67150.t00039 | At4g24770 | F22K18.30 | 31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/2/3, putative / RNA-binding protein cp31, putative | similar to SP|Q04836 31 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein RNP-T) (RNA-binding protein 1/2/3) (AtRBP33) (RNA-binding protein cp31) {Arabidopsis thaliana}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)

NAME	**START**	**P-VALUE**	**SITES**
AT4G24770.1	18	1.04e-13	CACCGTTCTA **AAACCCTTCCCTTCCTCTTCTTTTCTCTTC** TCCTTCCACT
Gossypium_hirsutum-6261	67	4.14e-13	CTTCTTCTTA **AACCCTCTCCTTCACTCTCCCCCCATCTTC** GCTTTATTCA
Nicotiana_tabacum-117133670	55	1.50e-12	CCGCCGTTTC **AAACCTCTGCCTTTCTCCTCAGTCCTCTTC** ATCTTATCCT
Vitis_vinifera-5408	28	1.44e-11	CCCAAAGCCA **AACCCCTTCCCTCTCCCTTCACAACTCCTT** ATCTTCTCCA
Citrus_sinensis-26113	34	2.31e-11	CTCTCTTGCT **AAACCTCTCCTCTCCCAGTCCTCTCTCTCA** CCATTCTACC
Glycine_max-217550	33	3.35e-11	TCTTGTTTTT **AAACCCTTCACTCACTCACTCACTCACTCC** TGTTCGTAA

67939.t00029 | At5g67630 | K9I9.20 | DNA helicase, putative | similar to RuvB-like DNA helicase reptin (Danio rerio) GI:27733814, reptin (Drosophila melanogaster) GI:7243682

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-100779	15	5.37e-13	AGAAATATAT **AAACCCTGAACCCTAAACTTTGTTCTC** TCTCCTCTCC
Gossypium_hirsutum-82915	85	8.70e-13	GTTTCTCACA **AAACCCTAAACCCTGCCTTTCCCTCCC** TCAATCATCC
Citrus_sinensis-63752	22	2.11e-12	GAGAACTAGA **AAACCCTAAACCCTAAACCACACGCTA** TCAAACCACA
AT5G67630.1	21	7.49e-12	GCTTTTCTCT **AAACCCTAAAACCTTAACTTTTTGCTC** TTCTCCCTCC
Glycine_max-211789	59	5.94e-11	TCCCTAAGCA **AACTCCGAAACCCTCTTTCTCCCTCGC** ACCGTCTTCG

67572.t00017 | At5g01650 | F7A7.170 | macrophage migration inhibitory factor family protein / MIF family protein | contains pfam profile: PF001187 Macrophage migration inhibitory factor

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-79158	54	1.78e-13	GGTTGGTGAA **AGAAAGAAAGAAAGAAAGAAAGAAAGAGAG** TGGTTAGGGG
Nicotiana_tabacum-18090	25	9.60e-13	GGGTTTCACA **GAACAGAGAAGAGGAAAAGAAGAAGAAGAA** GAAAA
AT5G01650.1	44	2.36e-12	AAAAAAATTG **GCGTCGAGTGATAGAGACGAAGAAGAAGAA** GAAA
Glycine_max-44857	129	6.99e-12	AATTGTGAGA **AACAACAGAGAAAGTAAGCAAGAAACCGAA** GAGAAGAAAA
Vitis_vinifera-34876	548	6.99e-12	GCTATAGGTG **GACAGGAGAAAAAGAGAGAGACAAGGGTAG** CAACTAGGGT

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-83724	348	4.67e-10	TTTTACTGGC **ACGAAGATAAATCCATAGTAAGACCTAGAA** GTTTTGTGAA

67175.t00041 | At4g29350 | F17A13.170 | profilin 2 (PRO2) (PFN2) (PRF2) | identical to profilin 2 SP:Q42418 GI:1353772 from (Arabidopsis thaliana); identical to cDNA profilin (PRF2) GI:9965570

NAME	START	P-VALUE	SITES
AT4G29350.1	40	6.04e-17	AACCAAAAGC **ACGCTACAGAAGAAGAGGAAGAAGAA** GAAGCAGAGA
Gossypium_hirsutum-588101080	35	3.09e-11	TATTTGTAAA **AACTCACACAAGTTTAGGAAGAAGAAGAA** G
Glycine_max-54271734	37	5.25e-11	TTGGTCCATT **ACGCCGGGGCAGCCAAAGAAAAAGAAAAA** TCCTCAATTT
Vitis_vinifera-22666	57	6.23e-11	CCTTCAAGAC **ACGAAAAACAGAAAAAACCAGAAGAAGAA** TTAACACCGG
Nicotiana_tabacum-15872	34	5.43e-10	TATTGTTCTG **AAGATTAAGAACAAAGGGACTAGGAAAAA** ACACAACAAC
Citrus_sinensis-85433	97	1.96e-09	CATCACTAAT **AATCTTCACCGGGCCCCGCAGAACAAGCC** GTGATCGAAA

67912.t00028 | At5g63530 | MLE2.16 | copper chaperone (CCH)-related | low similarity to copper homeostasis factor (GI:3168840); nearly identical to farnesylated protein ATFP3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-28294	310	1.42e-13	AAAAACCAGA **GGAAGAGAAGAAAGAAGAGGC** ACCCAAAGAT
AT5G63530.2	45	8.58e-13	TTTGGTATCA **GGAAGAGAAGAAACCAGAAGC** AGCAGAGGAA
Vitis_vinifera-37646	110	2.47e-10	AAAAGAAGCC **GGAGGAGAAGAAAATGGAGGG** AAAGCAGCGG
Citrus_sinensis-7027	47	2.02e-09	AACCTCAAAA **GAAATAGAAAATAAGAGAAGC** CTGCCTCTCC
Gossypium_hirsutum-855101081	65	3.29e-09	AATTAAAAAA **GAAAAAAAAGAAACAAAAAGC** AAAAGCAAAG
Glycine_max-1151271730	116	1.16e-08	AGAAGTGAAA **ATAACAGCAAAAAGTAGCAGC** TGCTGCAGCT

67170.t00036 | At4g28480 | F20O9.160 | DNAJ heat shock family protein | contains Pfam profile PF00226: DnaJ domain; ; similar to DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) (Heat shock protein 40) (HSP40) (DnaJ protein homolog 1) (HDJ-1) (Swiss-Prot:P25685) (Homo sapiens) and (Swiss-Prot:Q9QYJ3) (Mus musculus)

NAME	START	P-VALUE	SITES
Citrus_sinensis-66051	77	3.16e-15	TGAAAGTAAA **GAAGAGAAAGATAGGAGAAGAAGAAG**
Vitis_vinifera-44942	61	4.06e-14	ATCATACCCC **GCAAGAAGAGGGAGAAGAAGAAGAAG** AAGAAGAAGA

NAME	**START**	**P-VALUE**	**SITES**
AT4G28480.1	231	5.33e-13	GAAAAGTGAA **GAAACGAAAGAGAGAAGACAAAGAAG** AAGAAGGTGA
Glycine_max-1223271727	177	5.97e-13	CCGCAAACCT **GAAGAGAAAAAGAGCAGCAGAAGAAG** AAACACCAAC
Gossypium_hirsutum-550101081	78	8.24e-11	GCTCTGCGAT **AAAAGCAGAGGTTGAGTAAGAAGAAG**
Nicotiana_tabacum-113649	174	6.62e-10	ATTTATTGAA **GGAAAACCAAATAGGTCAAAGTGAAG** AAAAGAAAAG

60760.t00042 | At1g51650 | F19C24.25 | ATP synthase epsilon chain, mitochondrial | identical to ATP synthase epsilon chain, mitochondrial SP:Q96253 from (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-499271728	1	2.34e-11	G **GGAGAGAGTGAAGAGAGAAGA** AG
Nicotiana_tabacum-206133667	17	7.03e-11	TCGGTCAATC **GAAGAAAGTGAAGGAGGAGAA**
AT1G51650.1	38	8.22e-11	AACGGACGAA **GAAGGAAGACAAGGAAGAAGA** TCGGAG
Gossypium_hirsutum-82101076	2	4.66e-10	GA **AAGAAAAGTGAAGAACGAAAA** TCTCTCCCCC
Vitis_vinifera-44603	11	5.02e-10	GAAGATCAGA **GAGAGAAGGAAAGAAAGAAAA** TCA
Citrus_sinensis-43668	123	5.36e-10	AGACAGAGCA **AGAGAGAAAGAAGAAAGAAAA** AAGCAA

42869.t00028 | At2g28900 | F8N16.19 | mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein | contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-239133666	86	5.11e-18	CAAAGAAGAA **GAAGAAGAGAAGAAGAAGAAGAAGAAG** AAAAA
Vitis_vinifera-24533	623	5.82e-14	AAAGTAGTGA **GCACTGGAGAAGGAGAAGAGGAAGAAGAAG** AAG
Citrus_sinensis-36142	70	3.73e-13	CACTGAAACC **GAGAGAGTGAAGAAGAAACAGAACAAGAGC** AGAGAAGAAG
AT2G28900.1	89	1.44e-12	ATCCCAAAAC **CAAAAACAGAGGAAGAAAGAAGAAGAAAAG**
Glycine_max-361271726	89	2.67e-12	ATTCATAAAA **GCATAACTGAAGAAAACTAAGGAAGGAAGG** AAGGAAGGAA

67107.t00009 | At4g11660 | T5C23.90 | heat shock factor protein 7 (HSF7) / heat shock transcription factor 7 (HSTF7) | identical to heat shock factor protein 7 (HSF7) SP:Q9T0D3 from (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-87303	45	1.03e-15	TATCATTTAC **TCCACACGGAACCTTCTAGAAACAACAAAA** CCTAACCCAA
Glycine_max-241205	44	4.64e-15	ATCCTTATAT **TTCCAACGGAACCTTCTAGAACCACCATAA** CATCATTCTG

NAME	START	P-VALUE	SITES
Vitis_vinifera-20760	33	1.55e-14	CATCATTTAC **TCCACCCAGAAACTTCTAGAACCAGCACAA** AAAAACACCC
Nicotiana_tabacum-49904	46	9.65e-14	CACCTCTATG **TGTCGTCGGAACCTTCTAGAATAACCAAAA** ATCCCAACGG
AT4G11660.1	40	2.95e-12	ATCAATACGT **TCCTCTCAGAACATTCTGGAACTTCACAAC** ATAATCTCTC

60078.t00008 | At1g72210 | T9N14.4 | basic helix-loop-helix (bHLH) family protein (bHLH096) | identical to basic-helix-loop-helix transcription factor (Arabidopsis thaliana) GI:20520637; contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; PMID: 12679534

NAME	START	P-VALUE	SITES
AT1G72210.1	152	1.91e-12	TCTCCCTCTC **GAGACAAAAAGAGAAAGAGAAAC** ACTTTCTGTC
Glycine_max-147686	10	3.50e-11	GGGCCCGAGG **GAGAGAGAGACAGAGAGAGAGCC**
Citrus_sinensis-4243	42	7.56e-11	AGAGCAGAAA **GAACCAAGAAGAGATTGAGAATC** AAAGA
Nicotiana_tabacum-15300	155	8.29e-11	AATGTTCTAA **GAACAAGGAGGATATAGAGAACC** AAAGG
Gossypium_hirsutum-45999	19	1.11e-09	CTTCTTTTTT **GAAAGAGAAAGGAGAAAAGAAAA**

50828.t00049 | At1g03457 | F21B7.8 | RNA-binding protein, putative | similar to Etr-1 (Danio rerio) GI:7670536, BRUNO-like 6 RNA-binding protein (Homo sapiens) GI:15341327; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)

