

Name	description	Length	Im	GC%	ΔG	sequence
AT1G09700	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	55	78.3	41.8	-4.8	CGTATCTTGAAGTAGGTTCTTGCATAATCCCGTTTCGTGAACAGGTTGTGAAAC
AT3G62800	double-stranded RNA-binding domain (DsRBD)-containing protein, weak	45	78.6	46.7	-3.1	GCAACATCAATTCCTCTTGGACTTTTGGCGCTCAAGAAGCAACT
AT2G28380	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	46	78.9	47.8	-1.6	TGCAAAAGATGTTCTATACACACCCGTCTCATCCAAGATCCCTGGCGG
AT3G26932	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	48	78.5	45.8	-2.4	CCTTCTCTTCACTCTCAATGGGTCATCTTGGCATTTTCTCAAGG
AT5G41070	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	56	78.5	42.9	-4.6	TGCTGTCTCTTGAAGCAGGTTCTTGTAATACCTCTGTCTCATCAAGAATCTAGCAG
AT1G80650	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	46	78.7	43.5	-0.7	TGCATCCACATATGATGATCTTGCGCCATTTGGTTTCATAGAGG
AT4G00420	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	56	78.2	44.6	-3.8	CTTCAGTCACTTATTCAGTATGAGCAAGAGCTGAGCTTTGGATTCCTGTACC
AT3G20420	ribonuclease III family protein, similar to CAF protein (RNA helicase	60	78.4	43.3	-4.0	CAAAACAAATCTTTCCTCTAGCCAGGCTCTATCTTCTCAACGCTGATAGAGGCTTA
AT5G45150	ribonuclease III family protein, similar to CAF protein (RNA helicase	60	78.3	40.0	-1.8	CGACTTCCTTTACATCTTCAAGGTCACATCAGACAATCTTATTCCTCAGCAATAT
AT4G21670	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	45	78.7	51.1	-8.3	TGGCAACACATAGTACTGGTGTTCAGCAGCTTCAGCTTGAGGAG
AT5G01270	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	45	78.6	48.9	-2.2	AATGATCAGCTGCAGCCGCTTGGTTAGTCTTCGTTCCACTTCAC
AT3G03300	DEAD/DEAH box helicase carpal factory-related, similar to RNA helica	58	78.6	44.8	-3.8	CAGTAGAGGAGTTGAGATCCAAGGTTCCAAGGGAATAGCGATGCTTATCTGTATGCT
AT5G20320	DEAD/DEAH box helicase, putative, similar to CAF protein (Arabidopsis	48	78.5	45.8	-7.9	AGTATCAATCAGCAGCTTAAGTGATGCCAAGCACCCTGTTTGTATGTC
AT1G01040	DEAD/DEAH box helicase carpal factory / CAF, identical to RNA helica	48	78.3	45.8	-5.1	CATGCAGTTTCTTGAAGCAGCTAAACATACAGCTGTTGTGCAAGAC
AT1G48650	helicase domain-containing protein, contains similarity to DEH-box	46	78.3	47.8	-1.7	AAGAAATGGGCTCGGACAGGATGTGAAAACCTGGGATATGCATGG
AT5G04895	helicase domain-containing protein, similar to DEH-box RNA/DNA heli	55	78.5	41.8	-4.9	AAGGGTATGGAATTTTGGGAAACCGCGAATTAACAGAAATTCGGCTATAGTGATAC
AT4G20920	double-stranded RNA-binding domain (DsRBD)-containing protein, conta	57	78.5	40.4	-2.3	TCACTCCCAACAAACGTACACAGTATTCAAAACCTGCGACATCTGATAAAAGTGAAC
AT3G49100	signal recognition particle 9 kDa protein, putative / SRP9, putative	51	78.1	49.0	-2.0	GCCGTCACAGTGTCTATACTTCATCATACCCGATAGATTCGGGATCAGC
AT2G43640	signal recognition particle 14 kDa family protein / SRP14 family pro	51	78.9	45.1	-4.7	TGGCATATGATGCTTGAATCTTGTGTATCTTACGACCAACCCAGGATAG
AT1G48410	Member of a gene family conserved in plants, yeast, and animals. Mut	48	78.7	50.0	-2.6	CCGATGTGATCTACGGAAGGCTATGAGCAACTCTTTATCATCTGCCACC
AT1G31280	Argonaute gene	45	78.6	42.2	-2.5	TTCAATCCAAAGTTTCCAATGATTTACACCCCGCTCGGTCCATTA
AT1G31290	PAZ domain-containing protein / piwi domain-containing protein, cont	51	78.4	47.1	-2.8	CATAACTTGAGAACCACATAGCCGTTGTGAGAAGCAACGAGCTTAGACGAAGA
AT2G27040	AGO4 argonaute gene	51	78.5	47.1	-1.8	GGAGTGGTTCCGATCATAGATGTGTAACTTTCAGAGCTTTCGACAGAACAAG
AT2G27880	argonaute protein, putative / AGO, putative, similar to SP004379 Ar	46	78.5	50.0	-1.8	GTCATTTGGCAGAGCTTCCATGGTATGAGACGGGTTCTTGTTGTC
AT3G29400	PAZ domain-containing protein / piwi domain-containing protein, simi	53	78.3	43.4	-1.4	CTGCCCCTGCTTCCGATAGAACTTACAAATATCTGTATGATACCGTT
AT1G69440	encodes ARGONAUTE7, a member of the ARGONAUTE family, characterise	45	79.2	48.9	-4.7	CTCAAGTTGAAATCTTCTTGTGTGGTTTCGCCGTCGATGAGCCAGC
AT5G21030	PAZ domain-containing protein / piwi domain-containing protein, simi	52	78.4	46.2	-4.2	TACAAGTTCACAGAGCTCAATGGGAAAGTAGGTAGACGATTTGGCTTACCA
AT5G21150	PAZ domain-containing protein / piwi domain-containing protein, simi	47	78.7	53.2	-4.4	CGACTGAGATCGCAGTGGTGTCTCTTGTGTAGACATAGGACAGAGAA
AT2G43810	pinhead protein (PINHEAD) / zwille protein (ZWILLE), identical to SP	49	78.4	40.8	-3.2	ATGGATTTTGATCATAGAGCTTGTGTGGACAGCTCCGCAAGATTCGTT
