAAT **CTTCAATGTACAGAGGAACTA** AGTTAATCAA
Citrus_sinensis-11669	100	3.78e-12	ACATGGAAAC **CCTCAATGTACAGGGGAACTA** TGATGGAATT
Nicotiana_tabacum-46535	111	1.50e-11	AACAATGGAC **CTCTACTGTACAGAGCAACTA** GAATTTGCAT
Glycine_max-181527	100	2.73e-11	GATCCATCTA **TTTTCATGTACAGAGGAACTA** CGATGGTTTT
Gossypium_hirsutum-66992	105	9.14e-11	AACAAGGAAC **TTCTAATGTACAGTGGAACTT** CAGATTGCAT

67130.t00014 | At4g20270 | F1C12.190 | leucine-rich repeat transmembrane protein kinase, putative | CLAVATA1 receptor kinase, Arabidopsis th., PATX:G2160756

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-128776	1296	1.04e-13	TTAATGGTTT **TGTACAGTAGGATTGGTGGGG** GGGGTTATTT
Nicotiana_tabacum-69682	161	1.29e-12	GTTTTCCTCT **TGTACAGTAAGATTGGTGGGG** TTTTCTCAAG
Gossypium_hirsutum-84331	106	1.29e-12	CCTTTTCTTG **TGTATAGTAGGATTGGTGGGG** GTATTTTGTT
Vitis_vinifera-2766264	150	2.42e-12	AAGTTTTTTG **TGTACAGTAGGATTGGGGGGT** TGGGTTTCTT
AT4G20270.1	81	3.47e-10	TTTTAGAATT **TGTAATGATGGTTTGGTGGTG** ATATGAGTTT

67301.t00003 | At3g57200 | F28O9.50 | hypothetical protein

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-75166	137	4.75e-20	TGGAGCTCTT **CCCGATCATTACCCAAGCGCTGGTGTACAT** TTCAGATTTA

NAME	START	P-VALUE	SITES
Vitis_vinifera-51130	163	8.71e-19	TTCAAGGTTT **CCCGATCACTACCCAAGCGCTGGTGTAAAT** TTTTTAGAGA
Gossypium_hirsutum-57198	144	6.74e-17	GGGGGCTATT **CCCGATCATTACCCAAGCGGCACTGTACAT** TTTTAAGGTT
Nicotiana_tabacum-54403	156	3.32e-14	GGTTATTCCC **GATCATTATTACCCAAGCGGAGGTGTAAAT** TTATGTTGTA
AT3G57200.1	47	4.29e-13	TGATTTATGA **ACAGTTTTGAACCTGAGCTCTGGTGTACAT** TTAGGAAAGT

49197.t00003 | At2g40110 | F27I1.3 | yippee family protein | similar to mdgl-1 (Mus musculus) GI:10441648, Yippee protein (Drosophila melanogaster) GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-55953	28	5.11e-15	AATAATTCTA **TCCCAAATGTACATTCTTTAACCCAC** CACCCCATTA
Gossypium_hirsutum-85103	29	2.45e-13	TGGTCTAATT **TCCAAATTGTAAATTCTTTAAACCCC** TTAAAATTCT
Glycine_max-134390	12	2.78e-13	ATCCTACCAT **TCCCAATTGTACATTCCTTAACCCTG** TGTTGTTCAA
Vitis_vinifera-44929	11	7.99e-13	TAACCTTTAT **TTCAAAATGTACATTCATGAAACCCC** TATTGTTCTT
Citrus_sinensis-105507	14	1.21e-11	TACCCATCAA **TTCCACCTGTATATTCTTTAACCATC** AAATTTCCCA
AT2G40110.1	40	1.64e-10	TGACCATTTC **ATGTAAATGTAAATTATTCAACCTCC** ATTCCAATTT

52178.t00038 | At1g32400 | F5D14.17 | senescence-associated family protein | contains Pfam profile PF00335: Tetraspanin family