NAME	START	P-VALUE	SITES
AT1G03457.2	0	4.60e-16	**GAGAGAGAAGAAGAAGAAGAAGAAGAAGAA** GACGACGAAG
Gossypium_hirsutum-58192	50	3.15e-13	AAAAAAAAAG **GAGAAAAAATTAGAGGAAGAAGAGCAGGCA** TTG
Nicotiana_tabacum-19152	18	9.90e-13	TGCCCGAAAT **CAGCGAAGACCCGGCGGAGAAGAAGAAAAA** TAGTCAGAAA
Vitis_vinifera-17776	62	2.01e-12	TCGGGAAAGT **GAGAGAAAATAGAGAGAGAAAGTCCAAGAA** AGTAGAGAGA
Citrus_sinensis-20834	0	2.30e-12	**GAGAGAAACAGAGGCAAAGGACCAGAACCA** GAGAGAAACG

67936.t00031 | At5g67270 | K21H1.28 | microtubule-associated EB1 family protein | similar to SP|Q9UPY8 Microtubule-associated protein RP/EB family member 3 (Protein EB3) {Homo sapiens}; contains Pfam profiles PF00307: Calponin homology (CH) domain, PF03271: EB1 protein

NAME	START	P-VALUE	SITES
Vitis_vinifera-32014	26	6.90e-12	GAGAGTCAAG **ACAGAGAAAGCGAGAGAAAGA** AAGAGAGAAA
AT5G67270.1	46	2.02e-11	GAGCCGTTAG **AGAGAGACAGATCGAGAAAGA** ACCAGAGAGA
Glycine_max-451271732	13	1.29e-10	CCGGGGGAAA **CGAGAGCGAGAGAGAGAAAGA** A

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-74717	36	7.57e-10	GGAGCCTTCT **ACAGAGAAAGTTGAAGCAGAA**
Citrus_sinensis-53014	45	2.66e-08	CTCGGACGTT **AGAAAGAAATTTGAATTCAAA** ATCAAATAAG

68081.t00002 | At5g28640 | F4I4.20 | SSXT protein-related / glycine-rich protein | contains weak hit to Pfam profile PF05030: SSXT protein (N-terminal region)

NAME	START	P-VALUE	SITES
AT5G28640.1	21	6.67e-10	ACTTTTGTGG **AGGAGAGAAAGCGAG** ATAACACACA
Glycine_max-14890	56	2.42e-09	ACCCACAGAG **AAGAGAGAGAGAGAG** AGTTTCTCTC
Vitis_vinifera-43346	73	2.42e-09	TGTAACAGAT **AGGAGAGAAGGAAAG** GGAGAAGAAA
Gossypium_hirsutum-21618	45	1.07e-08	TAATAGTGAG **AGGCGAGAAAGAAAG** TTAAGAAACA
Citrus_sinensis-72850	396	1.10e-07	ACAGTCTTTC **TAGAGAGAGAGCGTG** TGTGTATAAG
Nicotiana_tabacum-40709	2	2.70e-07	AA **AAGAGGGAAGCAAAA** AAT

51873.t00012 | At1g05870 | T20M3.14 | expressed protein

NAME	START	P-VALUE	SITES
AT1G05870.2	7	7.31e-14	AGAAAAA **CAGAGAGAAACACACAGAGAGCTAGAGGA** GAGTGAGTGT
Citrus_sinensis-66940	8	7.02e-13	CACGCGTC **CGGAGAGAACTCTAAAAAGAGAGGGGGGA** GAA
Gossypium_hirsutum-71208	76	1.33e-12	AAATTTATTA **CAGGGAAAAGCAGGAAAGCAGAACTAGAA** CAAG
Nicotiana_tabacum-85852	0	9.74e-12	**CAGAGAGAAAAAAGACTGAAAAAAGAAAA**

68169.t00441 | At4g17790 | FCAALL.62 | expressed protein

NAME	START	P-VALUE	SITES
Glycine_max-214317	101	1.83e-15	TCCTGAAGGT **AAGGCAGAGAAGAGAAGAAGAGAAGGAAA** GAGGCTTGTC
Vitis_vinifera-28563	101	5.61e-15	TCACCAAGGA **AGGGAAGAGAAAAGAAAAGGAAAAGGAAA** AGAAATTATA
Gossypium_hirsutum-72158	15	1.21e-12	GAGGAAATGG **AGGGTAGAGAAAAGGTAAAAGAACCGAAA** CCCAGTTTCC
Nicotiana_tabacum-98993	95	3.66e-12	ACCCTTTTTT **AGCACATAGAAAGAGGGAGGGGAATGAAG** GAAGAGTATT
AT4G17790.1	270	9.72e-12	CGAGGAGACA **GAGACAGAGAAAAGGATTCGTGTAAGGAA** AAGCTTTTAA

67179.t00024 | At4g30240 | F9N11.90 | expressed protein | predicted protein, Arabidopsis thaliana

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-19660	58	2.12e-15	AAGCCGAAGA **GAAGAGAAGAGAAGCGAAAGGAAGAG** GAGAGAATTA

NAME	START	P-VALUE	SITES
AT4G30240.1	111	2.51e-15	AAAAGGAAGA **GAAGAGAAGAGAAGAGAAGGAAGCAG** AATCTAATTT
Citrus_sinensis-10591	123	6.24e-15	TCTTATCTCT **GAAGAGAGGAGGAGAGAAAGAAAGAG** AAGCATTTTC
Vitis_vinifera-31127	39	8.28e-13	CTTCTCCTTG **GCAGAGAAGAGAAGAGGAGTGCGTAA** GCTTATACAG
Glycine_max-163801	67	2.89e-12	TCGCCGTAAC **ACAAAAAAGGGAAGAGAGAGAAAGAA** CCACCCACCC

67844.t00014 | At5g53120 | MFH8.5 | spermidine synthase, putative / putrescine aminopropyltransferase, putative | similar to SP|O82147 Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (SPDSY) {Coffea arabica}; contains Pfam profile PF01564: Spermine/spermidine synthase

NAME	START	P-VALUE	SITES
Vitis_vinifera-51289	150	1.21e-18	GCGTTCCCTT **CAGAGACTGGAGCCGGAGAAGAAAAAGAT** AATCT
Gossypium_hirsutum-22101079	199	6.09e-18	TCATTAAGAC **CAGAGGCTGGAGCCGAAGAAGAAAAAGAT** AATCT
Glycine_max-1335271726	134	1.36e-17	TATCATTCAT **CAGAGACTGGAGCCTGAGAAGAAAAGGAG** AATTT
AT5G53120.5	52	3.28e-17	TCAACGTATA **CAGAGGCTGGAGCTGGGGAAGAAAAGGAT** TGTCT
Nicotiana_tabacum-57711	266	5.28e-13	CTCTGGTAGT **TGTAGACTGGATCCTAATAAGATAATTAT** TT

60004.t00032 | At1g72510 | T10D10.2 | expressed protein |

NAME	START	P-VALUE	SITES
Glycine_max-49521	295	1.77e-19	AGAAAAAATT **GAGGAAGGAGAGTGGGAGAAGGAGAGATAA** GAAGAAGAGA
Gossypium_hirsutum-19644	0	3.36e-18	**GAAGAAAGAGAGTGGGAAAAGGAGAGATAA** TAAAAAAAGA
Vitis_vinifera-38078	223	2.15e-17	AGAAGCGAAG **GTTGAAGGAGAGTGGGAGAAGGAGAGATAG** CGTCGAGAAG
Nicotiana_tabacum-94411	229	9.09e-17	AACAAAGGAA **GAAGAAGGCGCGTGGGAAAAAGAAAGATAA** TAGACAATAT
AT1G72510.1	248	4.04e-16	AAGTAATTTA **GAAGACGGAGAGTGGCAAAACGAAATATAA** AAAAAAAAGT

67199.t00035 | At4g34110 | F28A23.130 | polyadenylate-binding protein 2 (PABP2) | non-consensus TA donor splice site at exon 2, polyadenylate-binding protein - Triticum aestivum (common wheat),PIR:T06979

NAME	START	P-VALUE	SITES
Glycine_max-1759271733	459	3.09e-18	TATTGTGTCC **AATAACAAGAGGAGGGGGAAGAGAAACAAA** ACAAAAAAAA
Gossypium_hirsutum-55762	243	2.55e-17	TTTTTTATTT **AATAACAAGAGGAGAGGGAAGAAAGAAGAA** AAAAACCCCA
AT4G34110.1	269	1.84e-16	GTTTCAGTCT **AATAACGAGAGGGGAGGGAAGAGTAACTAA** AACCCCAAAA
Nicotiana_tabacum-51999	181	3.45e-16	TCTCCTTAAT **AATAACAAGAGGAGAGGGAACTAAAAAAGA** AAAAAAAGGA

51416.t00039 | At1g76010 | T4O12.22 | expressed protein

NAME	START	P-VALUE	SITES
Citrus_sinensis-5196	12	7.39e-18	GGGGGGGCAT **AAAAGAAGAAACGTAGCCGTAGAAGAGGGC** GCTTTATCTT
Nicotiana_tabacum-21342	8	2.05e-17	GAGGGCGT **AAACGAAGAAACGAAGCCGGAGAAGAGGGC** TCTTCTTTTC
Glycine_max-181703	16	6.65e-16	GGGAGGGCGC **AATAGAAAATACAAAGCCGTAGAAGAGGGC** TCGCTCTTTT
Gossypium_hirsutum-7526	3	3.06e-15	GGC **ACGAGCGGCACGAGAGCCGTAGAAGAGGGC** TCTCTCTTGG
AT1G76010.1	40	7.02e-15	GGGCGTATCA **AGGAGAAGAAACAAAGCCGTACAACGAGGG** CTCTTCCTGG

8264.t00023 | At2g45190 | F4L23.30 | axial regulator YABBY1 (YABBY1) / abnormal floral organs protein (AFO) / filamentous flower protein (FIL) | identical to YABBY1 (Arabidopsis thaliana) GI:4928749, abnormal floral organs protein (AFO) (Arabidopsis thaliana) GI:4322477; supporting cDNA gi|4322476|gb|AF087015.1|AF087015

NAME	START	P-VALUE	SITES
AT2G45190.1	9	1.06e-16	CAGCAACCC **AACAATCAAGAAGATCAGATCATGGTGGG** GTTTTTTATT
Citrus_sinensis-911	97	9.61e-16	TATAGTACTT **AACAATCAAGAAGATCAGAACAAGTTGGG** ATTTTATCAT
Gossypium_hirsutum-41240	17	3.92e-15	GGCAAAACTC **AACATCCAAGAGAATCAGATCAAGGTGTG** AGAAACCTAT
Glycine_max-11334	131	6.57e-15	ACAGTAACTC **AACAATCAAGAGGATCAGATCCATAGGAG** AAGTTTTATC
Vitis_vinifera-26135	133	6.28e-14	TTCTCACTCA **AAAATCAAAGAAGATCAGATCCAAGGTGG** TTAATCTCCG

50832.t00066 | At1g08830 | F22O13.32 | superoxide dismutase (Cu-Zn) (SODCC) / copper/zinc superoxide dismutase (CSD1) | identical to SWISS-PROT: P24704

NAME	START	P-VALUE	SITES
Vitis_vinifera-16060	901	4.12e-16	TCTCTCTAAA **AAGGGGTGTTCTGAGATCACATAGAAA**
Glycine_max-597271732	188	8.12e-16	TTCTCTGTCT **AAGGGGTGCCCTGAGATCACATTGAAC** A
Gossypium_hirsutum-41759	16	1.02e-15	AGATTCAGCG **AAGGGGTGCTCTGAGATCACATACCAA** A
Citrus_sinensis-62376	81	1.33e-15	TCCTCCCTCC **AAGGGGTGTTCTGAGATCACACAGCAC** A
Nicotiana_tabacum-57538	243	2.47e-15	CTAGCCATTC **AAGGGGTTCCCTGAGATCACATACAAA** A
AT1G08830.1	116	1.46e-14	ATTCTTTCCA **AAGGGGTTTCCTGAGATCACAAAGGCC** AAGTAACA

67119.t00024 | At4g18020 | T6K21.200 | pseudo-response regulator 2 (APRR2) (TOC2) | identical to pseudo-response regulator 2 GI:7576356 from (Arabidopsis thaliana)