AT1G14790	RNA-dependent RNA polymerase, putative, similar to RNA-directed RNA	48	78.4	43.8	-1.4	ACTTGAATTTCTTCCCACTTTTCTTCTATCATCAACCCGCGGATGGA
AT4G11130	RNA-dependent RNA polymerase, putative, similar to RNA-directed RNA	45	78.6	46.7	-1.8	ATCGCCACCAAGAACATTCATTTGGGATGTGGTCTTCTTCCCTCTTG
AT2G19910	RNA-dependent RNA polymerase family protein, contains Pfam domain, P	48	78.3	47.9	-4.0	CAGTGTACTGGTGTCTCCCAATTAATAGGACGCTTTAAACGACGACAC
AT2G19920	RNA-dependent RNA polymerase family protein, contains Pfam domain, P	48	78.3	47.9	-1.8	AAACTAGCACATCTGAGATTGATTTGGCCAGACCCAGAGATCTTCACTTCTCT
AT2G19930	RNA-dependent RNA polymerase family protein, contains Pfam domain, P	47	78.4	46.8	-4.4	TAGTAATGGGTTCTCCCGCTATCCCATGCAACATCTTTCGGTCTCT
AT3G49500	RNA-dependent RNA polymerase (SDE1), identical to RNA-dependent RNA	47	78.4	44.7	-3.8	CGCCAAGTTTCTTGAAGAAGAACGATTAATGCTTGTGGTGTGACAG
AT5G23570	X5 domain-containing protein / X5 zinc finger domain-containing prot	50	78.2	48.0	-2.3	GCCCATGCCGAGGCCATCTATCTGTTATCTGCTCTTATCCAGCTTAGTATAT
AT3G05040	expressed protein, weak similarity to exportin 5 (Homo sapiens) Gl-1	46	78.6	52.2	-3.4	GAGACCAAGGGAATGAAGAACACGAGGATAGAGAGCCATCCGGTTC
AT3G43920	ribonuclease III family protein, similar to RNA helicase/RNASEH1 CA	45	78.6	46.7	-2.5	TGCAGATGGTCTTCTTGTCTCGGTTTCCCTCTTCAAGAAACCTG
AT5G23020	2-isopropylmalate synthase 2 (IMS2), identical to 2-isopropylmalate	53	78.5	45.3	-3.5	ATATCCCAACTCTTAAAGCCGTTCTTTTACAGATGACGCTTCAAGCTTTC
AT4G37510	ribonuclease III family protein, contains Pfam profile PF00636 RNase	46	78.4	50.0	-2.1	AGCCACAGAACAGATTAACCCGGTGGCTCAGCTCTTCTCTATCT
AT1G24450	ribonuclease III family protein, contains similarity to Swiss-Prot P	49	78.4	42.9	-1.0	GTTCTGATCTGAGATTGATTTCACTTGTGTGACGATACAGGAACCGGA
AT4G15417	ribonuclease III family protein, similar to CAF protein (RNA helicase	47	78.4	48.9	-4.1	GACAGGATGGTGACCATCTCAACAACTATTCCTTCCAGACGGTCT
AT4G15420	PRL1-interacting factor K, nearly identical to PRL1-interacting fac	47	78.1	46.8	-3.6	CATATGTTGATCAGCCCTTAATCTGGGCTTCGATGGGCTCAAGTCTG
AT1G05460	RNA helicase SDE3 (SDE3), identical to RNA helicase SDE3 (Arabidopsi	47	78.4	46.8	-2.3	GGTGATCAAAAGCCCTGATAAGCGTGTCAGTTCATCATCATATCTTGA
AT4G13870	Werner Syndrome-like exonuclease (WEX), contains Pfam profile PF0161	47	78.5	48.9	-3.1	TATCTGGACAGCTCGCAACCTTCCCGGGGAAGCAACCTTTTCAAAAC
AT3G42540	5-3 exonuclease (XRN2), identical to XRN2 (Arabidopsis thaliana)	50	78.5	42.0	-3.5	GCCTTGATGAAACGCTCAACATTTCTTAAGTTACAGTTGCTTGAATCCGT
AT1G75660	5-3 exonuclease (XRN3), identical to XRN3 (Arabidopsis thaliana)	45	78.4	55.6	-5.1	CCCTATGTCACAGCTCTTCTTAAAGGAAGATGACACCGGGAATGAG
AT5G44900	5-3 exonuclease (XRN4), identical to XRN4 (Arabidopsis thaliana)	49	78.4	44.9	-2.4	ACAGGTATGTAAACATTAAGGCTCGGTTCTGCTCAATGACGGAACAC
AT4G20910	double-stranded RNA-binding protein-related / DsRBD protein-related,	45	78.4	46.7	-3.8	AAGATCATCTTCTGAGGGCGGAATGCCATGCTTTCAGAGGAGT
AT1G79880	La domain-containing protein, contains Pfam profile PF05383: La doma	46	78.4	45.7	-1.6	CCGAATCCAATCCACAGAGATTCTAATGTTTCAACGCTGCCAAC
AT3G27220	RNA recognition motif (RRM)-containing protein, RNA-binding protei	49	78.1	42.9	-4.7	GAGGGTGATGAAATGATCAACACCTTGGGATGATCTGGCTTAAAGCA
AT5G46250	RNA recognition motif (RRM)-containing protein, contains similarity	46	78.2	47.8	-2.7	CCGCTTCACTTCTTCTCATAGCCGCTAACCAACGAAGAACGATGAC
AT3G19090	RNA-binding protein, putative, similar to RNA-binding protein homolo	48	78.3	45.8	-3.6	GAAGTTTCTTCGGTCTTGGAGCAGCATTTTGGCGAGCATCTTGAAGA
AT2G43970	La domain-containing protein, contains Pfam profile PF05383: La doma	45	78.9	51.1	-2.4	CAGCGGCTTCTCAATTCCTTGAATCTCTTCAATTTGGTGTCTCT
AT3G66100	La domain-containing protein, similar to SP047096 La protein homolo	53	78.5	43.4	-4.8	TTCCAATATAGTCTGGATGTATTTGGTCAATTCGCGAAGTCTCTGTAATGCTG
AT4G35890	La domain-containing protein, contains Pfam PF05383: La domain	48	78.4	50.0	-1.7	GCAATCGGGGATAATACGACGACTGTGCCAATCTAGTAGGGAAGGGTA
AT5G21160	La domain-containing protein / proline-rich family protein, contains	46	78.7	47.8	-2.8	TGGAGATGAACCTCAATTTCAAGAACCTAGAGGCAATGACTGTCTGGT
AT3G41440	polyadenylate-binding protein, putative / PABP, putative, non-consen	48	78.7	43.8	-3.2	CCAACACCTTTGCTAATACCATTTGAATGAGCAATGACCTTGCAGAA