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-60101076	120	1.29e-17	GTTCCTTGTG **GAGTTTGTGTACAATACACAATTTTCAGGA** GCTTCACTGT
Nicotiana_tabacum-101409	94	6.98e-15	TCTCTTTGTG **GAGTCTATGTACAAAACACAGTTTTCAGGA** TCTTCACTTG
Citrus_sinensis-33470	79	9.06e-15	TCGTTTTGTT **GAGTTTGTGTAGAAAACACATTGTTCAGGA** GTTATAACCA
Glycine_max-68731	105	1.17e-12	TCCTTTTGCT **TAGTTTGTGTATCATTCACACTTTACTGGA** TCTCCTTCAC
Vitis_vinifera-19425	108	5.66e-12	TGTTTCTGTT **GAGTTTGTGTACAATACAACATTTTTTTCA** GGAGTTCTAC
AT1G32400.1	58	1.25e-10	TCTTTATTAT **TTCTGCGTGTAACAATCAAGAGTGTCAGTA** AAAGTAGGAT

60225.t00013 | At3g11660 | T19F11.6 | harpin-induced family protein / HIN1 family protein / harpin-responsive family protein | similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)

NAME	START	P-VALUE	SITES
AT3G11660.1	62	1.39e-10	CTTAGTGATG **TGAATTGTACATTTTGCT** TATACGAATA
Citrus_sinensis-32106187	132	1.39e-10	ATTAAAGAGT **TGAATTGTACATTTTGCT** ATAGAATAAA

NAME	START	P-VALUE	SITES
Vitis_vinifera-3370	90	1.39e-10	ATACGTCTTT **TGAATTGTACATTTTGCT** AAGAATAAAA
Nicotiana_tabacum-23042	127	1.39e-10	ACATAGTTGA **TGAATTGTACATTTTGCT** AAAAATAAAT
Gossypium_hirsutum-81708	125	3.76e-10	TGTTTGTAAG **GGAATTGTACACTTTGCT** ATACAATAAA
Glycine_max-206834	362	2.93e-09	ACTAGATGTT **TGTATTTTACGTTTTGCT** GTAGAAATGT

60504.t00029 | At3g18820 | MVE11.21 | Ras-related GTP-binding protein, putative | similar to Ras-related protein RAB7 GI:1370186 from (Pisum sativum), Plant Mol. Biol. 21 (6), 1195-1199 (1993); contains Pfam profile: PF00071 Ras family

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-45558	92	1.32e-14	TGGGGGATAT **ACTGTACATTAGTGTATGTGTGAGGAACA** AAATAGTCTG
Vitis_vinifera-12166257	97	1.43e-13	TGACGCTGCA **CTTGTACATTAGTGTTGGCATGGGAGGAA** AAACTCTGGT
Glycine_max-1662271727	77	8.27e-13	AGGAGACATC **ATTGTACATTAGTGTTTGCTCAAGAAACA** AATTGGTCCA
Citrus_sinensis-23437	90	8.27e-13	ATAAGGTTAC **ATTGTACATTAGTGTTTGTGTGAAACAAA** TTGGTTCATT
Nicotiana_tabacum-96453	123	1.86e-11	TCAAGTTGTA **CCTGTATATTAGCTTTTGCAAGGGGAGCT** GGTTGGTTCC
AT3G18820.1	75	9.99e-10	TTATTACTAT **GTTGTAAATTTTTTCTTTTGTGTGGAAAA** GGGATGAGAA

68169.t00412 | At4g14900 | FCAALL.410 | hydroxyproline-rich glycoprotein family protein

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-783101074	82	3.08e-18	TAAATGGTTT **GTTTGTAATCACTAACCGTTTAATGGTAGC** GATATCTGTG
Glycine_max-71271731	68	5.63e-18	TCGCAATGTT **GTTTGTAATCACTAACCGTTTAACGGTAGC** AGTTGTGTGT
Vitis_vinifera-13235	77	5.63e-18	TCAATGGTTT **GTTTGTAATCACTAACCGCTTAATGGTAGC** GATATCTGTG
Citrus_sinensis-11370	73	1.40e-13	TTCTAAATGG **GTTGTAATTCACTAACCGTTTTAACGTAGC** AATGGCTGTG
AT4G14900.1	30	3.30e-12	AAAGAAGATG **GTAAGTAACCAACCACTGATCTCTGGTGTC** TACGTTTTGT