NAME	START	P-VALUE	SITES
Citrus_sinensis-86563	183	1.49e-17	ACAATTGTTT **GTGGCCTGAGAAAGGATGCCAAACCAGC** T

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-71870	116	3.86e-16	AGACTTATCG **GCTGGCTGAGAAAGGATGCCAAACCAGC** T
Glycine_max-116655	206	3.04e-15	TGCTGCAGTA **GGGGACCGAGTAAGAATGCCAAACCAGC** T
AT4G18020.1	115	2.44e-13	AGCGGCGGTG **TTGGCCGCAAAAACGATGCAAAACCAGC** T
Nicotiana_tabacum-45130	91	2.10e-12	TCTTTAATTT **GGCTGCCTGAAAAGGATGCCAGTTCAGA** A

51794.t00024 | At1g71800 | F14O23.18 | cleavage stimulation factor, putative | similar to cleavage stimulation factor 64 kilodalton subunit GB:AAD47839 GI:5713194 from (Drosophila melanogaster), SP|P33240 Cleavage stimulation factor, 64 kDa subunit {Homo sapiens}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-109635	257	4.62e-20	AATGGTTCTG **AGGAGGAAGAAGATGGAGCAGCGCTTCACC** TTCTTCTGCT
AT1G71800.1	91	3.34e-18	CCCGTTACTT **AGCAGGAAGAAGATGAAGCAGCGCTTCACC** TTCTTCTTCG
Nicotiana_tabacum-77293	31	5.77e-16	TAAGAGGAAA **AGGATGAAGCTGAGTCATTGGAGCTTCACC** TTCTTCTTCT

67628.t00033 | At5g15350 | F8M21.240 | plastocyanin-like domain-containing protein | contains plastocyanin-like domain Pfam:PF02298

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-11254	20	5.28e-16	GCTCTTTTTG **GAAGGCTGAGAGTGCGGGAGTGAGAGAG** AGA
Vitis_vinifera-33562	45	8.94e-12	TTCTGGAGTG **GAGCACTCAGAGCAGAGCAGGGAGAGAG** AGAAGGCA
AT5G15350.1	38	1.58e-11	GCGCAACTTA **CAACATCTATAGAGAGAGAGAGAGAGAG** TTTAGTTAGA
Glycine_max-1509271727	1	3.31e-11	C **GGCCGGGGAGAGTGTTCCAGAGAGTTTG** TTAAAGAACT
Nicotiana_tabacum-77198	26	1.46e-10	GCTTAGCTAA **GAAACTCTAGAGTGTGCGAGTACTACTG** TAGCA

68169.t00064 | At4g14550 | FCAALL.254 | auxin-responsive AUX/IAA family protein | identical to IAA14 (GI:972931) (Arabidopsis thaliana); similar to SP|Q38825 Auxin-responsive protein IAA7 (Indoleacetic acid-induced protein 7) {Arabidopsis thaliana}

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-18061	97	5.30e-14	AAGAGTAGAG **AGAAAGAGGAAGAAGGAGAAGCAAAGA** GAGAAGATAG
Glycine_max-687271731	28	3.99e-13	ACATTATAAT **AGAAAGAGGACACAAGAGAAAGAAGGG** GGAGCTATAG
Citrus_sinensis-20090	38	3.09e-12	TATTTCCCCA **AGGAAGAAAGAAAGAAAGAAAGAAAGA** AAGAAAGAAC
Nicotiana_tabacum-57199	107	3.09e-12	TTTTGTTAAC **AAGAAGTGGAAGAAAAGGAAGAAGAGA** TAATTTC

NAME	START	P-VALUE	SITES
AT4G14550.1	27	3.93e-11	CTTCACCCCC **AACAAGAGTTATCGAGAGAGAGAGAAA** ACATATTCTG

51078.t00034 | At1g60060 | T2K10.11 | expressed protein

NAME	START	P-VALUE	SITES
Citrus_sinensis-35397	25	3.74e-16	TATAGAGAGA **GGAAAGAGTAGTAAGAGAAGAGAAAGAGA** GAGAGAGAGT
Gossypium_hirsutum-18541	35	5.82e-13	AGATATATCC **GTAGAGAGGAGGGAAAAAAAATGAAAAGA** ATGAAACAGA
Vitis_vinifera-33375	46	7.07e-13	CTCCTTGTAA **AGATACAGTTGGGAAAGGAGATCAAGAGA** AGATTTTAGG
Glycine_max-119804	126	9.41e-13	AGATAGCTAG **GTAAGAGGGTGTAAGGGAAGAGAAAGAGA** TCATAGAAGA
AT1G60060.1	33	5.12e-11	CTTTACTCAG **AGAACCAAAAGAAAAATAAAGAGAAAAGA** ACCCAAAAAA

67286.t00047 | At3g53620 | F4P12.320 | inorganic pyrophosphatase, putative (soluble) / pyrophosphate phosphohydrolase, putative / PPase, putative | similar to magnesium dependent soluble inorganic pyrophosphatase (Solanum tuberosum) GI:2706450; contains Pfam profile PF00719: inorganic pyrophosphatase

NAME	START	P-VALUE	SITES
Vitis_vinifera-20066263	94	2.61e-13	ATGAAGAAAG **AGGAAACAGAGCGGGAACGCG** TTCACCTCCA
Glycine_max-224271	8	5.73e-13	GGTGAAAC **AACAAGGAGAGCGGGAACGCG** TTGCGTACAC
Citrus_sinensis-71106188	33	3.48e-12	CCAATGCAAA **GGGAAAGAGAGCGGGAAGGGA** ACCAGCGTCA
Nicotiana_tabacum-13132	33	4.11e-12	AAGTAGTGTT **AACCAGCAGAGCGGGAAGGGG** GAGAACGCGT
AT3G53620.1	103	4.69e-12	CACAGAAGCA **GAGACATAGAGCGGGAACGCG** TTTAGTCACA

67904.t00002 | At5g62000 | MTG10.1 | transcriptional factor B3 family protein / auxin-responsive factor, putative (ARF1) | contains Pfam profile: PF02362 B3 DNA binding domain; identical to cDNA ARF1 (auxin response factor) binding protein GI:2245393

NAME	START	P-VALUE	SITES
Citrus_sinensis-17333	222	1.58e-12	TGAGCTTTAG **CAGATGAGAGATCTGAGCT** TGAAAGGGAC
Gossypium_hirsutum-25443	230	1.58e-12	GAGAGTTAAT **CAGATGAGAGATCTGAGCT** AAAAAAGAGA
Glycine_max-1475271734	173	3.69e-11	ACGAGTGTCG **CGGATGAGAGATCTGTGGT** GAGGTCTCTG
Nicotiana_tabacum-116318	307	1.33e-10	TTTGTGCTTG **GAGATGAGAGATCTGTGTT** GAGAATTATT
AT5G62000.2	264	6.54e-10	AAGTGGACTA **CCGAAGCGAGTTTTGAGCT** TTTTCAGAGA

7001.t00032 | At2g47490 | T30B22.21 | mitochondrial substrate carrier family protein | contains Pfam profile:

PF00153 mitochondrial carrier protein 67323.t00043 | At3g62650 | F26K9.80 | expressed protein | putative mitochondrial carrier protein At2g47490 - Arabidopsis thaliana, EMBL:AC002535

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-57962	63	9.65e-19	TGCGACTTTG **GTTCTCTGCGATCTCCCTCTCGAGAGAGGA** ATCTTTGAAT
Gossypium_hirsutum-10900	159	4.54e-17	TGCCACTCTG **GTTCTCCGCCATATCCCTCTCGATAGAGGA** CTCCTTTCGT
AT2G47490.1	193	1.31e-16	TGCGACGCTT **GTTCGCCGCGAAATCCCTCTCCCGAGAGGA** TACAACCTTT
Glycine_max-65497	175	2.27e-16	GACCACCCTG **TTCCTCCGCCATCGCCCTCTCCAGAGAGGA** TTCTTTTTTC
Nicotiana_tabacum-33378	122	1.17e-15	TGCGACTGTG **GTTCTGTGCGATCTCCCTCTTAAAAGAGGA** CTTTAAGAAT

67219.t00034 | At4g38970 | F19H22.70 | fructose-bisphosphate aldolase, putative | strong similarity to plastidic fructose-bisphosphate aldolase (EC 4.1.2.13) from Nicotiana paniculata (NPALDP1) (GI:4827251), Oryza sativa, PIR2:T02057 (SP|Q40677)

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-19104	5	2.75e-12	GGGAG **AGAGCTTGTGTGAGGAGATAAGA** TTTATAGAGC
Gossypium_hirsutum-1367	18	3.97e-11	TTGTGTCAAA **AAAGCTTGAGCTGAGAGATAAGA** GAAAGCACTG
Glycine_max-180634	23	5.76e-11	ATACAACTAC **AAAGGTTGCTGTAGGAGATAAGA** TATTGAAGTA
AT4G38970.1	67	4.59e-10	CAAAGAAACC **AAAGGCAGAGAAAAGAGATAACA** CACACAAAAA
Nicotiana_tabacum-19385	21	4.15e-09	GTAAGAGTGA **GAAGAGAGTGTGCTGAGATAAGG** AGATTATAGT
Citrus_sinensis-103630	25	1.76e-08	CTCAGAACCC **ACAGCAAGAAGAAGCAAAGAGGA** AA

67051.t00023 | At4g03415 | F9H3.20 | protein phosphatase 2C family protein / PP2C family protein | similar to protein phosphatase-2C; PP2C (GI:3643088) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain;

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-315101074	989	1.52e-15	TTTTAACTTA **ATCGGATGTTTTGTTTGTGGAGCTGATGAA**
Glycine_max-1064271730	330	1.03e-14	TATATTATTC **ATCAGATGTCTGCATTCTGGAGCTGAGGAA**
Vitis_vinifera-34565	92	1.16e-14	TCCTGTTTTC **ATCAGATGTATTCGTTGTGGGGTTGAGAAG**
Nicotiana_tabacum-79781	18	4.95e-13	GATTCCCGGG **ATCAGATGATCACTTTGTGAGTCTGAGCAA** A
AT4G03415.1	186	1.27e-10	AACGGTGGAG **ATCTGTTTTTTTGTGTGTGGCTATATAACA** ACCTTATTGT

67037.t00013 | At4g00880 | T18A10.18 | auxin-responsive family protein | similar to small auxin up RNA

(GI:546362) {Arabidopsis thaliana}

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-85076	75	2.27e-17	GATAGAATAT **GAGCAACATTCCAAGATCTTTAACAGACTC** TTGTTCTACT
Citrus_sinensis-68498	47	3.10e-17	CATCTATCAT **GAGCAACATTCCAAGATCTCTTACTGACTC** TTCTCTTACC
Glycine_max-100733	47	1.77e-16	CATTTATCAT **GAGCAACATCCCAAGATCTCTCACCGACTC** TTCCCTAACC
Gossypium_hirsutum-25857	198	2.30e-15	AAATTATCAT **GAGCAACGTTCCAAGGTCATTAACAGATTC** TTCTTTGACT
AT4G00880.1	57	2.87e-12	CATCCATCTC **TTACAACCCTCCAAGAACACTGGCTGTTTT** CCTTCACTTT

67283.t00006 | At3g52660 | F3C22.60 | RNA recognition motif (RRM)-containing protein | heterogeneous nuclear ribonucleoprotein R, Homo sapiens, PIR:T02673; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-94051	155	6.45e-18	TTCCTTCACA **GTTGTCTTGCAAGCTTGCTTTATTAGATAC** ATAAA
Citrus_sinensis-73662	184	8.24e-18	TCTCTTAACC **GTTGCCTTGCAAGCTTGCTTTAATAGATAC** ATAAA
Vitis_vinifera-23116	92	1.65e-16	GGCACTAATT **GTTGCCTTGCAAGCTTACTTAATTAGATAC** ATAAG
AT3G52660.1	163	4.81e-15	AGCTCTCTCA **GTTGTACTGCAAGCATTCTTTTCTAGATAT** TTAAG