AT4G34110	polyadenylate-binding protein 2 (PABP2), non-consensus TA donor spli	45	78.3	46.7	-4.7	ATGTAATTCAGTCTTGGATCGCTCTTGCAGCGTCTTGGGGATG
AT1G27260	polyadenylate-binding protein 3 (PABP3)	49	78.7	51.0	-2.4	GGAGTGTAGTTCAGGCGCTCCATTCGACGGAATGACATCGTTAGGGTTAC
AT2G23350	polyadenylate-binding protein, putative / PABP, putative	48	78.4	45.8	-3.8	ATAACTGTAGTTCAACTTCTGATGATGCTTCTCCGATCTCCGGTGT
AT1G71770	polyadenylate-binding protein 5 (PABP5), identical to QB G05196 from	47	78.3	48.9	-1.3	AGCATATGTGAGACTTTCATTCGACGACTTCGATCTTCAAGGTTAG
AT3G16380	polyadenylate-binding protein, putative / PABP, putative, similar to	48	78.3	43.8	-2.5	TCACATGTTTAAAGCGAGTATAGCAATTCGAGCTGAGCTGAAGGTGAA
AT2G36660	polyadenylate-binding protein, putative / PABP, putative,	48	78.5	43.8	-4.4	GCCACATATAGTGGTTTCCCGTGAACCAATTTGCCATGAAAGGTTTTC
AT1G49760	polyadenylate-binding protein, putative / PABP, putative, similar to	46	78.2	50.0	-2.9	CCACAAGCGGATAGATATCTCAACCAAGCATCTTCTCTGTTGCT
AT1G01725	Expressed protein	50	78.2	46.0	-4.0	ACGGAATCTTGCCTGAAAGTATCTCTGTCTGATAGGATCAAGAGCGTT
AT1G67930	golgi transport complex protein-related, similar to golgi transport	52	78.6	46.2	-1.6	GCAITCCAGACTCTATCGGTTAATAGATAATCGCTCTCTGTATGATCTGT
AT1G68940	armadillo/beta-catenin repeat protein-related / U-box domain-contain	47	78.6	53.2	-6.5	GAGTCTCTCTCACTCCCTTCTGTAGATGGCCAGAGAGGTTCCAA
AT2G47390	Expressed protein	52	78.3	42.3	-2.3	GTCGCTCTCCAGATTTCGTTCTTGTGCTGTATTTATGTCAAAACAGTCA
AT2G40770	SNF2 domain-containing protein / helicase domain-containing protein	45	78.9	46.7	-5.1	CCCAATCCCAATTCATCTGCAGCATCTGCATGACATGGGTTCAAG
AT2G35870	Expressed protein	60	76.8	30.0	-4.7	CTACAGCTTATCAAAAAAATTCGAAGCTTCCAAATCTTAAITCTGTAACATGTGGA
AT3G05090	transducin family protein / WD-40 repeat family protein, contains se	48	78.7	50.0	-2.7	GGACAGTTATTCAGCGGCTCTTGTATGACGGGGCTGGATTAGCTCTT
AT5G58550	protease inhibitor/seed storage/lipid transfer protein (LTP) family	47	78.7	46.8	-1.6	TCTTCTTTGATGCTTGAAGTCTGTGGAGACGGCTTTATGTTCAACG
AT3G16050	A37 (A37) mRNA, complete cds	51	78.5	47.1	-3.6	GCCACGAAGTACCTGAGCTAATCCGCAATTAACAGAGAACGGGATGGTTTT
AT4G36380	cytochrome P450 90C1 (CYP90C1) / rotundifolia3 (ROT3), identical to	47	78.5	51.1	-3.5	ATGACACTATCTCGTCTTCTCAGCGCTCCAACTGTACCGGTTACCA
AT5G06190	Expressed protein	60	76.5	45.0	-4.9	TCTCTCTGATACGAGCAAGTCCCAATTCCTAGTACTATTAGGACATAGAGACTGGA
AT5G10700	Expressed protein	53	78.2	41.5	-1.2	GCAAAATTCATCATCTGCGTTTCCCTTTAACTTCCAGCTCACTTATGAT
AT5G18790	ribosomal protein L33 family protein, ribosomal protein L33, Rickett	60	75.7	35.0	-2.3	TGTTGATGTCAGTACATAGTTGATCTGATTTATGATACAGCTGATGAATGATGTC
AT3G34770	fatty acid hydroxylase (FAH1), identical to fatty acid hydroxylase F	50	78.5	46.0	-4.0	TGGCATCCGTTAATAAGATAGTGTGACAGTGTTCCTCCAGCTCACTTCGT
AT3G05080	Expressed protein,	50	78.5	44.0	-6.0	TGCTCTACAGATTTGGGATCTGTCTGTGTGTTTATCATCGATGGAAGT
AT3G11996	pseudogene, hypothetical protein	45	78.6	48.9	-3.0	TCAGTGGGATGAAGAAGGCTCTGAACGCTGTGATCAGATATGC
AT3G43359	pseudogene, similar to putative helicase, blastp match of 49% identi	45	78.7	51.1	-6.2	ACACCGGGAACTATTCTCAGACATCCGGAAGGGCAGCTTCGTAT
AT3G22945	pseudogene, cyclophilin (fragment), blastp match of 59% identity an	45	79.1	51.1	-4.4	ACCTCGTCTTCAATGCTCTGAGCAGCTGGAGTCTTCAACAACT
AT4G31290	ChaC-like family protein, contains Pfam profile: PF04752 ChaC-like p	46	78.4	47.8	-4.8	TGCCAGCTTATAACATAGTCTCTCTCATGCCAATCTCGTGCAT
AT4G19100	Expressed protein	57	78.7	42.1	-3.1	CATCGTTGCGTGTAATGGTGCTATACGGGATATCTTAAGCGGTTAATGAAGTAAT
AT5G14560	Expressed protein,	50	78.4	46.0	-3.7	GTGATTTGTCTTCCCGATCACCACAACTTCCCGGTAATTCCTTCCCTTG
AT5G60240	Expressed protein,	55	78.6	43.6	-6.2	GAGAGAGAGATCCGAATCTCGTTTCAATCTCGATCTTCTGTTTTCATACCG
AT5G31989	gypsy-like retrotransposon family (Athila), has a 6.7e-11 P-value bl	46	78.2	50.0	-4.1	AAGAGGAGAGTGATGTGAACGACTGCGTCCCGCGTCTATAAAGAGG
AT1G01720	no apical meristem (NAM) family protein, contains Pfam PF02365: No a	50	78.4	44.0	-1.9	TTTGTGTTGAATCCGGCGAGAGACCCAATCATCAGCTTACGATGATTC
AT1G05450	protease inhibitor/seed storage/lipid transfer protein (LTP)-related	51	78.5	47.1	-3.7	AAGAAGCAGACCTCTCAGGATCAGAAGTTTGCAGATCTGAGGAGAAGTGG
AT1G67920	Expressed protein	45	80.6	53.3	-2.7	AACCTCTCTCACTCCGGTTGCTGACGACGCGTTGTCTTAATCT