60243.t00012 | At3g09980 | T22K18.21 | expressed protein | contains Pfam profile PF04949: Family of unknown function (DUF662)

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-671101077	179	2.22e-18	TAGAAAGGGA **AATGCCCCTATAAACAGGTTTGTAACTAAA** CTCTTGGCGA
Citrus_sinensis-31379	196	3.55e-15	TTAGGAAGGG **AATTACCCGATAAACAGGTTTGTAACTAAA** TGCATCATGT

NAME	**START**	**P-VALUE**	**SITES**
AT3G09980.1	207	2.97e-14	AACTTCAAAA **AATACTCATCAAGACAGGTTTGTAACTAAA** CGCTTCTTCT
Nicotiana_tabacum-98716	194	5.27e-14	TCTTAAAGGG **AAAAACCCTGTAAACAGGTTTGTAACTATA** ACAAGTCTCA
Vitis_vinifera-21503	171	8.39e-13	AGGAAAGGGT **AATGCCCTTTAAAACAGGTTTGTAAACTAA** ACAATGTCTC
Glycine_max-1849271728	174	2.73e-12	AGGGCTATAT **ACCCTACAAACAGCCAGGCTTGTAACTAAA** TACTTGCATT

67039.t00045 | At4g01100 | F2N1.16 | mitochondrial substrate carrier family protein | contains Pfam profile: PF00153 mitochondrial carrier protein

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-25728	35	1.80e-17	TATGAGGTGT **GTGGTATTTTTGTAGGCAAGGGGATAGAGA** GAAAGGTAAA
Vitis_vinifera-9643	35	6.16e-17	TTGAACCAGT **GTGCTATTTTTGTAGGCAAAGGGAAAGAGA** GAAGGTAAAT
Citrus_sinensis-88787	33	1.76e-14	TTGGACAGAG **GTGTTATTTTTGTAGGGAAGGGGTTAGGGA** AAAGGTAAAG
Glycine_max-169000	31	2.26e-13	TTGATTGCCT **GTTATTTTCTTGTAGGCAAGGGGATGCAGA** GATGATAAAT
Nicotiana_tabacum-81718	32	5.86e-12	TTTCATGCAT **ATGATAATTTTGTAGGCAAGGATACAAGGG** TTACAATAAC
AT4G01100.1	35	9.64e-11	AGAAAGCGCA **CTTCTATTTTTGTAGCCAGAAGAGAAGTTC** AACAAAGTTA

67318.t00033 | At3g61470 | F2A19.70 | chlorophyll A-B binding protein (LHCA2) | identical to Lhca2 protein (Arabidopsis thaliana) GI:4741940; similar to chlorophyll A-B binding protein, chloroplast (Precursor) SP:P13869 from (Petunia hybrida); contains Pfam profile: PF00504 chlorophyll A-B binding protein

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-49673	156	6.22e-13	TGTTGAGTGT **TGTACAAATACCTTTATGAAATTAGA** AGCAATGAAT
Vitis_vinifera-2793	158	9.15e-13	GCTCATGCAG **TGTACAAATACCTCTATTAACTTAGA** TTCCATTTAA
Nicotiana_tabacum-13387	153	1.09e-11	GATTAAGCAG **TGTACAAATATCTTTGGGATCTCCTA** AGTCCTAACA
AT3G61470.1	52	2.20e-11	TGATCATGTT **TGTACAAATATCATTTTGAACTTAAA** ATTATTATGT
Glycine_max-169555	159	5.64e-11	GATTATTCAA **TGTACAAATACCTATTTAAGTTTAGA** TGCATTTAAT
Citrus_sinensis-78681	119	2.23e-10	CCTCTATCTA **TGTACAAAGACTTGTGTGATCACTTA** GATGCCATGA

60468.t00021 | At3g15880 | MSJ11.27 | WD-40 repeat family protein | contains Pfam profile: PF00400 WD domain, G-beta repeat (7 copies)

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-42530	23	1.29e-15	AGAGCACAAG **TTCTTTTACATGCTTGGCTTACTGGCAC** TCTAAATTTA
Glycine_max-123271734	22	4.53e-14	GAAGACAAGT **TTCTTTTACATACTTGGCTTGCTGGCCA** TTTTAAGAAC