67169.t00023 | At4g28190 | F26K10.70 | expressed protein

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-86421	377	1.86e-16	TCCTTCAACG **TTTTCTCCACCAGATCTCTCGGAGTGA** CTCAGCAAAG
Vitis_vinifera-4703	91	7.37e-16	CTTTTCAACG **TTTTCTCCACCAGATCTCTCGGGGTGA** GCCGTGGAGA
Nicotiana_tabacum-133670	0	2.56e-14	**GCTTTTCCACCAGATCTCTTGGACTGA** CTCCTTGGAG
Glycine_max-127019	147	1.96e-11	CATTTAGACG **TTTTCTCTGTCAGATCTCAAGGCTTAA** CGTGGTGTTG
AT4G28190.1	102	3.54e-11	ATAAGCTTTT **GCTTTGATATCAGATCTCTCTTACGGC** TTTTGAGATG

67993.t00028 | At5g15460 | T20K14.70 | expressed protein

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-70873	48	2.58e-11	TTCAGCCAAC **CCAGATCAGTTTTGGACTCAA** TTCTGCAGAA
Glycine_max-265238	359	5.42e-11	CAATTGCCGC **CCAGATCAGTGATTGACCCAA** TTGAGAAAAA
Citrus_sinensis-35106185	14	6.13e-11	AAGGGAGTGA **CCGGATCAGTTTTTGAGCGCA** CCAAAGTGAG
AT5G15460.2	107	5.89e-10	CTCATCAAAC **TCAGATCAGTAGCGGACCCAA** ATAGGATCAA
Vitis_vinifera-28547	343	7.52e-10	CAGAGCTCGC **CCAGATCGATTTCAGAGCCCA** AAATACCTGA

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-3866	316	1.01e-08	AGGACAGTTT **CCAGATCAGTTTTTCCTATCA** ATTTAAGGCT

60010.t00047 | At1g70600 | F24J13.17 | 60S ribosomal protein L27A (RPL27aC) | identical to 60S ribosomal protein L27A GB:P49637 (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-65986	100	3.04e-16	CATATACGCA **GTAGCAGCACAGGAGGGAGAGAGGAGAG** A
AT1G70600.1	3	2.41e-15	CTA **GCCGCAAAGAGAGAAAGGGAGGGAGGAGAG** TGTAGCAGAT
Citrus_sinensis-124106181	631	2.63e-14	AGTGCACTCC **GCAGAAGGTAAGGAAAAAGGAGGAAGAGAG** CTTCCTAGTC
Glycine_max-1297271732	67	6.44e-14	CTCTCTGAGA **AAAACAGATAGTGTGGGAGAGAGAAGAGCG** GAAGAGAAA

67199.t00030 | At4g34050 | F28A23.190 | caffeoyl-CoA 3-O-methyltransferase, putative | nearly identical to GI:2960356 (Populus balsamifera subsp. trichocarpa), GI:684942 (Medicago sativa subsp. sativa) isoform contains a GT-TG intron which removes an internal segment of the protein.

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-59198	66	1.76e-14	CATTACGGCC **GGGGGAAACCAAAGGAAAGGAAATTAAGAG** AAAGCAAATA
Glycine_max-263299	36	1.30e-13	CTCTTTCAAA **AGGGAGAAGAAAAGGAAAGGAAACAAAACG** CACAAAGGAT
Gossypium_hirsutum-89640	36	2.48e-13	ACTCGCTCAG **GTCCATAAACAAAGGAAAGCAAAGAGAAAG** AAGCTTTTCA
AT4G34050.1	37	3.02e-11	TCACCCAAGA **AGACAAAAACACAGAGAGAGAAAGAGAGAG** AA
Vitis_vinifera-20666259	52	1.87e-10	AAAGTTTCCG **GCGAATACTAGAAGGAAAGGAACAGAAGAT** CTCTAGAA
Citrus_sinensis-51392	15	4.23e-09	AAACTCCAAA **ATCCAACATCAAAAGAAAAGACTTGCGTCA**

67714.t00023 | At5g35914 | MIK22.4 | pseudogene, similar to Unknown protein | similar to En/Spm-like transposon protein; blastp match of 37% identity and 1.2e-29 P-value to GP|21397269|gb|AAM51833.1|AC105730_7|AC105730 Unknown protein {Oryza sativa (japonica cultivar-group)}

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-18202	50	4.38e-16	ATCCCTATTT **TCAGGATTGTGTGGGAGCGGTTGATGG** TATACATATT
AT5G35914.1	550	2.17e-14	TTAATTTATG **TTAGGACTGTGTTGGAGCTATTGATGG** CACACACATA
Citrus_sinensis-43958	29	2.57e-14	GGGCTTCAAC **TCAGGATTGTATTGGTGTCATAGATGG** T
Nicotiana_tabacum-68321	16	7.11e-14	ACCCATATTT **TGAGGATTGCATTGGCGTGATCGATAG** C

50886.t00054 | At1g09840 | F21M12.23 | shaggy-related protein kinase kappa / ASK-kappa (ASK10) | identical to shaggy-related protein kinase kappa SP:Q39019 GI:717180 from (Arabidopsis thaliana)

NAME	START	P-VALUE	SITES
Vitis_vinifera-19575	239	1.54e-18	GAAACGCTTC GAGGAAGATAGGTGCTTGGATGGGATGG AAGGCAGAAT
Citrus_sinensis-63220	100	5.97e-14	CAAGCGCTTC CAGGAAGATAGGTGTTTGGGTGGTACAG AAGGCACGAC
AT1G09840.1	241	1.15e-13	ACGACAGCTC AAGGAAGATCGGCTCTTTGATGGGATGG GACACCAAGA
Nicotiana_tabacum-22102	0	1.75e-12	GAGGAAGAGCTGTATTCACATGGGATGC TGTTTTAGCT
Glycine_max-122468	12	6.76e-12	ATTACGGCCG GGGGAAGAAAGGTAATAGAGAGAGAAAG GGAAGAGGAG

60047.t00030 | At1g72730 | F28P22.8 | eukaryotic translation initiation factor 4A, putative / eIF-4A, putative | similar to Eukaryotic initiation factor 4A-10 GB:P41382 (Nicotiana tabacum); identical to (putative) RNA helicase GB:CAA09211 (Arabidopsis thaliana) (Nucleic Acids Res. 27 (2), 628-636 (1999))

NAME	START	P-VALUE	SITES
Glycine_max-60811	93	5.39e-20	CCTTCCCTTC AACTCCACGGCGCAGATCCGAGGAGTTTGG GAAACCCTAA
Citrus_sinensis-20106188	68	5.39e-20	CTTCCCTTTT AACTCCACGGCGCAGATCCGAGGAGTTTGG TAACCCTAGC
Vitis_vinifera-8766262	14	6.73e-19	CTTCTTCTCC GACTCCACGGCGCAGATCCGAGGAGTTGGG AAACCCTAGC
Gossypium_hirsutum-70101078	41	5.74e-18	TTTGCCTATC AACTCCACGGCGCAGATCCGAGGAGTCTCT ATTTCTCAAT
AT1G72730.1	86	1.52e-17	TTCTTCTTTC AACCCCACGGCGCAGATCCTACGAGTTTGG TCTTTGTCTC
Nicotiana_tabacum-132413	65	2.81e-17	GTGTTTCCTG AACTCCGCGGCGTAGATCCGAGGAGTTTTT GGAAAAAAAG

51682.t00023 | At1g30510 | F26G16.13 | ferredoxin--NADP(+) reductase, putative / adrenodoxin reductase, putative | strong similarity to SP|P41345 Ferredoxin--NADP reductase, root isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) {Oryza sativa}, ferredoxin-NADP reductase precursor (Zea mays) GI:500751

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-7395	63	1.64e-14	GCCAAACAGT CTTGTCCTTTCCCAAACTCCAAAGGATCAC TACAATCCCT
Glycine_max-21459	77	1.20e-13	AAACAAAAAA CCTGACCTTTCCCTTTCTCCAAAGGATCAT CGAACTAAAC
AT1G30510.2	56	4.96e-13	AAGAAGGAAG CTTGGCCTTTGAGGAGATTCAAAGGATCGT GTTGCTTACT
Gossypium_hirsutum-49878	35	4.96e-13	GAGGAAGAAA AGCGTCTTTTGGCAGTCGCCAAAGGATCAT CGTTCGAATC
Vitis_vinifera-6635	55	2.00e-11	GGCTGCAGGA ATTCGGCACCTTGGATCGCCAAGGGGTCAT CCTCACTCGC

48842.t00026 | At2g19490 | F3P11.9 | recA family protein | contains Pfam profile: PF00154 recA bacterial DNA recombination protein

NAME	START	P-VALUE	SITES
Vitis_vinifera-64383	14	4.13e-12	CGAAGGTCTC AAAAGGGAGGGAAACCAAA CCAAAAACCC
Citrus_sinensis-64125	67	3.93e-11	AGTTTCAGTA AAAAGGGACGGAACCCAAA AGTCCAAAAC
AT2G19490.1	20	7.92e-11	AAAAATAGTT GAAACGGAGGGAAACGAAA ACCTAAAACC
Glycine_max-211601	104	1.36e-10	ATGGAATGGA AAAAGGGAGGGAAATCAAA CAAAACGCTC
Gossypium_hirsutum-32314	93	1.17e-08	ACCCCAAATG AAAACAGAAAGACCCGAAG CATTTTTTAG
Nicotiana_tabacum-91467	47	2.96e-08	CTAAAGCGCC AAAATAGAAGCGGCAGAAA TGCTCTACTG

67990.t00031 | At1g31730 | F27M3.7 | epsilon-adaptin, putative | similar to SP|Q9UPM8 Adapter-related protein complex 4 epsilon 1 subunit (Epsilon subunit of AP-4) (AP-4 adapter complex epsilon subunit) {Homo sapiens}; contains Pfam profile: PF01602 Adaptin N terminal region

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-62620	292	4.69e-18	TCCAAGCTGG AGCAGTTGAAGACAATTGGTAGGGAGCTCG CA
Citrus_sinensis-16208	27	2.38e-15	GCAAAGCTGG AGCAATTGAAGACAATAGGAAGGGAGCTCG CA
Glycine_max-205799	0	2.40e-14	AGCTGAAGACGCTGGTGGGGAGGGAGCTGA CA
AT1G31730.1	218	4.84e-12	CGGAGAAATC ACCGCTCAAACTTTGTTGCTAGGGATTTGA GTGAGTGAGA

60531.t00007 | At3g15010 | K15M2.15 | RNA recognition motif (RRM)-containing protein | similar to UBP1 interacting protein 1a (Arabidopsis thaliana) GI:19574236; contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

NAME	START	P-VALUE	SITES
Vitis_vinifera-66261	69	4.95e-12	GTTCTCCACT AGGGTTAGGGTTTAACCG AGGATCTCTC
AT3G15010.2	61	2.10e-10	CTGGACTAGA AGGATTAGGGATTTACCG GTGAAAGAAT
Gossypium_hirsutum-54711	55	6.46e-10	TGAATTTTGT AGGGTTAGGGTTTTAAGG GTAAAGCATC
Nicotiana_tabacum-5723	15	1.11e-09	CCGGATTCCC GGGATTAGGGTTTAACCT CCGGTCAGTT
Glycine_max-83201	22	4.08e-09	TTAGAGTTAG ATTATTAGGGTTTAACCG TTCCTCCCCT
Citrus_sinensis-67751	12	6.84e-09	TTATCTCATT AGGGCTAGGGTTTTGCTC ACAAAATTCT

60014.t00080 | At1g80410 | F5I6.38 | acetyltransferase-related | low similarity to acetyltransferase Tubedown-1 (Mus musculus) GI:8497318, N-TERMINAL ACETYLTRANSFERASE GB:P12945 from (Saccharomyces cerevisiae); contains Pfam profile PF00515 TPR Domain