AT1G68935	Expressed protein	57	78.5	43.9	-3.5	TAGTGAGATTCAACAATACACTGTACGAGCCCAATGATGATCACTAGGACACAAA
AT2G47380	cytochrome c oxidase subunit Vc family protein / COX5C family protei	57	78.8	45.6	-4.9	GGAACCAAGTATTGAGCGGCTTAATTAATCTTCTCAGCAGTCAACATGATCTCAC
AT2G40765	Expressed protein	48	78.5	43.8	-7.5	GGTCAATGAATGTTCTTATTCACCAACAAATGGTTGGACGACCCAGGA
AT2G35860	beta-Ig-H3 domain-containing protein / fasciclin domain-containing p	55	78.5	43.6	-2.7	ACGGAATAAACCGTGACCCCAATCTTCAAGAGCTTCCATCAATTTACTCTCT
AT3G58540	Expressed protein	45	78.8	46.7	-3.0	CGCCATGACTGGATCTGTTGATCTGATGATGTAATAAAGGCTTCG
AT3G16040	Expressed protein	48	78.9	50.0	-1.7	CCATATCTGTGCTCATGCTACTCTTCTTACCAAGCTTGGGCTCTTCA
AT4G36370	Expressed protein	47	78.6	44.7	-5.7	ATGATCACTTCAATTACTTCGACGCGCGGCGATGACGATGATATCAT
AT5G06180	Expressed protein, similar to unknown protein (sp Q9ZE28)	46	79.9	45.7	-1.6	TACCAGACGCGCACCAATCAACACCGGGCATCTTCTTCAACAGCTTTT
AT5G10695	Expressed protein	45	78.5	53.3	-4.1	CTATTTACGCTCAACCACTTGAACCGGCTCTCCCGAGTACGGAC
AT5G18780	F-box family protein, contains F-box domain Pfam:PF00646	51	78.4	39.2	-2.0	TGAAATTTGAATCTGGTGCTCAATTCAGGCTGACGATAGTACCTAAGA
AT2G34760	pseudogene, tubulin beta chain-related, similar to beta-7 tubulin G	54	78.5	46.3	-1.0	GGAATCTTATAAGTGCAGCAGCAAGTGACAGACGAGGCTATGACAGCTAATG
AT3G31993	CACTA-like transposase family (Pta/En/Spm), has a 3.3e-25 P-value b	49	78.7	44.9	-2.2	CATCAATTTTTCGCGAACTAGCCGGGCTTCTTCAATCAACATGCTAC
AT3G43358	copa-like retrotransposon family, has a 7.8e-69 P-value blast match	50	78.5	44.0	-0.3	CGAGGACCGATGTAACGCAATCCACCAATCTATAAACCCCAACTTTCAT
AT3G22950	ADP-ribosylation factor, putative, similar to ADP-ribosylation facto	52	78.4	44.2	-4.7	ATGAAGTTCTTAAAGCTATCTTGGCCACCAAGTCCCACTCAAAAGCGAAT
AT4G31280	hypothetical protein,	50	78.4	42.0	-4.0	CACGTGACGATGGAAGAACGGAACAGACAAAAAATATGACAGGTTCCGCT
AT4G19095	Expressed protein	56	78.4	37.5	-3.3	AGTTGCGCTGATATAACCCAGAACGATGATGATCAAACTTGTCCAACTCGTTAAAT
AT5G14550	Expressed protein, contains Pfam profile PF03267: Arabidopsis protei	60	78.3	41.7	-6.4	GTCTAAGCAATACAGCTTGTGTTCAATCATCTGGTGTGATTCACCCCAATCTACCTGTATAC
AT5G60230	tRNA-splicing endonuclease, putative, contains similarity to Swiss-P	45	79.4	46.7	-5.2	CCATTTCCTATAGGCGCCATGGATTAAGCTGGGTTGATTTGAT
AT5G31919	gypsy-like retrotransposon family, has a 0.0019 P-value blast match	52	78.5	48.1	-4.2	AGAGCAACTTCCAGAGGACCTATGTGAATTCAGCTTACCAACCCCGAGGTAA
AT5G51090	unknown protein	46	78.3	52.2	-2.6	ATTTTGGAGCTTCACTTAAGGCCCTTGAAGCTTGGTGTCTGAG

RatH1	sine repetitive element	48	78.5	50.0	-5.6	AACCGCGCACCCTCTAAGCTTCGCTAGGGTCTTTACCAATTGAGCTAA
RatH2	sine repetitive element	45	78.9	51.1	-5.0	TAGTCAGGCCCGCTGCATTTCTGACTACCAGGTAAACCAATTGGG
RatH3	sine repetitive element	45	78.4	53.3	-2.8	GCCTCATACATCTCTAGAGGGCGGAGCCACACCCAGGTAAATTCAT
ATSG07350	tudor domain-containing protein / nuclease family protein, contains	45	77.9	51.1	-3.9	CAAAAGGCTCACTATACCTCTCTCTGCGAGCCATCTTAGGTGCCA
ATSG05270	expressed protein	47	78.2	44.7	-2.5	TTGAGATTAAGTTGTCAACGAATCTGGAAATCGCTGCTGGTTGTGAAG
AT4G17520	nuclear RNA-binding protein, putative, similar to nuclear RNA bindin	50	78.7	46.0	-2.6	TGGATTCTCTAGTCACCGGAGTAATATCATCTCTTGATGGTTTCCCAATTC
AT3G13460	expressed protein, contains Pfam profile PF04146: YT521-B-like famil	45	78.1	48.9	-4.0	GCTGTGTGACGCTCGTGTAGTGAAGATTTAGCGCGTGGTATTTGAT
AT2G25910	3-5 exonuclease domain-containing protein / K homology domain-contai	45	78.6	44.4	-1.7	AATTAGAAATTCGCGGTTGCAAGCTTCTTAAATGCGGAGGATTCGAT
ATSG61780	tudor domain-containing protein / nuclease family protein, contains	45	78.7	48.9	-0.1	GGTCCATTAACAAATCATTTGCGGGTTCCAGGAGTATCGAGGCTA
ATSG16830	nuclear RNA-binding protein (RGGA), identical to nuclear RNA binding	45	78.1	53.3	-1.4	GCTTCAGTCTCAGCAGCTATCTCTTCCCTGGAGTTCCCAATTC
ATSG47210	nuclear RNA-binding protein, putative, similar to nuclear RNA bindin	45	78.8	51.1	-2.3	ACGACCTCCACCATACGTTTATGCGCAGTACCATGACCTGTCTCT
AT1G55500	expressed protein, contains Pfam profile PF04146: YT521-B-like famil	50	78.9	46.0	-3.2	GCATAACCTGTCATGGATGCGAGGTGTGATCACTCTGTAATCGCAATT
ATSG61020	YT521-B-like family protein, contains Pfam profile PF04146: YT521-B-	50	78.5	42.0	-5.5	GACATTAACACTTTTGTGTGATGTGGCCACCAATGTCTGTTTGTGATCTG