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-41675	23	1.47e-13	AGAGCACAAG **TTCTTTTAAATGCTTGGCTTGCATGTCC** ATTCCTAATC
Nicotiana_tabacum-97186	514	5.27e-12	AGTGTAATCT **TTCTATTACATGCTGAGATTTCAGACAC** ACGATG
AT3G15880.2	142	2.18e-11	GCTGCCACCA **TTCGAGTCCATGCCTGGCCGAGAACTCG** AACGCATGAT

60464.t00012 | At3g15980 | MSL1.4 | coatomer protein complex, subunit beta 2 (beta prime), putative | contains 7 WD-40 repeats (PF00400) (1 weak); identical to coatomer protein complex, beta prime (beta'-COP) protein {Arabidopsis thaliana} (GI:9294445); similar to Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP) (p102) (SP:P35606) (Homo sapiens)

NAME	START	P-VALUE	SITES
Vitis_vinifera-18766263	10	7.30e-19	TAAGGTTAAT **CCAAAAGCTGCTGAATCTTTGGCTGATCCT** GAAGAGTATC
Gossypium_hirsutum-45683	1	7.30e-19	T **CCAAAAGCTGCTGAATCTTTGGCTGATCCT** AAAGAGTATC
Citrus_sinensis-72084	2	5.48e-18	AC **CCAAAAGCTGCTGAATCTCTGGCTGATCCT** GAAGAGTATT
Nicotiana_tabacum-10419	34	1.02e-12	ATAATGTTAA **CCAGAAAGCAGCAGAGCTTTGGCTGATCCT** GAGATATCCC
Glycine_max-98130	21	9.72e-12	TGAAGGAGCC **CCGTCAGCTGAGAAGCATTTGGATGGGGCC** GTGTGAAAAT
AT3G15980.2	72	1.69e-11	AAACCTCTCC **CCCAAAAAAGAAAAACATTTTGCCGCTTCT** AACATTTCTA

67045.t00018 | At4g02260 | T2H3.10 | RelA/SpoT protein, putative (RSH1) | identical to RSH1 (RelA/SpoT homolog) (Arabidopsis thaliana) GI:7141304; contains Pfam profiles PF02824: TGS domain, PF01966: HD domain, PF04607: Region found in RelA / SpoT proteins

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-56249	49	2.29e-13	CGGTCGCAAG **CTCGGTATGAAAGTTTTGTCCCC** CCATAGAGAG
Citrus_sinensis-102659	49	3.60e-12	AAAGGCAAGA **CTGGGTATGAAAGTTTGGTCCCA** GAAGTCTGAA
Glycine_max-509271730	50	1.91e-11	GGCCATTCCG **CCGGGGAATTAAGTTTTGTCCGC** AGCAGCGTAG
Nicotiana_tabacum-27658	42	7.77e-11	TGTTGAAAGC **TTGGGAAAAAAAGTTTTGTCCTC** TAAAACCATA
AT4G02260.1	18	5.25e-10	GACTCACGTT **CTTGGCCTTGAAGTTTTGTCATG** TTCACTGGAA

50818.t00051 | At1g67325 | F1N21.24 | zinc finger (Ran-binding) family protein | similar to ZIS2 (Homo sapiens) GI:4191329; contains Pfam profile PF00641: Zn-finger in Ran binding protein and others

NAME	START	P-VALUE	SITES
Glycine_max-3757	5	2.25e-19	GTACT **AGGACATGTTTGAGGGTTGAGAAGGTCCAG** AGTTGTCATC
Citrus_sinensis-34938	5	2.25e-19	GTACT **AGGACATGTTTGAGGGTTGAGAAGGTCCAG** GGTTTTCTTC

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-6978	5	2.25e-19	GTACT **AGGACATGTTTGAGGGTTGAGAAGGTCCAG** GGTTGTCGTC
Gossypium_hirsutum-89831	5	2.25e-19	GTACT **AGGACATGTTTGAGGGTTGAGAAGGTCCAG** AGTCGTCGTC
Nicotiana_tabacum-107784	5	2.35e-17	GTACT **AGGGCTTGTTTAAGGGTTGAGAAGGTCCAG** AGTTGTCGTC
AT1G67325.1	4	3.51e-16	GTCG **TAGACATGTTTGGGGGTTGAGAAGGGTGAG** TCTAATCCAG