NAME	START	P-VALUE	SITES

NAME	START	P-VALUE	SITES
Citrus_sinensis-3941	39	3.46e-17	GTTCACAGTA **GGGTAGGGTTGCAGCAGATAAACGCCACC** ACCGTCACCG
Nicotiana_tabacum-28179	31	4.51e-17	ATCTCTCTCT **CAGTAGGGTTGCAGCAGATAAACGCCACC** ATCTCCGTTC
AT1G80410.1	23	2.46e-14	CTTTGTTTCG **CAGTAGGGTTGAAGCGGATAGTACGCCAC** CTCTATCTCT
Gossypium_hirsutum-80078	34	2.17e-12	TTCCAGTTCA **GAGTATGGTTGAAGAAGCAGATAGACGCC** ACCGTTTCTC
Glycine_max-541271726	7	1.13e-11	GGGCCTC **GCTTTGCTTTGCAGCTCACAAAACGCCAC** CAGGCTTTTC

67306.t00009 | At3g58500 | F14P22.90 | serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A4) | identical to SP|P48578 Serine/threonine protein phosphatase PP2A-4 catalytic subunit (EC 3.1.3.16) (Protein phosphatase 2A isoform 4) {Arabidopsis thaliana}; contains Pfam profile PF00149: Ser/Thr protein phosphatase

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-8153	41	1.40e-17	CCAAACCAAA **CTAGGGTTAGGGTTATCCCTAATCCGCA** TAAAGATTTT
Citrus_sinensis-38552	26	7.28e-17	TGATCTCACT **CTAGGGTTAGGGATATCCCTAATCCGGA** CACCGTTATC
AT3G58500.1	91	6.15e-15	TCCATCCAAT **TTAGGGTTAGGGCTGCCCCTAATCTGGA** AACCTTTGCC
Vitis_vinifera-314	62	2.58e-13	GCAGCGAAAT **CTAGGGTTAGGGTTAGTGTCAGCTTCCA** ATCTGGCTGT

67201.t00043 | At4g34710 | T4L20.290 | arginine decarboxylase 2 (SPE2) | identical to SP|O23141 Arginine decarboxylase 2 (EC 4.1.1.19) (ARGDC 2) (ADC 2) (ADC-N) {Arabidopsis thaliana}

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-227133666	307	1.25e-21	GCTTCTTTTG **AGGGGGTAGCCGGGGCCTCGGCCTCGGCGG** GTTTTAATAG
Glycine_max-1277271727	314	3.16e-21	TCTTCTTTTG **AGGGGGAAGCCGGGGCCTCGGCCTCGGCGG** CTTTCAAAGC
Gossypium_hirsutum-31096	339	9.36e-21	GCTTCTTTTG **AGGGAGTAGCCGGGGCCTCGGCCTCGGCGG** GTTTTAAAGC
AT4G34710.2	291	3.76e-20	TCTTCTCCTG **AGGGGGTAGCCGAGGCTCCGGCCTCGGCGG** TTTTTAAACC

67577.t00046 | At5g02960 | F9G14.270 | 40S ribosomal protein S23 (RPS23B) | ribosomal protein S23, Fragaria x ananassa, PIR:S56673

NAME	START	P-VALUE	SITES
Citrus_sinensis-102190	0	3.44e-16	**GGGGAGGGTTTTACTAAGCGGCTGCTG** TTTCTTCTCT
Vitis_vinifera-51762	91	6.81e-14	TAATCTCCAG **GATTAGGGTTTTACTCGGCGGCTCCTT** CTTCCTCCTC
Nicotiana_tabacum-102167	12	1.10e-12	TTTTTTCTTA **TATTAGGGTTTTGCTAGGCGGCTGACT** CCTTTCTCCT
Glycine_max-82567	5	2.02e-11	CGGCC **GGGGAGGGTTTTGTGCTGTTGTCGCTG** CTCATCCTCC

NAME	START	P-VALUE	SITES
AT5G02960.1	25	4.80e-11	GCCTTCACTA GGTTTAGGGTTTTCTCAGCCGCTTAAG AGCTTATCAT

67046.t00014 | At4g02450 | T14P8.5 | glycine-rich protein | similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807)

NAME	START	P-VALUE	SITES
Vitis_vinifera-17566260	17	4.48e-11	TTTTCTTCTA CTGCCTTCTAGGGTTTTCCA TTTCGCGACC
Gossypium_hirsutum-42651	40	7.41e-11	TACCGGTTTG CTGGTTTCTAGGGTTTTTCA ATCTATACTT
AT4G02450.1	88	4.90e-10	CGTGTTTCCT CTTCTCTCTAGGGTTCTCCT TCAACAGTTT
Glycine_max-190546	73	3.02e-09	GGGTTTCTCT CTTCAAACTAGGGTTTTACA GAATATAAGC
Citrus_sinensis-71943	89	3.19e-09	CAACTCTCTC TCTCGCTCTAGGGTTTTACT GTTTTCTTTC
Nicotiana_tabacum-43884	78	3.80e-09	GCCGCTTCAC TTTGTTTTTAGGGTTTTTCA GAGTCTCTCT

51058.t00035 | At2g22430 | F14M13.17 | homeobox-leucine zipper protein 6 (HB-6) / HD-ZIP transcription factor 6 | identical to homeobox-leucine zipper protein ATHB-6 (HD-ZIP protein ATHB-6) (SP:P46668) (Arabidopsis thaliana)

NAME	START	P-VALUE	SITES
Vitis_vinifera-28762	287	4.56e-17	CTTCTTTCTT TTTGATGGGTTCAGAGGGTGAGGAAG TACTGAAAAA
Glycine_max-255224	284	3.74e-14	TTATGAATTA TTTGATGGGTGAAGAGGGAGAAGAAG TGGTGAGAAA
Gossypium_hirsutum-71350	168	4.44e-12	ATGTCTATTG TTGGATGGGAACTGAGAGTAAGAAAG AAACTGTGTT
Nicotiana_tabacum-15942	189	1.21e-11	TTGTACTTCT TATGATGGGCTCAGAAGTGGAGGAAT TAATTAAAAA
AT2G22430.1	129	1.73e-10	TTCTCTTTTC TTGATGGGTTTAAGAGAGTAAAGATC ATCAAGTACT

25234.t00005 | At2g37630 | F13M22.13 | myb family transcription factor (MYB91) | contains Pfam profile: PF00249 myb-like DNA-binding domain

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-1614	247	1.17e-16	GGATCACAGA GCAATGGGAAGTGGTGTTTTCCCCTGGAA
Vitis_vinifera-15486	87	8.29e-16	TGAAATTGAG GCAATGGGCAGTGGCATTTGCATCTGGAA
Nicotiana_tabacum-23758	327	1.09e-15	GGAGTTTGGG ACCATGGGCACTGGTGTTTGCACCTGGAA
Citrus_sinensis-15342	195	6.60e-13	AGAATTTTAC ACAATGGACAGCGTTGTTTACTCCTGGAA
Glycine_max-302271731	141	1.29e-12	CAAGTTCCAA GCAACTGGTTGTGGGATTTGCACTTGGAA
AT2G37630.1	168	2.55e-11	GAAGGATGGT GAGATGGGAAGAAGTGATGTCAGGAGGAG TAGGAG

68001.t00020 | At5g17640 | K10A8.120 | expressed protein

NAME	START	P-VALUE	SITES
AT5G17640.1	376	1.18e-12	ATCTCTGAAC **CAATGGGGAAACATTTCTGACA** TTTA
Vitis_vinifera-40004	475	5.13e-12	AGCTTTTGGT **CAATGGGGGAAGGCTTGTGACG** ACA
Glycine_max-77319	415	5.70e-12	GCTTTAAAAG **CAATGGTGGGACAATTGTGACA** AAT
Citrus_sinensis-16072	28	7.31e-12	TATTTTGATC **CAATGGGGAAAAATTTCTGACA** GGA
Gossypium_hirsutum-70716	385	1.66e-11	GCTTTTTATA **CGATGGGGAAATATTTGTGACA** ATA
Nicotiana_tabacum-114062	298	7.84e-09	TTTTGAATGA **CAAAGTTATGAGGATTTTGCCA** GGCTTTTGGA

15156.t00007 | At2g02710 | T20F6.15 | PAC motif-containing protein | similar to nonphototropic hypocotyl 1 (Zea mays) GI:2687358; contains Pfam profile PF00785: PAC motif

NAME	START	P-VALUE	SITES
Glycine_max-241609	292	6.82e-14	AGCGCGAGTT **CACATGGGATTGGGAACAACCG** CGAGAAGCAG
Gossypium_hirsutum-94160	176	1.98e-12	TATTACTACC **CACATGGGATTGGTTCCAACCG** CGAAACCCAG
AT2G02710.3	134	1.31e-11	CCTGAAAACC **CACATGGGATTGGAACTAAACA** CTAGACTGAC
Nicotiana_tabacum-120862	311	7.31e-11	AAGTTGTTGC **CACATGGGATTGGGGTTAATAA** TCTTAGGTGA
Citrus_sinensis-83694	15	4.10e-10	CGTCCGCGGA **CGCGTGGGCTTTGATAAAACAA** ATCAGCGGGC

67287.t00052 | At3g54020 | F5K20.320 | phosphatidic acid phosphatase-related / PAP2-related

NAME	START	P-VALUE	SITES
AT3G54020.1	315	1.91e-16	GACCCAAACT **GTTGGGGTTTGAAGTAATATGGAAGTGG** AAGATTAACA
Vitis_vinifera-17466258	326	1.76e-13	ACACTTAAGA **GTTGTTTTGTGATGTAATATGGCACTGG** TTTGCCACAT
Gossypium_hirsutum-688101080	236	1.91e-13	GACCTTAACC **GGTGGGCTTTGAACTACTATGGTACTGG** TTGTTACACG
Glycine_max-88564	418	2.43e-13	TCTATCATCA **GTGTGGTTATGAGGTAACATGGAAGTGC** TCCTTGCGCG
Citrus_sinensis-23906	378	1.35e-12	GTTAATGATG **TTGACTTTGTGAAGTACTATGGAAGTTG** TTGTTACACG

67261.t00012 | At3g48210 | T24C20.90 | expressed protein

NAME	START	P-VALUE	SITES
Vitis_vinifera-27133	0	2.20e-14	**AAAGTAGAAATGGCGGGCTGAGC** GTCCAATTTC
Nicotiana_tabacum-83641	61	2.45e-13	TTTTGAAAAG **GAAATGAAAATGGCGGGCTAAGC** ATACTGTCTC
AT3G48210.1	20	2.78e-12	AACTCGAATC **AAAATTCAAATGGCGGGCTAAAC** TTCGATTCAG

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-82452	30	2.92e-12	ACAAAAATTG **AAAGCAAAAAGGGCGGGCTTAGT** CGATCGTTAA

60025.t00021 | At1g71980 | F17M19.13 | protease-associated zinc finger (C3HC4-type RING finger) family protein | identical to ReMembR-H2 protein JR702 (Arabidopsis thaliana) gi|6942149|gb|AAF32326; contains Pfam domain, PF02225: protease-associated (PA) domain and Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger); identical to cDNA ReMembR-H2 protein JR702 mRNA, partial cds GI:6942148

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-269430	98	1.46e-12	CCATTTTGAT **ATGGAAGCTGATGTTTCTATT** ATTTTTGCCG
Nicotiana_tabacum-130945	121	1.46e-12	TCTGTAGAGA **ATGGAAGCTGATGTTTCTATT** CTTTCAACAA
Vitis_vinifera-18348	88	3.26e-12	TCCGTGTCAA **ATGGAAGCTGATGTTCCCATT** TTCGAAACCC
Gossypium_hirsutum-90555	229	3.26e-12	TATTTCGCTA **ATGGAAGCTGATGTATCCATT** TCCTTCTCAA
Citrus_sinensis-6360	16	4.69e-12	CTNTTTTCTC **ATGGAAGCCGATGTTTCAATT** TATTTTGTTT
AT1G71980.1	222	7.20e-12	TGTGATTTAA **ATGGAAGCTGACGTGTCAATT** TCCTGAAAAA