AT2G26120	RNA-binding protein, putative, similar to GB:AA39463 from (Zea mays	52	78.2	38.5	-4.1	AGATGTCAATGTTTACAAAACCCATAACCAACATGCACTTTGTGTGAATCC
AT1G67770	RNA-binding protein, putative, similar to terminal ear1 gb:AA39463	56	78.5	42.9	-2.6	TAGCTTAACGTTCTTGAATGTTCCTTAATGACTCAAGACCTGGATACGAGCAT
AT1G37140	RNA-binding protein, putative, similar to terminal ear1 Gl-3153237 f	52	78.2	46.2	-1.6	CTTGAGTTCTGAAATGTCGAGTCAGCTCTCTTCTTCCCTGATATCTAGCCA
ATSG07930	RNA recognition motif (RRM)-containing protein, similar to terminal	54	78.9	44.4	-4.8	CCGGATATGTCAATGCTGGAAACGTTTACCAGCTCATTAGGCTGAATCTTAG
AT1G76940	RNA recognition motif (RRM)-containing protein, contains Pfam PF0007	45	78.4	48.9	-3.1	CATGGAAACAGAACCCACTTCTCGTATGTCACGCTGAGGAGTA
ATSG44200	nuclear cap-binding protein, putative, similar to SPI52298 20 kDa n	56	78.4	44.6	-4.6	GTGCTTCGAGTTCTCTTGAACATAITCCCAATACCACTTAGCAGGATCGTAA
AT1G07920	elongation factor 1-alpha / EF-1-alpha, identical to GB:CAA34456 fro	46	78.1	50.0	-0.7	CCTTGGAGTACTTGGGGTGTAGGATCACTCTTGTACAAACGCA
ATSG03240	polyubiquitin (UBQ3), identical to Gl-928809	56	78.3	39.3	-2.4	TTGAGAGTTGAAATACAAAGGCCGCTTACAAAGCCCAACGAAGGTACATAAAGAA
ATSG05320	polyubiquitin (UBQ10) (SEN3), senescence-associated protein; identic	55	78.3	43.6	-2.0	GCTGATTTCTTTCGGGTGAGAGTCTTAAACAAGATCTGCATCTTGATCACGGTAG
ATSG8740	peptidyl-prolyl cis-trans isomerase / cyclophilin / rotamase / cyclo	49	78.6	46.9	-2.7	CGTCGATGTCATGTCGAAGTATACCTTAGGGAACGCCATCTTCTGTGT
AT3G13920	eukaryotic translation initiation factor 4A-1 / eIF-4A-1, eIF-4A-1 g	45	78.3	51.1	-3.3	GCAGATCTCGCCATGCTGGAGCAAAAGTTGGTAAGCGAGAGTAAAG
AT1G19910	vacuolar ATP synthase 16 kDa proteolipid subunit 2 / V-ATPase 16 kDa	45	78.1	46.7	-5.4	ACAAGCAACTTAGTTGTTGTGATTCGCTTAAACACCGGCATCG
ATHB14A	A.thaliana beta-tubulin-4 gene, complete cds	58	78.3	41.4	-1.1	CAGGACTCAATCACATACATGAATACAAAGCTGCAATGGAGAATGTACTACAG
AY060403	Arabidopsis thaliana putative actin 2 protein (At3g18780) mRNA, complete cd	NA	NA	51.1	-4.6	AGCACAAATCCGGTTGTACGACCACTGGCGTACAAGGAGAGAACA
AY063089	Arabidopsis thaliana putative actin 8 protein (At1g49240) mRNA, complete cd	46	78.6	52.2	-2.7	GAGACACACCATCACAGAGTCCAAACAATACCGGTTGTATCGACC
AJ550162	Arabidopsis thaliana mRNA for LRR receptor-like kinase 1 (rch1) ge	49	78.5	44.9	-5.5	GGATAATCGGTTAAGCGCGGAAATCTTTCGGGATAAAGCCATCTAAT
AF055372	Arabidopsis thaliana AT4 mRNA sequence	46	78.6	43.5	-1.5	CATCAACCTTCATGCAATCTTCTCGCTCCATTCACACAACTCT
AF236376	Arabidopsis thaliana IPS1 mRNA, complete sequence	45	79.7	48.9	-3.1	CAAGAACAACAACACGCGCGGGAGTGGGTACACCCCAACATAAT
AT1G4973	Arabidopsis thaliana GLUT1 mRNA, complete cds	58	78.4	44.8	-4.2	CAGCTTTGCATAGCTTCAATTCGTCGTCACCACTTCATAGTTACTACAGGAATG
DP9218	Arabidopsis thaliana AtCR20-1 mRNA	58	78.5	39.7	-4.0	ATCCGGATCGAGAAATATCTCTGTTGATTTAGAGAAATTTACGTAAGATGATCGAGATC
ncpRNA002	ncpRNA	47	78.5	44.7	-1.1	ATTGGCGCATCAAGAACTCTCCCGATTTCAGGATTCAGGACCAT
ncpRNA004	ncpRNA	45	78.3	53.3	-4.9	GGTCAGTACTCAACCATGGCACTAGGTGTACCAACGGGGAATGTT
ncpRNA014	ncpRNA	45	78.5	48.9	-1.7	GTTCTGGTGTGTAAGAAAGTCACTGGGACCGGAAACCTTAGCAAAA
ncpRNA015	ncpRNA	49	78.3	46.9	-2.4	CAGTAATCCGATACCAACATGACGATCCGGAGAGAAAGGCCACCACTA
ncpRNA017	ncpRNA	60	77.5	40.0	-5.7	AAACTCTCTTTTGGATACGACCAAGTTTGTATCAGAGAAAGGAATGTTCTGTGTCT
ncpRNA021	ncpRNA	53	78.5	47.2	-3.6	AAGTGTGTGATTTTAACAGTCGCGCTTCAACGACGTGGGTATGAGGAAGGTCT
ncpRNA026	ncpRNA	49	78.4	44.9	-3.7	ACGCCAAAGTTTGTGTTATCGGTTATCTCAACAGTACCAACCGTGTCTTCA
ncpRNA029	ncpRNA	55	78.5	45.5	-3.9	GTCGTATAGCCCTATGGACGTCTAGTTAGAACTCTTCAAAACCGGATCAATCTC
ncpRNA030	ncpRNA	45	78.6	51.1	-2.9	ACAAAGATGACCAACGCTGTAGTTGTAAGCCCAACGCTGCCGTCT
ncpRNA033	ncpRNA	48	78.3	50.0	-5.1	GAGAAGACTTGACCGGAAATATCTTATACGGGCGGAGAAACGCCAC
ncpRNA034	ncpRNA	56	78.5	44.6	-2.4	CGATGAAGACTTACCTACATAGAAGAGTTTCAAGGAATCTACGAGGAGAAAGAA
ncpRNA040	ncpRNA	45	78.4	51.1	-3.5	ATTGACGAGCTCTCAAACTCTAGGCAATAGCACGACGCTGTTCT
ncpRNA041	ncpRNA	51	78.5	41.2	-3.2	CACCGCTTATCATTTGAAACTGGAAATGCCGAAGAAATAACTGTCTCAG
ncpRNA043	ncpRNA	48	78.4	50.0	-4.6	GACATCGCCGTATCTGACTAACCACCGTGTGATCTGTCTAGAACGAT
ncpRNA048	ncpRNA	56	78.5	39.3	-3.1	ATCTTCGAACAGCTTCTACCAAGATTAAGCTTTCTTTTTCACGCTCCGCTTTTGCA