67774.t00016 | At5g43330 | MNL12.18 | malate dehydrogenase, cytosolic, putative | strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SP|O24047 {Mesembryanthemum crystallinum}, SP|O48905 {Medicago sativa}, (Prunus persica) GI:15982948; contains InterPro entry IPR001236: Lactate/malate dehydrogenase

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-173133669	77	3.00e-14	AGTATGTGAT **AATAGAAGTGGCTTCAGTTTTGAATAAGGC** CATTGTTGAT
Gossypium_hirsutum-18647	49	5.64e-14	GGTTTGCCTT **AATAGGATTAGCTGCAGTTTTGAATAAAAA** ACCGTTCTAG
Glycine_max-978271733	57	9.25e-13	GGTTTGCCCA **CAGAAGTGTAGCTTCAATTTTGAATAATGC** TCCTTCTAAG
Vitis_vinifera-18866257	66	2.68e-12	ATGAGGATTG **AAGAGGCATTTATGCAGTTTTGAATAAGGA** AGAAAAACCT
Citrus_sinensis-65097	53	6.93e-12	TTGTCTGAGT **AGTTGGTATAGTTACAGTTTCGAATAAAAC** CATTGTTGAA
AT5G43330.1	23	1.79e-10	CAGCTGGTTT **AATCAGTGAAAGCTTTGTTTCGAATAAAGA** AGTTTTGTTA

67610.t00034 | At5g10450 | F12B17.200 | 14-3-3 protein GF14 lambda (GRF6) (AFT1) | identical to 14-3-3 GF14lambda GI:1345595 from (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-37462	27	6.17e-16	CAGTCATATT **CCTCTCCAGGAGGAGGTGGGCTTTGAA** TGTCATTTTG
Gossypium_hirsutum-96326	30	8.45e-15	TGGTCCTATT **CTTCATCTGAAGGAGGTGGGCTTTGAA** TGTCATTTGA
Glycine_max-132636	29	1.35e-13	GGGTGGTATT **CTTCCTCTCATGGAGGTGGGCTTTGAA** TGTCATTTCT
Citrus_sinensis-8209	24	1.34e-12	GATCCGTTTG **CTCCTCTGGGGGGAGGGGGGCTTTTGA** ATGGGCTTGA
Nicotiana_tabacum-9166	330	1.58e-12	TGACATTAAA **CTGCTCCTCCAGGAGGTGGGCAATGTC** ACACAGCAAC
AT5G10450.2	4	1.94e-10	GGAT **CTAGATGAAGGGGGGGAGGGTTGTTAC** GCGATGTTTC

67111.t00016 | At4g12570 | T1P17.160 | ubiquitin-protein ligase, putative | similar to SP|P39940 Ubiquitin--protein ligase RSP5 (EC 6.3.2.-) {Saccharomyces cerevisiae}; contains Pfam profiles PF00240: Ubiquitin family, PF00632: HECT-domain (ubiquitin-transferase)

NAME	**START**	**P-VALUE**	**SITES**

NAME	START	P-VALUE	SITES
Vitis_vinifera-25284	21	3.52e-15	CATCTCATTT **TGGGATAAGAAGGGTTTTTGACTGCACA** GAGAGATTTG
Citrus_sinensis-90905	16	2.53e-14	TTGTCTGCCC **TGGCGTCACAAGCGTTTCTGACTGCACA** TAAATTTGTA
Glycine_max-194771	16	1.17e-12	ACACCTGCAA **TCTGAATAGAAGTGGTTTTGACTGCACA** TAAAATTATC
Gossypium_hirsutum-163101074	32	3.83e-12	ATTTTGGTGG **GGGCTAAAAATCGGGTTTTAACTGCACA** GATAAATTTG
AT4G12570.1	117	1.12e-10	TTTAGTGTTA **TGGTCATGCCTCTGTTTATGACCGGAAG** ATTTCTTAAC