67802.t00004 | At5g47100 | K14A3.5 | calcineurin B-like protein 9 (CBL9) | identical to calcineurin B-like protein 9 (GI:5866279) and calcium-binding protein AtCBL9 (GI:16151825) (Arabidopsis thaliana); similar to calcineurin B-like protein 1 (GI:3309082) (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-122046	87	1.08e-14	TTTATTGGTT **AAGATGGTTTTGATGATATATTGTAGTGA** AGCTGGTTAC
Vitis_vinifera-43041	135	2.60e-14	CGAGCTCGGT **CGGATGGTTTTGATGATGTACTGTAGTGA** AGCCTAGGCG
AT5G47100.1	182	3.23e-13	GGTGTTTTTA **AAGATGCTTATGATGATGATGGGGAGTGA** GTAATATCAG
Gossypium_hirsutum-45995	71	2.36e-12	GTAGGGTCTA **AAAATGGTTTTGCTGAGAGAACATAGTAA** AGCCTTGGCG
Glycine_max-117578	111	2.95e-11	CAATTTTCTG **AACACGCTTTTGAAGAGGGTAAGTTCGAG** CACCGGTACT

67596.t00025 | At5g06510 | F15M7.4 | CCAAT-binding transcription factor (CBF-B/NF-YA) family protein | contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-120857	66	1.05e-18	GCTTCAAATT **GTACCGACATGGCTCCTAGCAAATGGGGTT** TCTCTTCTTG
Gossypium_hirsutum-60217	109	3.23e-18	GCTTGAAATT **GTGCCGACATGGCTCCTAACAAATGGGGTT** TCTCAGCCTC
Glycine_max-255288	0	2.04e-16	**GGACCGACATGACTCCAACCTGATGGGGTT** AAACACTGCT
AT5G06510.1	16	1.56e-15	TTCTAATTTG **GAACCGACATAGCTCCCAACTAATAGGAAT** CTCAAGCTTC

67161.t00029 | At4g26570 | T15N24.20 | calcineurin B-like protein 3 (CBL3) | identical to calcineurin B-like protein 3 (GI:22136404) (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-1564	158	1.22e-18	GTACAAATAG **GAAATGGTTAAAAGGTATGGAGTGTTTTGA** TGTGCAGAGA
Gossypium_hirsutum-23112	111	1.22e-18	GCAGAATCAG **GAAATGGTTAAAAGGTATGGAGTGTTTTGA** CGTGTGGAAG
AT4G26570.1	171	6.75e-17	GACGAACCAG **GAAATGGTTAAAAGGCATGGAGAGTTTTGA** TTTACAAGAT
Glycine_max-242984	263	1.76e-16	CCTGGAGTTG **GAAATGGTTAAAAGTTATGGAGTGTTCTGA** TTTGCAAAAG
Nicotiana_tabacum-58781	196	5.76e-16	GACATAACAG **AGAATGGTCAAAAGATATGGAGTGTTTTGA** AGCAGAGGCT
Vitis_vinifera-18528	81	4.43e-13	TTCCTCTTCA **GGCTTTCTCTGCAGGTATGGAGCATTTTGA** TGTGCCAAAA

51031.t00032 | At1g09240 | T12M4.5 | nicotianamine synthase, putative | similar to nicotianamine synthase (Lycopersicon esculentum)(GI:4753801), nicotianamine synthase 2 (Hordeum vulgare)(GI:4894912)

NAME	**START**	**P-VALUE**	**SITES**
AT1G09240.1	51	1.64e-11	GAAAAATCAA **TAACCTCATAGTGTCGAC**
Vitis_vinifera-35086	91	1.64e-11	AGACTTCCCC **TAACCTCATAGTGTCGAC**
Citrus_sinensis-104374	90	3.49e-11	CCAATATCAA **TATCCTCATAGTGTCGAC**
Glycine_max-260565	68	6.96e-11	TATCAGTAAT **AAACCTCATAGTGTCGAC**
Gossypium_hirsutum-529101075	88	1.40e-10	AAATTTCCCA **TAACCTCGTAGCGTCGAC** A
Nicotiana_tabacum-89825	123	1.87e-10	AATTTCTTCA **TATCTTCATAGTGTCGAC**

67325.t00031 | At3g63200 | F16M2.50 | patatin-related | low similarity to patatin-like latex protein allergen Hev b 7 - Hevea brasiliensis, EMBL:AF113546; contains patatin domain PF01734

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-16092	86	1.52e-16	AAATTTTCCG **CCATTAATGCCTCTCAGCGAGAAAGTGTGA** TCGATAGCGT
Gossypium_hirsutum-81859	149	4.18e-15	CTTCTCGCCG **CCATTAATGCTTATCAGCAATATAGCGTGA** ATAGAGCCAA
AT3G63200.1	140	3.40e-14	CGCATTCCCC **CAATTAAAGCCTCTCTGCTCCAAACCGTGA** TATACTCTTT
Nicotiana_tabacum-98776	420	6.67e-14	CAATTTCGCA **TCATAAATGCCTCTCCGAAGAATATCGTGA** CTTTTTTCCT

60048.t00049 | At1g71692 | F26A9.6 | MADS-box protein (AGL12) | identical to GB:AAC49085 GI:862650 from (Arabidopsis thaliana) (Plant Cell 7 (8), 1259-1269 (1995))

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

NAME	START	P-VALUE	SITES
Glycine_max-172479	65	1.94e-19	GGCTGCAGCA **ACCTCGAAGCTAGTTCAAACTAGTGGGAGG** TTGTGTGCAT
AT1G71692.1	57	1.94e-19	TAAGTGGGGA **ACCTCGAAGCTAGTTCAAACTAGTGGGAGG** TTGTTTCACG
Nicotiana_tabacum-35191	55	1.94e-19	AAGTGCAACA **ACCTCGAAGCTAGTTCAAACTAGTGGGAGG** TTGTCTGCAA

60042.t00066 | At1g75080 | F9E10.7 | brassinosteroid signalling positive regulator (BZR1) | identical to to BZR1 protein (Arabidopsis thaliana) gi|20270971|gb|AAM18490

NAME	START	P-VALUE	SITES
AT1G75080.1	65	1.74e-15	ATTCCAGCGA **AGGAAAAGCGTATTCCTCGTGAGCACT** AACTTCTCAC
Citrus_sinensis-96873	27	1.69e-14	NCTACAGCGA **AGGGAAAGCGTATTCCTCGTGGCCATT** TTAGCCTTTT
Gossypium_hirsutum-79198	87	6.80e-13	TTTCCACCCA **AGCTAAAGCGTATTCCTCGTTACTCGT** GATCTTCTCC
Glycine_max-198583	21	1.75e-12	AGAAACAAGT **AGAAGCAGCACATTCCTCGTGAGGGGT** CGTTACTAAC
Nicotiana_tabacum-36495	56	2.09e-12	TCTATAAAAC **TTTGAGAGCGTATTTCTCGTGAGTAGT** AGTCCCCCAA

49200.t00042 | At2g27510 | F10A12.19 | ferredoxin, putative | similar to non-photosynthetic ferredoxin from Citrus sinensis (GI:1360725), Ferredoxin, root R-B2 from Raphanus sativus (SP|P14937); contains Pfam profile PF00111 2Fe-2S iron-sulfur cluster binding domain

NAME	START	P-VALUE	SITES
Citrus_sinensis-72106181	53	2.57e-11	AACCCACTCG **CCACCTCGCGCGCTCCGCC** GCTCGATCTC
Vitis_vinifera-47555	12	6.95e-11	CGGGCTGCCC **TTCCCTCGTGCTCTCCGCC** ATTTCTCGCT
AT2G27510.1	12	2.47e-10	TCCACCAACC **CCCTCTCGCACTCTCCGCC** ACCTTCTTCC
Gossypium_hirsutum-67940	100	4.24e-10	GAAACTTAGA **CCCCTTCGTATTCTCCGCT** CATACCCCAA
Nicotiana_tabacum-9501	71	2.29e-09	TCTGCTTTTT **CTCCCTCGAGAACTCCGCT** TACTTTCGTT
Glycine_max-150100	33	4.79e-09	CGTGACTCAA **TCACTTCGTTTTCTCCGCT** TTCATCTTCT

67295.t00030 | At3g55520 | T22E16.180 | immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative | POSSIBLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) SP:P30416(Mouse);P59 PROTEIN (HSP BINDING IMMUNOPHILIN), rabbit, SWISSPROT:P27124:FKB4_RABBIT

NAME	START	P-VALUE	SITES
Gossypium_hirsutum-52673	0	9.08e-17	**GCCACCAGAATCGACGGCGATTCCTCCCGA** AAAATCATCC
Vitis_vinifera-1266260	0	1.03e-15	**GGCGACGAAATCAACGGCAATTTCCCCCGA** TATATCGCTT
Citrus_sinensis-49537	5	1.32e-14	CCACG **CGTCCGAAAATCCACGGCAATTTCTCCCGA** TTTATTGTCC

NAME	**START**	**P-VALUE**	**SITES**
AT3G55520.1	97	1.09e-13	ACAGTCTATG GCCACCGATCTCTACGGCGATCTCTTTCCG GTTATCACTT

67286.t00004 | At3g53340 | F4P12.40 | CCAAT-box binding transcription factor, putative | similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP:P25209) (GI:22380) (Zea mays); contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-52438	1	6.40e-12	T CTTCTCCAGCGTCCGATC TACCTTCGCC
AT3G53340.1	8	1.15e-11	GCTCCTAT CTTCTCCAGCGTCGGATC AGATCAGATC
Nicotiana_tabacum-117133664	11	3.03e-11	TTTTTCCCAC TTTCTCCAGCGTCCGATC CTCCCTTTTC
Glycine_max-221563	64	6.27e-11	ACCTTGCTTT CTTCTCCAGCGTCCGATT CTCTCACCGA
Gossypium_hirsutum-49791	27	3.50e-10	TCTTTCCTCT TTTCTCCAGCGTTCGATC CCCTCTCTTT
Citrus_sinensis-64829	28	4.81e-08	CCTCTCCCCC CTTCTCCAAACTCGCGCG CCAAATACAA

67858.t00037 | At5g54940 | MBG8.21 | eukaryotic translation initiation factor SUI1, putative | similar to SP|P32911 Protein translation factor SUI1 {Saccharomyces cerevisiae}; contains Pfam profile PF01253: Translation initiation factor SUI1

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-390101081	67	7.62e-14	CTAGTGATTC GTGTTCAAAGAACCAAACAAGCCAAGTAC
Glycine_max-223382	89	1.22e-12	CCGTGTTACT TGTTCCCAAGTCTCCAACAAGCAAAGTAC
Nicotiana_tabacum-20870	80	3.02e-12	TAGTTTCGGA GGGTGAGAAGTTCTCTTCCAGCTAAGTAC
Vitis_vinifera-26066259	135	5.61e-12	TTCATTGCCC GTATTTCTAGTTTTCATCCAGCAAAGTAC
AT5G54940.1	111	5.70e-11	TTTTCGAATC GGATTGAGAGAATCAAACAGCTTAAGGGC AGTTTCTTAG

6067.t00024 | At2g34160 | T14G11.28 | expressed protein

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-414271733	6	4.33e-15	CGGCCG GGGAAGAGAAAGAGATTTGGATTTGGGG GAGCATTTGG
Vitis_vinifera-11805	0	3.57e-13	GGGGGCAGAGGGAAATAGGGTTTTGGGG GTTTAGGGCT
Citrus_sinensis-31621	78	3.08e-12	CACCAAAACA GAGAAATCTAAGAATTAGGGTTTTGGGT AATAAGTTCT
Gossypium_hirsutum-10039	97	5.33e-11	TTCGTCCGAT TTGCAGAGTCAGAGGCTGAGATTTAGGG TTTAGCAGAA
AT2G34160.1	44	1.34e-10	CCCTTAACTC GAGAAAAATTAGGGTTACGGATTCCGAT TAGCAAGC