ncpRNA049	ncpRNA	47	78.5	48.9	-0.6	CTAGAACGCTGGGGTCTTCATCTCTTCCGCGATCTCAATCTCTGTA
ncpRNA051	ncpRNA	48	78.5	45.8	-2.5	CTCTTCCACAATTGTATGTTGGCAACATTTCTATCTTCCCACTCTGC
ncpRNA052	ncpRNA	45	80.4	53.3	-3.1	GTTGAGAAAAACGGAAGACGCGCGGACATGAGCCGGATAACACC
ncpRNA053	ncpRNA	45	78.8	48.9	-2.2	CTGTTCTCTACCAATGTGGCTACACTTCGCTTGAATGTCTTGA
ncpRNA058	ncpRNA	51	78.4	39.2	-4.4	AAAGTCATGTCTGATTTGACGTATTAATGCGGACAGCCACAAATGGACAAA
ncpRNA060	ncpRNA	60	78.1	45.0	-2.5	TCCATCTTCTAGTTCTATAGACGAGAAAGGTTGGAGCCTCAGCGGAAATAAGAGACGA
ncpRNA062	ncpRNA	55	78.8	40.0	-2.1	TGACATTGAAAAACATAGATGTTGGTGTTCAGAAAGGGCTGGATTCATCTTTTGC
ncpRNA072	ncpRNA	45	78.4	51.1	-6.2	ATCGGACACGCTCCGAACGCGAGATAAAGGATAAAGTCTTCCCTCT
ncpRNA075	ncpRNA	53	78.5	43.4	-7.2	GATCTAATCGGAAAGATAAACCGGACAAACGCCGGAAGCTTTATCCGTTAAAC
ncpRNA076	ncpRNA	59	78.5	40.7	-7.2	TATATTCATCTTAGACAGACATCTGACATAGAGCGCGTAAAGAAACCGGCTGAAACT
ncpRNA079	ncpRNA	49	78.5	44.9	-2.2	CACGGACAATCTTGTTAAGTTGAAATCGCATTCGGCAGCTCTTGAACCT
ncpRNA082	ncpRNA	50	78.6	44.0	-3.1	ATACAATTGTAGAAACTCCGAAGAAAGGCTCGAGCCGGACATTTGTGATG
ncpRNA083	ncpRNA	50	78.5	46.0	-3.3	CCCACCATTTGTAATCTTAGCATGTGTATGTTGTCTAAGCCACACCACTA
ncpRNA086	ncpRNA	52	78.5	44.2	-1.2	GGAGGAGCCACATCCACAATAGAAATCATCTTGGTTAGAAATAGGCTCCCATTT
ncpRNA111	ncpRNA	54	78.5	40.7	-2.9	TCGTTTGTATGCGGATTCCTCTTGTTAAGTAAGCGGTTCTACACAAGAATCAAC
ncpRNA113	ncpRNA	45	78.8	48.9	-6.8	CTATAATTCGCGATTTCAATTCACCGCGGAGTCTTCGCGTAGAA
ncpRNA123	ncpRNA	46	78.4	52.2	-4.9	ACGAACATCGCCTCTTAGAACCGGACGCTAGCAAGGACGACCTCTAT
ncpRNA131	ncpRNA	46	78.5	45.7	-1.6	TGACTCTCATAGAAACCCAGAACACCGCGATATGATGTTGAATCT
ncpRNA146	ncpRNA	60	77.8	36.7	-0.1	AAAATTGACAAAGGAAACATATAGAGCCGCGGTAAACTAAGAACATCTGTGACGAATCCAA
ncpRNA149	ncpRNA	49	78.5	40.8	-3.2	AGTTTGTAGCTGCTTAATAAGCCAGTGAACACGCCCATGAATTAACAACA
ncpRNA150	ncpRNA	60	78.2	40.0	-5.2	GGACTCTTATCGGAAACACGCTGTGACTTTAGAAATCAACTGTGAACATGCCGATAAG
ncpRNA151	ncpRNA	47	81.1	46.8	-2.9	ATTTGACATGATTCGGGGCTCAACGTTGGTTGCGATCATCTGTAT
ncpRNA156	ncpRNA	53	78.3	43.4	-1.6	TCAACACATAAATCTTGTAGAGGCGACCGGAGCAGAACTATTAATCTCGAAA
ncpRNA157	ncpRNA	48	78.5	47.9	-3.8	ACAAGAGGTTGTGAGAGCTTTAGGACGGCAATCGAAGGATTTGTCT
ncpRNA311	ncpRNA	47	78.2	44.7	-2.4	AGAACTCGAAAAACACGAGCTGTATGCGGATATGATCTTCCGCTTT
ncpRNA316	ncpRNA	52	78.5	44.2	-2.7	TGATTACATAGCATGACCGGCTCTGTGTGTGTTCACTGCTCATTTAAGTGA
ncpRNA325	ncpRNA	55	78.5	40.0	-3.2	TGGAATCTCCATAGGACAAAGGAAATCGAGATCTTACTTGACCAAAATGGTG
ncpRNA326	ncpRNA	59	78.2	37.3	-1.6	AAGTTGAAGATGATGAATTCATGATGGAGAGAAACGTTAGGCTGGTTATGAGACTGATT
ncpRNA351	ncpRNA	45	78.5	48.9	-0.3	TGGGTAGACTGTTCCTTCTGCGGATCTCCATCCAAATGAAAGA
ncpRNA370	ncpRNA	54	78.5	48.1	-2.5	GCGTAAATTCATAGTTAAGGGTGTCTTATAGCCCTACTAGTCAAGCACGGG
ncpRNA374	ncpRNA	48	78.5	50.0	-6.0	CCATTCATGCCAGACTCGGATGCTAGAGAAATGCTGGAATGCTCTCTC
ncpRNA375	ncpRNA	45	78.5	53.3	-1.4	GTCACAGCCACTCAGCAACAAGTACTCGAGTAGCACAGGAAGCA
ncpRNA387	ncpRNA	60	76.9	41.7	-1.3	TGTGTTCTCTACTAATGCTCTCAGGACAGGAATTAGGAAATGGGTATAGTTGTTT
ncpRNA415	ncpRNA	45	80.3	48.9	-3.5	ACTCAAAACCGGTTCAAAACGCGCTTACGACGACCAACCGTTCAAT
ncpRNA431	ncpRNA	45	79.4	55.6	-5.9	GATTCCTCTGATATGCGCTACGACCCCTTAGGGTAGCCGACAGT
ncpRNA437	ncpRNA	46	78.6	45.7	-0.8	TAGTTGGAACGCGCAGAAATGAAACTGCGAGCAGCAAGGAGCAAAACA
ncpRNA446	ncpRNA	45	79.5	51.1	-1.5	ACCAGCTTCTCTAATAGAGACGGCGCGCGGTTGAAATGAGTCTT
ncpRNA461	ncpRNA	60	78.5	40.0	-8.7	ATATCAAAGGTTAAGCAGCTTTATGCTCAAACTAGCCACTTATGACAACTGATTGACG
ncpRNA502	ncpRNA	47	78.4	46.8	-3.5	TAACATAACTCTATAACGATGCGGCTTTGCTGCTCGCGGACCTCGATTA
ncpRNA504	ncpRNA	48	78.4	50.0	-2.7	ATCGTCTAGGACAGATCGACGGTGGTTAGTTCAGAAATCGGCGAGTGC
GSLTFB60ZF08	ncpRNA	56	78.5	39.3	-3.1	ATCTTCGAACAGCTTCTACCAAGATTAAGCTTTCTTTTACCAATCGCCTTTTGCA
ncpRNA508	ncpRNA	47	78.4	46.8	-2.4	CAAAGCATCCATACAGCAAGAATGGGAGACAGCTAGAAATCCCAACA
GSLTFB7ZC05	ncpRNA	59	78.5	44.1	-6.0	TAACCTGACAACTTCAGTAGTGTTCATCCAGGTAATCTTGGCTCTGCTAGGCTTTTGAC
ncpRNA509	ncpRNA	46	78.5	50.0	-2.9	TATCACTTAGAATCCGAGCTTGGTTCTACGCCAGTGCTCTGCTGT
GSLTFB94ZE11	ncpRNA	48	78.4	45.8	-3.2	ACAAAACCTGGTGCTCTCGTCAAAAATCTACGACGCTCTGCTGCTCTAA
ncpRNA511	ncpRNA	47	78.6	53.2	-5.1	GCTCCAGGTAATCCATATCGATATTTAGCGCTGAGCGGCTTGGTA
ncpRNA512	ncpRNA	45	78.4	48.9	-0.8	GCTCGACGATGAAGTTATGACGATCTCCGCTTACTCTTCAAT
ncpRNA513	ncpRNA	50	78.5	50.0	-4.5	CGCTCTGATCCGAGCTGTCTAATAGGAGAGATCATCACTCTTCTGTCACTA
ncpRNA514	ncpRNA	46	78.5	45.7	-1.1	TGTCAAGTTTGGCATTACAGGTTTGGAAATTTCCCATAGACACTTTTG