51597.t00063 | At1g78080 | F28K19.29 | AP2 domain-containing transcription factor RAP2.4 | identical to AP2 domain containing protein GI:2281633 from (Arabidopsis thaliana)

NAME	START	P-VALUE	SITES
Glycine_max-180944	57	1.68e-17	TGGCTGCTAC **TGCAATGGAGTTTTTGGCAATTGCAGGG** CTAGTACTAT
Citrus_sinensis-66130	90	5.24e-16	TAGTGGCGGC **TGCAATGGAGTTTTTGGCATTTGCAGCG** CCAAGCTTAT
Gossypium_hirsutum-42342	98	1.11e-15	TAAAGCTAGC **TGCAATGGGGTTTTTGGCAGTTGCAGTG** GCATGTATTT
AT1G78080.1	25	2.71e-12	TTCAGCCGCT **TGCAATGGAGTTTTTGTGAAATTGCATG** ACTGGCCCAA
Nicotiana_tabacum-81384	109	4.31e-12	GGGACAGCCA **TTGCAATGAGTTTTTGGTAATTGCCTGG** TTAGCCCTTA

67222.t00016 | At4g39780 | T19P19.170 | AP2 domain-containing transcription factor, putative | similar to AP2 domain containing protein RAP2.4,Arabidopsis thaliana

NAME	START	P-VALUE	SITES
Citrus_sinensis-25409	75	1.51e-16	TAAAGAGTGG **CATCTGCAATGAAATTTTTGACATTTGCAG** AGTTGCTATT
Glycine_max-82524	123	1.40e-15	TCTTTGGCTG **CTTCTGCAATGGATTTTTTGACATTTGCGG** ATGTTTTGCT
Nicotiana_tabacum-6133670	94	4.56e-14	AGGTAATGGC **CTCTTGCAATGAGGTTTTTAACATTTGCAA** GAGGTCAGTC
Gossypium_hirsutum-22865	100	1.34e-13	TCTGCAGTTA **TCTCTACAATGAAATTTTTGACATTTGTAG** AGGGTATTTA
AT4G39780.1	67	1.60e-13	ATATTAATCT **CTCTGCAACTGAAATTTTTAACAGTTGCGG** AGAGAATCGT

67217.t00026 | At4g38710 | F20M13.270 | glycine-rich protein | cylicin II - bovine, PIR2:I46014

NAME	START	P-VALUE	SITES
Vitis_vinifera-15164	167	2.29e-15	TTTCTATGAT **GCAGTATGGAGACAATTTTGGTAGG** CATTCTCAGT
Gossypium_hirsutum-283101072	127	8.51e-13	TATTGTCAAT **GCAGTATTTAAACAATTTTGGTAGG** CTTCGAATTA
AT4G38710.1	102	6.91e-12	TTGTGTGGGG **GAACTCTAGAGAAAATTTTGGTAGG** GTCTTTTTTT

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-187653	278	6.45e-11	TAATACTGAA **ACAGTTGAGAGACATTTTTGATAGC** AGTGTTGGTA
Nicotiana_tabacum-67764	79	9.07e-11	CATGTGATGC **GAAGCATTAAAGCAATTTTGATAGA** ACTGCTCAAT

67801.t00014 | At5g47010 | MQD22.15 | RNA helicase, putative | similar to type 1 RNA helicase pNORF1 (Homo sapiens) GI:1885356

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-256841	37	5.76e-18	GATGGGTTAT **AGTCTTTGCAATCAGCAACTGGGTTTGTGC** CTGTCTTTTG
Citrus_sinensis-47426	125	6.57e-17	GATGGGTTAT **AGTCTTTGCATTCGGCAACTTGGTATGTGC** TGTCATGTGT
Gossypium_hirsutum-81688	39	3.47e-14	GATGGGGTAT **AGTCTTTTGCATCAGCAACTTGGGTTGNGC** TGGCCTTGGT
Nicotiana_tabacum-77045	27	6.28e-14	TGTAACGGTT **ATGTTTTGCATACAGCAACTTGGTTTGTGC** TGTCATGTGA
AT5G47010.1	136	1.54e-11	CGCCTTTCTG **GCTCGCTTAACGCAGCAAACAGGTAAATGG** TTATGCAAAG