51169.t00008 | At2g21250 | F7O24.1 | mannose 6-phosphate reductase (NADPH-dependent), putative | 6-phosphate reductase (Apium graveolens)(GI:1835701), NADP-dependent D-sorbitol-6-phosphate dehydrogenase (Malus domestica)(SP|P28475)

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-5	5	1.56e-15	TTACG **GCGGGGACACGAGAACAGCCACCCAGAGAG** TGTCCGTGTG
Glycine_max-100864	0	2.28e-13	**GCGGGGACACTTGATTAGCTGAGGAGGAAG** AGAGAAAAAC
Gossypium_hirsutum-65407	63	1.24e-10	CAAGTCCTTC **GTAGGGATAGCAGATTTGATTTACAGAGAC** CAAAGGGGGG
AT2G21250.1	39	1.34e-10	ATTTACCCAA **TCAGGGATTCAGGAAGAGAAGCAGAGAAAG** AA
Nicotiana_tabacum-25078	4	2.85e-10	CGGC **GCGGGGAGAATACAAGTTCCAAGCAATCAA** CCAAAGCAAG
Citrus_sinensis-81223	18	8.91e-10	CCGCGGACGC **GTGGGAAAAGTGGCAATAGCAAGCAAAGTC** ACAGCAAGTT

52195.t00053 | At1g19310 | F18O14.3 | zinc finger (C3HC4-type RING finger) family protein | contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-2707	88	1.27e-14	GACTTCTTTG **GATCGGTCGATTGCCATATCGATCGGTC** CTTCTATCTC
Citrus_sinensis-64782	44	4.04e-14	TGACTTTGTG **GATCGATCGATTCGCAAATCGGTCGGTC** GATTTCTTCA
AT1G19310.1	96	8.19e-13	GATTGCGATC **GTTCCGTCGATCCCTTCATCGCCCGATC** TAAATCTCTA
Vitis_vinifera-21326	32	5.43e-12	ATCCGTCGGT **GGTGGGTCGCTCGGCCGATCAATCGATA** ACTCTGTTCC
Glycine_max-117212	44	1.53e-10	CTATTGACTT **CCTCAACCGATCCACTCTTCTCTCTATC** TGCAG

60008.t00027 | At1g74040 | F2P9.9 | 2-isopropylmalate synthase 1 (IMS1) | identical to 2-isopropylmalate synthase (IMS1) (Arabidopsis thaliana) GI:12330687; identical to cDNA 2-isopropylmalate synthase (IMS1) GI:12330686

NAME	**START**	**P-VALUE**	**SITES**
Gossypium_hirsutum-71228	20	1.47e-10	CCTCGGTGCT **GACGGCGCCTCCACTCTC** ATTTCCCTCC
Citrus_sinensis-55230	43	2.20e-10	GCAAGCAGCA **GCAGCCGCCTCCACTCCC** GCTCCCGCTA
AT1G74040.1	36	2.61e-10	GTCGCCCGTC **GCCGCCGCCGCCACACTA** TCATCTCTCT
Nicotiana_tabacum-67322	7	1.35e-09	GATTCTC **TCCTGCGCCGCCACTCAC** ACCCTTCATT
Glycine_max-130126	4	8.73e-08	ACGA **GCTTCAGCACACTCTCTC** TATCTAGGGT

51794.t00034 | At1g71860 | F14O23.24 | protein tyrosine phosphatase 1 (PTP1) | identical to protein tyrosine phosphatase 1 GI:3170531 from (Arabidopsis thaliana); contains Pfam profile: PF00102 protein-tyrosine phosphatase

NAME	START	P-VALUE	SITES
Citrus_sinensis-97230	98	4.49e-14	ATTTCAAAGC GCCCTCGGTGTCGCCGGAAATCGGCC
Vitis_vinifera-64418	68	2.39e-13	CTCAATCCTT GTTCTCGCCCCAGCCGAAGATCGGCC
Glycine_max-162271	87	2.98e-13	GTCTCTACTC GCTCTCGTCCCCGCCGGAGATCCACC
Nicotiana_tabacum-2420	102	8.25e-13	TCAGTTCGGA GCCGGAGCCGGAGCCGGAGATCGGCG
AT1G71860.2	111	1.70e-11	TCCTGCCGTC GCGTTAGATCCCGCCGTCAATCGGTC
Gossypium_hirsutum-39684	98	1.40e-10	ATTTCGAATT GCGTTTCTTCAAAGCGGAAACCGGCC

67801.t00019 | At5g47060 | MQD22.20 | senescence-associated protein-related | similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana);

NAME	START	P-VALUE	SITES
Glycine_max-265107	211	1.52e-13	CCTTCCTTGG TTCGTTCCCTCCACAAACCAAAAACCCAAC AAAAGAACGT
Nicotiana_tabacum-200133665	17	2.84e-13	TTTCCACTTT CCCATTCTCTCTACAAACCAAACAAGGAAA TTAA
AT5G47060.1	23	3.58e-13	CTCTCTCTTT CACTTTCTCTCTAAAAACCAGAAAAAAAAA AA
Vitis_vinifera-6911	23	1.17e-11	GGTTTGCACT CTCCCTCTCTCCTCGCATCAGTCACCCAAC CCCTCTTTAT
Gossypium_hirsutum-74512	32	4.74e-11	CTTCTCTTTA CTCCTTCACTTTAATTCCCACAAAAAAGAC CAGACCTTTG

67766.t00023 | At5g42560 | MDH9.24 | abscisic acid-responsive HVA22 family protein | weak similarity to SP|Q00765 Polyposis locus protein 1 (TB2 protein) {Homo sapiens}; contains Pfam profile PF03134: TB2/DP1, HVA22 family

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-58021	72	4.66e-16	CTCACCTCTT CTCCGCCGACATCGCAACGGTTCGCCGGAG CATTACGGCG
Gossypium_hirsutum-96638	120	1.42e-14	CGCCGACTGC CGCCGCCGACATCGTAACCACTGTTCGCCG GCGATCTTCT
Vitis_vinifera-24462	78	1.61e-14	TCTCTTCTTA CGCCGCCGACATAGTAGCGGTTCGCCACCG TAGCGTTTCG
Glycine_max-63912	80	1.59e-13	CCCCTCCGCA TCTCGCCGACAACGTAACGGTTTCGCGGTG GCCGTTTCTG
Citrus_sinensis-7787	5	1.19e-12	CCACG CGTCCGCGACTTCGCAACCGCTAGCGGTGG CATTTCGGTG
AT5G42560.2	143	3.77e-10	CGTCTCTGAT TCTCGTCGCCGCCGTACACAGTTGTTGTTC TCTGCCGG

49202.t00036 | At2g25520 | F13B15.18 | phosphate translocator-related | low similarity to SP|P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}, phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-56149	80	2.93e-15	TTTCACCTCC **CCTCTCCACCACCCACCACCGCCACC** GCGAAA
Gossypium_hirsutum-85798	58	2.54e-13	CCTTCCTCAC **CCTCACCCTCTCCCACCGCCGCCTCC** TCCACCATTT
AT2G25520.1	63	3.85e-11	CTCTCTTAAT **CCTTTATCCTGCGCACCACCACCACC** ATCTTCTTCT
Glycine_max-201836	132	5.98e-11	ATAGCTATAG **CATCACACACACACACCACCGCTAGG** GTTAGGGTTA
Vitis_vinifera-47387	45	8.50e-11	CCCACCTTGC **TCTATCCTGCGCACCCCCCTGCCCCC** TCCGTGTATC

60557.t00017 | At3g14080 | MAG2.4 | small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative | similar to U6 snRNA-associated Sm-like protein LSm1 (Small nuclear ribonuclear CaSm, Cancer-associated Sm-like) (Homo sapiens) SWISS-PROT:O15116; contains Pfam profile: PF01423 Sm protein

NAME	**START**	**P-VALUE**	**SITES**
Vitis_vinifera-22350	480	1.33e-16	TGAGGCGGCA **GGGAGATTTCTGAGCTGCCAATGCCATTTG** TTTGTTTTTT
Nicotiana_tabacum-100712	198	4.42e-14	GGCATTATTA **GTGGGCTATCTGAGCTGCCAATGCAAATTG** AATTGAAATC
Citrus_sinensis-25545	313	5.22e-13	TGGGAAAAAA **GAGAGAATTTTGAGCAGCCAATGCAATTTT** TGATTTGGTG
Glycine_max-71215	238	1.15e-12	TGACATTGAA **GTGTTCAATTGGCACTGTCAATGCCATTGG** TGTGGTTTGT
Gossypium_hirsutum-8694	186	7.45e-11	GGTGGGTGTC **GATTGTGGAGGCCAAATCCAATGCCATTTG** TTTAGAATTG
AT3G14080.2	311	1.52e-10	TAGAAAGACC **GAAAGTTTTCTTCAATTTCAAAGTCAGTGG** CG

51806.t00053 | At1g18660 | F6A14.25 | zinc finger (C3HC4-type RING finger) family protein | contains Pfam profile: PF00097 zinc finger, C3HC4 type

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-51713	17	5.25e-17	TCCGGAGAGA **CACGTAGTGGAATATAGTCCGTGTATGAAA** CGAAGGACCG
Glycine_max-59457	106	1.58e-16	AAAGAGCCAA **GACGTAGTGGATTTTGGTCCATGTATGCAA** CGAAGGAGCC
Vitis_vinifera-19287	20	1.49e-15	AGACTCTTGA **GACGTGATTGAATGTGGTCCGTGTATGAAA** TGAAGGATTG
AT1G18660.1	142	3.71e-15	AGAGGATAAC **CACGTAGAGGATTCTAATCCGTGGTTGCAA** ACGAAGGACC

60531.t00026 | At3g15090 | K15M2.24 | oxidoreductase, zinc-binding dehydrogenase family protein | low similarity to NOGO-interacting mitochondrial protein from Mus musculus (gi:14522884); contains Pfam profile: PF00107 zinc-binding dehydrogenases

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-47000	36	3.59e-16	CCTCTTCTCT **CTCTGCGGACCAAAACACAGACACGTTCC** AATTCCCCCT
Gossypium_hirsutum-21110	3	1.08e-15	CTT **CTCTGCGGACTAAAACACTTCCACGTCTC** TCCTTTGCTT

NAME	START	P-VALUE	SITES
AT3G15090.1	13	2.00e-15	AACAAAGCCG **CTCTGCGGACGCAAATGCTGCCACGTCTT** CAATTTCCGT
Nicotiana_tabacum-61120	35	1.39e-14	CCAATTTTGT **CTATGCGGATAAAATAGCAGACACGTCCC** CTTCATTCTC

60238.t00047 | At3g09320 | F3L24.19 | zinc finger (DHHC type) family protein | similar to Golgi-specific DHHC zinc figer protein (Mus musculus) GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain

NAME	START	P-VALUE	SITES
AT3G09320.1	91	1.01e-11	ATCCACTCGC **CGGAGACGCCGTCGTTT** CGACGCCGGT
Citrus_sinensis-21250	46	1.01e-11	CACGCACACA **CGGAGACGCCGTCGTTT** TATAACGCCG
Gossypium_hirsutum-29272	17	1.01e-11	CCACCACCAC **CGGAGACGCCGTCGTTT** GTCACGCCGG
Glycine_max-1268271729	140	1.81e-11	CTTTTATTTT **GGGAGACGCCGTCGTTT** CGGCAACGCC

67931.t00009 | At5g66320 | K1L20.10 | zinc finger (GATA type) family protein |

NAME	START	P-VALUE	SITES
Nicotiana_tabacum-34404	129	1.66e-14	ACCGAGTCAG **CTTCCTCTTCGTGTTCGTCTTCCTCCACC** ACAACC
Vitis_vinifera-48899	7	4.09e-14	ATCACTC **CTCCCCCTCCTCCTGCGTCTCCCTCTCCC** TCTCCCTCTC
Glycine_max-22314	86	1.04e-13	TCCACCACCT **CTTCCTCTTCCTCTTCTTCACCCTCTAGC** CCCTTGCTAA
AT5G66320.1	138	2.41e-13	TAATCTCTTT **CTTCTTCTTCTTCTTCTTCTTCTTCTCGC** CACCGCTCCT
Gossypium_hirsutum-21820	143	3.36e-11	CTCTTTTCAA **CTACACCTTCGCTCTTGCCTTCGTCTCTT** CAGGAA