ncpRNA517	ncpRNA	49	78.1	46.9	-1.7	GAGCAAAAACAGAAAGAGATACATTTTGGATCGGGGTCCTTCAAAAACCT
ncpRNA518	ncpRNA	45	78.4	55.6	-4.0	GGTTCTCTTACCAACGGTGGTTGGCTCTTGCTTAGCTTCTTCCGCT
GSLTPGH65ZA08	ncpRNA	48	78.4	50.0	-4.6	GACATCCCGGTATTTGACTTAACACCCGTCGATCTGTCTAGAACGAT
ncpRNA519	ncpRNA	51	78.6	45.1	-2.0	GCTCATAGACTCCCTGTGCAAACTCTTTTGTGCTCCGGAAGGATTTCTAAT
ncpRNA520	ncpRNA	52	78.3	40.4	-4.0	GAAATCGACACTGATGCGTGTGTTAATTTCTATCTCAGGCTTTTACCGGAAAG
ncpRNA521	ncpRNA	60	77.5	43.3	-1.2	TCCTCTAATACTTGTATGTCGTAGGACATCAGGATGTATCTTGTGACCAATCTGTATCTG
ncpRNA522	ncpRNA	58	78.4	41.4	-2.3	AAACTCTAGTCCACAATACTCTTGTATCATCACCATACTCAACCTCTCCACATCCCA
ncpRNA523	ncpRNA	45	78.4	51.1	-3.1	ATGCTACACACTAGTGCAATCCCTGCTCTCAAGCTGTTTCCGCTGT
GSLTSIL15ZF04	ncpRNA	49	78.5	42.9	-1.8	AGCATATGGGGTTGGGAAATTTGGATATCTAGCATGAGCAAGGCCAAAT
GSLTSIL18ZG09	ncpRNA	55	78.4	40.0	-3.7	TGTTTAGACTCTTACACAAACGCAATTTCAACTTCCGCTGACAGTTGAAATCTGA
ncpRNA524	ncpRNA	49	78.5	46.9	-1.4	TTATACGGGACATGGGAGAGCGGCAATACAAATGGTCAAGCTGTGATCT
GSLTSIL25ZA05	ncpRNA	47	78.5	44.7	-1.1	ATTTGGCGCATACGAAATCTCCCGGATTCACAACTCTAGAACGCCAT
ncpRNA527	ncpRNA	45	78.5	48.9	-2.6	CATCTGTCAATCTCGAATGCAAGCGGCTAGATGTGATATCTCTG
ncpRNA528	ncpRNA	48	78.4	47.9	-1.7	GAGAAGAAATCTGTCGACAGACAGGACCTGACATCTCAGACTCATCTCAGAG
GSLTSIL42ZB01	ncpRNA	53	78.5	45.3	-4.2	CAGAGCCGGTTTACAAAAGCTGACCTTAAAGTCAGATGATTTCACTTCCGCTTAGC
GSLTSIL43ZF08	ncpRNA	45	78.6	51.1	-2.2	AAAAGTAACCTGGGACGGAACCTTACTGACCAACGCGCGGCACTTT
ncpRNA530	ncpRNA	47	78.8	48.9	-2.0	TACTCAAATTCACCTAATTTGGGGAAGGCGTCTGCGGATCTACTCTTC
ncpRNA531	ncpRNA	46	78.5	45.7	-0.6	ATGTGAGCCGAACGATATTTGGACGAAGCGACTCATCAACACCAAT
ncpRNA532	ncpRNA	54	78.2	40.7	-1.5	TCATTCACCAACCTCTATAAGTAAAGTACTTGGACATCTTCAAAATCA

GLSLTSIL54ZF08		npcRNA	56	78	44.6	-2.2	CAACGGAAAAATGTACAGGTAAACGGTACGACGAGTAAGACGTGTACAGTGAAAGGT
GLSLTSIL66ZC05		npcRNA	47	78.4	48.9	-4.6	ACTAACTCTTTTACAAAGGAACGGCCGGCGAGGAATATTCGAGGTG
npcRNA533		npcRNA	51	78.3	45.1	-3.9	AGCCATTTTCGAGAAACTGTAGTCCAAAAGGGGACCATGTTTACAGAGCAAG
npcRNA534		npcRNA	48	78.4	47.9	-6.1	AATGGGTGGAAGCCCTTATATCTTAICTTTCGCAACTCCGCTCACAT
GLSLTSIL6ZH01		npcRNA	45	78.6	42.2	-2.3	ATGTGGAATCCGGTCATCGCAATTGTGAATTCACAGCTCTAAAA
npcRNA535		npcRNA	45	80.9	55.6	-3.9	TCCTCCCTAAGTTACGCATTGGGCGCTTTTGCTACGCTCACTCAC
GLSLTSIL7ZC06		npcRNA	46	78.5	45.7	-1.2	TGAGCCATTAGAAACCCCGATTCCACCTCGAAACGAGGCCAATAA
GLSLTSIL80ZH03		npcRNA	52	78.3	46.2	-7.0	GTTTCATCATAGGTGATGAATGATGAGGACGGGTGAGCTAAGTCCATGTACC
npcRNA537		npcRNA	48	78.7	52.1	-3.5	CCACCCCCATACTGCCCCAGATTATCTTAATCCATCGATAGGCTAGC
npcRNA538		npcRNA	60	78.5	35.0	-4.6	AACCCGAAGACATAATCGCTTGATAGATTTCGCAATCGAAGTTCTTTATGAAAGCA
npcRNA539		npcRNA	50	78.7	44.0	-3.4	GACCGTAGTTGTTGGGCTTGAAGCAAGCTTTTCTGAAGTCATCAACGAT
npcRNA540		npcRNA	46	80.7	50.0	-6.2	AGAACCAGGAAGATGTCGGAAGAGAAGCCGACCAACCATCCATGGAT
npcRNA541		npcRNA	45	78.3	48.9	-1.7	GATGAAGACGAAGGCGCTAGTCGAGTGCTATGGCTCAAAAAAG
npcRNA078		mir162a	60	74.3	31.7	-0.7	CACAAGTAGTAAATAGCTGGATCTTTATTTGCCTTATGAACCAATGGCAAAAAACATAT
npcRNA078		mir162a	52	78.3	36.5	-2.8	CAACGAAACATAAATTTCCGGAATCGGATCAAAACGAAACACATCAGATCTGA
npcRNA078		mir162a	46	78.3	45.7	-3.0	TTTTTAATGTGTTACAGGAAGAGATCGATGAACCGCTGCCTCCAG
npcRNA078		mir162a	60	78.2	36.7	-0.7	CCAATAAACAAAAAGATTCAAGTCAATAAGAAAGATACAGAGGCAAAACGCTGGATGCAG
npcRNA078		mir162a	58	78.5	41.4	-1.8	CTCTTCATCTGCTCTTAAGAACACAAAAATCCTCAGCTTTCAGAAAAAGTAATCGGA
npcRNA078		mir162a	60	78.2	38.3	-1.1	CGGACTTGACTCTGTTTCCCTCAGCTTTTATTTTAAATGTGTTACAGGAAGAGATCG
npcRNA078		mir162b	60	75.1	31.7	-1.4	CTGCTCCAGCGACTTCACCTTTCCTCATTCATAATAATCCCTTTAGACAGGGATATGAAGAA
AB006708 30800-30401 w		mir162b	56	78.3	41.1	-7.6	AGCAGCTGAGAAGACTTATCGAATCCATTGTCTGCTTCTCAGCAATACTCAAAAT
AB006708 30800-30401 c		mir162b	60	78.2	43.3	-5.2	CCGAGCCCGATGTGAGACTCTATCATATAATAATCCCTTTAGACAGGGATATGAAGAA
AL022580 56501-57000 w		mir168a	60	78.4	40.0	-5.5	ATCTTCCAGATCTGATAGGATTACGAGTTTTTTACACCTCGAGGATCCGATTCAGTTG
AL022580 56501-57000 c		mir168b	57	78.3	38.6	-0.5	CATCAGAAAAAGGTGAAAGAGATAAAGGAGGAGAAAAACAGTTACCAAAATCTCCGCAAA
AB020744 40501-40000 w		mir168b	60	78.3	38.3	-3.1	AACAGATAAATGTGTGAGATCTGATAGTTGGATCCTTATTTTTCACCTCGGACTCCGA
AB020744 40501-40000 c		mir168b	60	72.5	26.7	-3.5	TGGTTACACGGAAACAAATTTAAAGAAAAATAATGTATCAATAACATCTTCAATAGTAGA
F12K2 3960-4885		siRNAs	60	73.3	31.7	-2.5	TCAAACGCTATGTAGACTTAAATAATTTTCTAAGATCTTACGAACGCTATGTGGAC
F12K2 3960-4886		siRNAs	60	71.4	26.7	-2.7	GCAAAAAGTTATCTTGAATATGTTTTCATATTAATGTTATTTTCTACTTAATGAACAGTTG
F12K2 4885-3960		siRNAs	59	72.8	30.5	-1.8	AGCGTTCGATAAGATCTAGAAAAATTAATTTAAGTCTTAACATAGCGTTTGTATGGATCT
F2J10 25960-26880		siRNAs	60	72.1	25.0	-3.9	TTTTGCATATCTTAAATATGTTTCGTTTAAACATAAAAAATATACAAATATCTCCGGAC
F2J10 25960-26880		siRNAs	60	71.4	31.7	-5.9	TGGACTTAGAATATCTTCTTACCATCTATCAATCAATACACTCTGTAATAATAGTTGAA
F2J10 26880 25960		siRNAs	59	73.8	28.8	-3.9	TGGGAGATGTCGGGAATGATATTTGTAATATTTTATGTTAAGCAAAACATATTTAGGA
F17A14 12900-13800		siRNAs	60	72.5	31.7	-4.0	AGAAAAATATCTTAAAGTCAACATAGCGTATCTCAAGTTCACAAATATCGACGAACATAGAA
F17A14 12900-13800		siRNAs	60	74.1	31.7	-2.2	TGAAATGTGTTCAAGTAAATGAGATTTTCAAGTCTTCAAGTCTTCAAGTCTTCAATACAGT
F17A14-13800 12900		siRNAs	58	72.7	31.0	-1.0	AACCTGATTAGCAACTGTCTTCTTACAGCACTTGAATAATCTCAATTACTTGAACACATT
F17A14 14850-15840		siRNAs	60	75.5	36.7	-3.3	TGTAACCTCTTGTGATCGGATGGTAGAAACATAGGTTCTTAAATCCCATATAGGTTATCGA
F17A14 15840-14850		siRNAs	60	74.2	36.7	-1.1	CATATACTCGAATACCTATATGGGATTAAGAGACCTATGTTTCTTACCATCCGATCAACAAG
MCE21 930-1880		siRNAs	56	78.6	42.9	-1.3	CCAGTCCCTTGATAGCGAGACCTTCTTACCCTTAAATTTTGTGCAATAATA
MCE21 1880-930		siRNAs	60	77.9	38.3	-2.6	TGTTGGTTATATTAATGCAACAAAAATTAAGGGGGTAAGGAAGGTCTCGCTATCAAGGG
npcRNA526		antisense of AT1G12060.1	49	78.4	51.0	-2.1	GCAGCAGCGAGGATTACAGTCTGGCTACCGTCTTATAGGATCCGAAAC
npcRNA510		antisense of AT1G29355.1	52	78.6	44.2	-1.5	CCTTTTCGCTTGAATCTCTTGGTTATATCGAAGCAGCTGGACAAGGAGAAGA
npcRNA529		antisense of AT1G67370.1	53	78.5	45.3	-4.2	CAGAGCCGGTTACAAAAGCTGACCTAAAGTCAGATTAATCAATTCGCCGTGAC
npcRNA516		antisense of AT1G76500.1	45	82.6	57.8	-7.1	ATCCGGGTTCCGACCCAGTTACCTCTGGTTCAACCGGGAAACGTC
npcRNA525		antisense of AT1G13660.1	45	78.4	51.1	-0.9	TTCACCAGCCGAGATCAACTCAGTCTCCTCCTCAAGAAACCTCTATC
npcRNA507		antisense of AT3G21760.1	46	80.5	52.2	-3.9	AGTCAAAAGCCACGGTGGAAAAACTTACTGACCCGGGTCCACCAGAT
npcRNA515		antisense of AT5G21020.2	58	78.6	44.8	-8.2	GGCTTCTCATCTCACACGTATAGGTTCTTCTCTATTTACGACACAGTGTATCTGAGATA
AT1G12060	IQ domain-containing protein / BAG domain-containing protein, contains Pfam		45	78.5	55.6	-2.2	CCGAGCTTCTTGATCGTCGGATCTTAAACAGGGACGGAGTCTAG
AT1G29355	expressed protein		51	78.5	47.1	-2.8	TCTTCTCTTGTCCAGTCGTAGTGAAGAGATCAAAAGGATCGAGACCGTCA
AT1G67370	meiotic asynaptic mutant 1 (ASY1) mRNA, complete cds		46	78.6	47.8	-1.8	CATCACTATGGTGGCGCTCATCTGGCATTTTGTCAAGAGTCTCTCATC
AT1G76500	DNA-binding family protein, contains Pfam domain, PF02178: AT hook motif		45	80.5	55.6	-5.3	GTTGAACCAGAGGTAACCTGGGTCGGAACCCGGATCCTTGTGGAG
AT2G13660	expressed protein		55	78.5	47.3	-0.6	AAAGGCCAGTAGGTACAATCGAAGGCAGAGATAGAGGTTTCTTGGAGGACTGAGT
AT3G21760	UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam pro		59	78.5	45.8	-4.9	CAGCTCAGTAGTGTCCGAGTCTTGGAGTCACTAACGTCATAGTTTCTTAACGTCGTAAA
AT5G21020	expressed protein		51	78.5	47.1	-7.6	TCTATAATAGCCGAGGCTGTGGACTGAAGCTGGTTTAAACAAACAGATGG
npcRNA536	antisense of GSLTPGH8ZC04		45	80.6	53.3	-2.7	AACCTCTCTCATCTCCGGTTGCTGACGCGACGGTTGTCTTATCTT
GSLTPGH8ZC04	antisense of GSLTSIL78ZH02		51	78.5	47.1	-1.5	GCATCCAGACTCTATCGGTTAACAATAGAAATCGCTTCTTGTATGACTTCG
NC 003071.3: 19527822-19527934	mir164A		56	71.8	28.6	-0.5	AAGAACAACGAAAAACACATATATCAATAAGGTTAAGGGGATATAAATCAATGG
NC 003076.4: 287581-287733	mir164B		48	71.9	37.5	-2.8	GTGTGTGTTTATCGATATAAGTATATTTCCACGTGCGTAAACATTTGAA
NC 003076.4: 9852678-9852779	mir164C		48	72.2	37.5	-1.5	TCATCAAACTCCAAATAATCTCCAATGGCCACGTATATGTAGCTACTTA
NC 003071.3: 19183178-19183347	mir166A		55	72.2	33.3	-0.2	AAACAATCAATACGCAATGTAATGAATCTGAGAAAGTAAGGTAAAGAGATCAAAAC
NC 003074.4: 22933181-22933300	mir166B		45	74.1	37.8	-0.6	CAAACTCTCTTCGTAAATTCGGATGTGAGGGAGTGATAATTTGGG
NC 003070.5: 78927-79037	mir165A		51	72	30.9	-1.2	AACCTGAATAGCTTAACCTCATGATAATCTGATCTTAGCAGATTCACAAAT
NC 003075.3: 369831-370012	mir165B		45	71.9	40.0	-2	CAAGGTTTTGTAGTTTCTCCAGAGTGATGTAAGGCAATTAACATG
NC 003074.4: 4359001-4359226	mir169A		51	72.1	39.2	-2	CACACTTTCGTACATTCGCGTTTCTACTAGCTATACCCACTTGATATAT
NC 003076.4: 8527472-8527652	mir169B		51	72.5	33.3	-6.4	TATAAATACTCATACGGTCGATGTAACTCCGTTTACACATCTAGATATTGAA