41871.t00025 | At2g41410 | F13H10.4 | calmodulin, putative | identical to SP|P30188 Calmodulin-like protein {Arabidopsis thaliana}

NAME	START	P-VALUE	SITES
Citrus_sinensis-55510	73	7.79e-16	CCCGTTCAAT **TCATTCCCCCTTCTCCTTCTCTTTCCTC** TTTTCCCCTT
Nicotiana_tabacum-10949	29	2.25e-11	TCCCTCCATT **TAACTCGCTCCTTCCTCTTTCTTTCCTC** GCACCAACTC
AT2G41410.1	48	3.70e-11	TCTCCCCATT **TAATACCCTCCTTCCTCGTTCTTTCCTC** TCAAACCAAA
Glycine_max-53230	2	8.35e-11	GC **TCTTTCTTCCTTCTCCTTCTCTTCTCTG** CTTCTCTTTT
Vitis_vinifera-54379	26	5.84e-10	CGACCACGCG **TCCGTCTTCATTGTCTATCTGTTTCCTC** CCTTTCTTCT
Gossypium_hirsutum-25843	43	1.57e-09	ATCCTCACCT **TCTCACCCCCTACCCATCCTATTTTCCT** AATCCCCCAG

31701.t00020 | At2g18870 | F19F24.7 | hypothetical protein | contains 1 transmembrane domain; tandem duplication of fibronectin type III domain protein (GI:3004551) (TIGR_Ath1:At2g18880) (Arabidopsis thaliana)

31701.t00021 | At2g18880 | F19F24.8 | fibronectin type III domain-containing protein | contains Pfam profile PF00041: Fibronectin type III domain

NAME	START	P-VALUE	SITES
Glycine_max-119045	50	3.51e-19	GGAATTGTGA **ACAGGCTTTCTTCTGGACCTGAGGTTCAGA** AACTCTGTGG
Gossypium_hirsutum-19336	245	3.86e-17	GGTATAGTCA **ATAGGCTTTCTTCGGGACCTGAAGTTCAAA** AACTATGTTC
Vitis_vinifera-12270	67	6.18e-17	GGCATCGTTA **ATAGGCTTTCTTCTGGCCCAGAGGTTCAGA** GGCTGTGTGC
AT2G18880.1	190	1.21e-12	TCTGCGGACC **ACACCATTTTTTCCGCTCATCAACTTCAAG** GGGATAATTT

60540.t00026 | At3g20060 | MAL21.6 | ubiquitin-conjugating enzyme 19 (UBC19) | nearly identical to ubiquitin-conjugating enzyme UBC19 (Arabidopsis thaliana) GI:22530865; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme

NAME	START	P-VALUE	SITES
Glycine_max-181824	0	1.11e-13	**CTCTTCTTCTTCTTCTTCTTTTTC** TTTTCCTCTC
Citrus_sinensis-5215	67	3.99e-13	CTAATTCGTT **CTCTTCTTCTTCTTCTTCTTCTTC** TCATTTTCAC
AT3G20060.1	43	1.21e-12	ATCTCTATCT **CTCTTCTCCTTCTTCTTCAGTTTC** GATCATTCTT
Nicotiana_tabacum-77964	26	9.21e-12	CAACCCTTCT **CTCTTCTTCTTCCCCTTCAGTTTC** TAAAAAATAA
Gossypium_hirsutum-55299	84	7.80e-10	CTTTGTGTAT **CTGTTCTTCGCATTCTGCTTTTAA** CTACTTTGGT
Vitis_vinifera-47275	132	1.18e-09	ATTCAGAGGT **CTCTTCTCTTCTTCTTTCTTCTGA** TAATCTGTTG

52195.t00056 | At1g19330 | F18O14.5 | expressed protein

NAME	START	P-VALUE	SITES
AT1G19330.1	124	2.20e-12	TTTCCCTCTC **TCAGCAATGCATGATCTTCGA** TTTTCTATCA
Citrus_sinensis-106037	56	3.28e-12	AAATTTAAAC **TCAGCAATGCGTGATCTTCAA** TTTAAATGCA
Glycine_max-478271734	66	6.28e-12	ACATTCTTCA **TCAGCAATGCACGATCTTCAA** TACGAATGCA
Gossypium_hirsutum-58656	129	8.35e-12	ATATACGTAT **TCACCAATGCATGATCTTCCG** ATCCAATGTA
Vitis_vinifera-5840	137	3.60e-11	GAATACGGCT **TCTGCAATGCATGATCTTGCG** ATCAAATTCC
Nicotiana_tabacum-83769	98	2.22e-09	TAGAACTAAG **TCAGTATTAGTTGGTCTTCAG** GGTGTTGTTA

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	508	3.24e-17	CCGCTTCTCT **GAATCCCTTTCTGTTAATCATCTGTCTTT** CAAGCTAAGA

NAME	**START**	**P-VALUE**	**SITES**
Citrus_sinensis-66130	424	3.24e-17	CCGCTTCTCT **GAATCCCTTTCTGTTAATCATCTGTCTTT** GGAAAATCTG
Gossypium_hirsutum-42343	145	3.24e-17	CCGCTTCTCT **GAATCCCTTTCTGTTAATCATCTGTCTTT** TGAATCAAAA
AT1G78080.1	163	1.27e-15	GTTGTTTCTC **GCTTCTTCTTCTGTTAATCATCTGTCTTT** CAAAAAGAAA

51777.t00032 | At1g50010 | F2J10.11 | tubulin alpha-2/alpha-4 chain (TUA2) | identical to tubulin alpha-2/alpha-4 chain SP|P29510 GB:P29510 from (Arabidopsis thaliana)

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-70279	38	5.17e-15	TTTCTGTTTA **AACGGCGTCTTGATAAACGCCGCTCT** TCTCCTCTTT
AT1G50010.1	61	1.01e-13	GATCTAAAAG **AAGAGCGTCTTCATAAACGCCCTTCT** TCTTCTTCGT
Vitis_vinifera-64762	0	1.31e-13	**GGAGGCGTCTTGATAAACGCTATTCT** CATTCTTTTC
Glycine_max-1832271728	78	2.23e-13	ACAACCCAGA **GAGCGCGTCTTAATAAACGCTCTTCT** CTGAAAACCC
Gossypium_hirsutum-305101078	38	5.07e-13	GGGGATCCAC **AGCGGCGTCTTGATACACGCCCCCTC** TTACTTATAT

60473.t00009 | At3g21610 | MIL23.18 | expressed protein | contains Pfam domain, PF02681: Uncharacterized BCR, COG1963

NAME	**START**	**P-VALUE**	**SITES**
AT3G21610.2	245	2.77e-17	TCTTGCCTTC **GCTCTTGCTCAGTTCCTCAAAGTCTTCAC** TAATTG
Nicotiana_tabacum-91202	397	2.77e-17	CCTTGCGTGT **GCTATTGCTCAGTTCCTCAAGCTCTTCAC** CACCTGGTAC
Citrus_sinensis-7368	168	6.06e-17	TCTCGCCTTT **GCTCTTGCTCAATTCCTCAAGATCTTCAC** CACTTGGTAT

67136.t00012 | At4g21560 | F18E5.180 | vacuolar protein sorting-associated protein 28 family protein / VPS28 family protein | contains similarity to Swiss-Prot:Q02767 vacuolar protein sorting-associated protein VPS28 (Saccharomyces cerevisiae)

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-1588271729	86	7.20e-19	AGAACCCTTC **TCTTTGCGCGTGTCCCGTTCTCTTCTCCAA** TCCTCCTCCA
Gossypium_hirsutum-2220	40	7.20e-19	AGTTTAGTTC **TCTTTGCGCGTGTCCCGTTCTCTTCTCCAA** TCCTCCAAAA
AT4G21560.2	321	2.41e-18	TTTGTTTTCG **TCTTTGCGCGTGTCCCATTCTCTTCTCCAA** AGTTCCCTAT
Nicotiana_tabacum-57586	132	2.41e-18	AAGATTAGTA **TCTTTGCGCGTGTCCCATTCTCTTCTCCAA** ACTTGTTGAA
Vitis_vinifera-31827	218	5.94e-18	AGGTTGGTTC **TCTTTGCGCGTGTCCCGTCCTCTTCTCCAT** TACGCAAAAC

67039.t00043 | At4g01250 | F2N1.6 | WRKY family transcription factor | contains Pfam profile: PF03106 WRKY DNA -binding domain

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-48870	40	2.13e-13	CTGGCCAAAG **TCAGCGCCTTCTTTTGTCTTCT** TTTCCTCTGC
Glycine_max-42236	23	1.15e-12	TCGCCAAAAG **TCAGCGCCTTCTTTTGTCTTTT** CTCTCTCTCA
AT4G01250.1	0	3.11e-12	**TCAGCGCTCTCTTTTGTCTCCT** CTGCTTTTTT
Gossypium_hirsutum-53733	136	5.04e-12	CATTAAAAAG **TCAGCGCCTTTTTTTGTCTTTT** ACATTCTGTT
Vitis_vinifera-22295	13	6.24e-12	GCTTCCAAAG **TCAGCGCTTTGCTTTGTCTCCT** TTTGGGGTTT

67861.t00024 | At5g55530 | MTE17.25 | C2 domain-containing protein | low similarity to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain

NAME	**START**	**P-VALUE**	**SITES**
Glycine_max-116256	190	2.12e-14	CTCGATTCAC **GAACTGGGTCATCCTCTGATTGTGGATTA** TTGGATTTCA
Vitis_vinifera-21682	75	1.71e-13	CTCGATTCAC **GAACTGGGCCGTTCACAGGTTTTGGATCA** GAGCCACTGA
Citrus_sinensis-36629	140	4.24e-12	CTGGTTTAGT **GAAGTGAGCTGTTGTTGGATCTTGGATTA** GAGCAAACAG
Gossypium_hirsutum-30576	207	1.11e-11	TCTATTTTGG **GAATTGGGTTGTGTCCAAATCTTGAATTA** GAGCCGTAGA
Nicotiana_tabacum-20564	120	1.41e-11	TTCGAATTTC **GAGTTGGGTCTTCTTCTGATATTCGATTT** TCTGCCTAAA
AT5G55530.3	60	7.86e-10	GAAATCAGCT **GCCTCAGATCAGAGCTTGGTTTTGGATTT** AGGCAAGATT

67163.t00018 | At4g27130 | T24A18.80 | eukaryotic translation initiation factor SUI1, putative | similar to SP|P32911 Protein translation factor SUI1 {Saccharomyces cerevisiae}; contains Pfam profile PF01253: Translation initiation factor SUI1

NAME	**START**	**P-VALUE**	**SITES**
Nicotiana_tabacum-126823	88	9.03e-19	CCATCTCTCC **AAACCCTAATTTTCGGATCAGGTCTGAGCA** TCCAAGTTTT
Citrus_sinensis-5998	66	2.60e-18	CTCGATTATT **AAACCCTAATCTTCGGATCAGGTCTGAGCA** TTCCGGTTGT
AT4G27130.1	185	5.93e-16	CAGATCCACG **AAACTCTACTTTTCGGATCAGGTCTCAGCT** TCTCTATCGT
Glycine_max-192063	92	1.36e-14	TGACGTATCG **AAACCTTAAATTTGGGATTAGGTCTGAGCA** ATCTGGTTGG
Vitis_vinifera-19366265	116	1.48e-13	ATTCATTTCT **GAAACCCTATTCTCGGATCAGGTCTGATTA** CTCTGGTTGT
Gossypium_hirsutum-28114	39	1.83e-13	TCTCAAGAAA **GCCCTAAACACCTCGGATCAGGTCTCAGCT** TGTGGTTGTT