

Supplementary Table 1.

Gene	Symbol	Protein Name	Phosphorylated Peptide	Phosphorylation Site	I-Area Ratio	I-R ²	I-Debunker score	II-Area Ratio	II-R ²	II-Debunker score	III-Area Ratio	III-R ²
92154	ABBA-1	Actin-bundling protein with BAIAP2 hom	K.TPTVPDS*PGYMGPTR.A	S601	1.76	0.95	0.999958250	1.18	0.98	0.999971836	0.98	0.98
92154	ABBA-1	Actin-bundling protein with BAIAP2 hom	R.AGS*EECVFYTDETASPLAPDLAK.A	S612	1.40	0.99	0.999977464	1.03	0.99	0.999986373	1.00	0.99
92154	ABBA-1	Actin-bundling protein with BAIAP2 hom	K.GGGAPWPGGAQTYSPSSTCR.Y	S300	0.49	0.98	0.999985406	0.97	0.99	0.999983906	2.03	0.97
23	ABCF1	ATP-binding cassette sub-family F mem	K.QQPPEPEWIGDGESTSPSDK.V	S22	1.09	0.98	0.872361494	0.81	1.00	0.847115585	0.97	0.97
27	ABL2	Isoform IA of Tyrosine-protein kinase A	K.VPVLIS*PTLK.H	S936	0.76	0.98	0.999991559	1.06	0.99	0.999989547	0.99	0.96
3983	ABLIM1	Actin binding LIM protein 1	R.TLS*PTPSAEGYQDVR.D	S433	1.27	0.99	0.999994010	1.16	0.98	0.999989861	1.11	0.99
31	ACACA	acetyl-Coenzyme A carboxylase alpha is	R.FIGSVSEDNS*EDEISNLVK.L	S29	1.23	0.99	0.999992898	0.72	0.99	0.999992499	0.83	0.99
65057	ACD	Adrenocortical dysplasia protein homolo	R.TPS*SPLQSCTPSLSPR.S	S424	1.51	0.90	0.999936226	0.82	0.88	0.997623142	0.46	0.93
22985	ACIN1	Apoptotic chromatin condensation induc	K.ASLVALPEQTASEEET*PPPLLTK.E	T414	0.90	0.92	0.922696554	0.91	0.92	0.993049132	0.95	0.99
22985	ACIN1	Apoptotic chromatin condensation induc	K.ASLVALPEQTAS*EEETPPPLLTK.E	S410	1.02	0.99	0.997470008	0.80	0.99	0.999702808	0.96	0.99
22985	ACIN1	Apoptotic chromatin condensation induc	R.TAQVPS*PPR.G	S1004	0.97	0.98	0.774393811	0.75	0.99	0.899996943	0.99	0.98
103	ADAR	Double-stranded RNA-specific adenosin	K.TAESQT*PTPSATSFSGK.S	T306	0.66	0.98	0.999984604	1.15	0.99	0.999973267	0.27	0.90
103	ADAR	Double-stranded RNA-specific adenosin	K.TAESQTPT*PSATSFSGK.S	T308	0.69	0.89	0.999961630	1.15	0.99	0.999914421	0.28	0.43
120	ADD3	Gamma-adducin	K.SDVEIPATVTAFAFSDDTVPLS*PLK.Y	S423	1.03	0.97	0.997510657	1.14	0.97	0.999695489	1.73	1.00
60312	AFAP1	CDNA FLJ46074 fis, clone TESTI20019	K.SGTSSPQS*PVFR.H	S668	1.22	0.91	0.999843254	0.76	0.99	0.991945223	1.15	0.98
27125	AFF4	AF4/FMR2 family member 4	R.NQEIQGEDAFPPSS*PLFAEPYK.V	S32	1.26	0.73	0.572031506	0.93	0.74	0.136685670	1.16	0.72
27125	AFF4	AF4/FMR2 family member 4	K.AVGMPSP*PVSPK.L	S1055	0.11	1.00	0.966165920	15.08	0.90	0.342304021	1.55	0.96
25909	AHCTF1	AT-hook-containing transcription factor	K.ESAWS*PPPIER.L	S2221	0.57	0.91	0.993522166	0.76	0.80	0.999958967	2.51	0.98
25909	AHCTF1	AT-hook-containing transcription factor	R.NLS*FNELYPSGTLK.L	S1550	0.51	0.96	0.999920964	6.64	0.90	0.999985140	2.74	0.99
25909	AHCTF1	AT-hook-containing transcription factor	R.LIS*PLASPADGVK.S	S2231	1.50	0.87	0.999987415	0.78	0.95	0.999972057	2.86	0.95
25909	AHCTF1	AT-hook-containing transcription factor	R.LIS*PLAS*PADGVK.S	S2231;S2235	0.67	0.68	0.999979689	0.79	0.95	0.999992134	3.32	0.96
79026	AHNAK	Neuroblast differentiation-associated pro	K.ASLGS*LEGEAEAEASSPK.G	S5752	0.79	0.93	0.999992740	2.18	0.95	0.999992603	0.72	0.98
11215	AKAP11	A-kinase anchor protein 11	R.SVS*PTFLNPSDENLK.T	S1242	0.99	0.98	0.999982496	0.81	0.98	0.999987706	1.07	0.90
11214	AKAP13	Protein kinase A anchoring protein Ht31	R.S*AVLLVDETATTPIFANR.R	S1876	3.54	0.91	0.993424871	1.14	0.97	0.978118055	1.06	0.96
11214	AKAP13	Protein kinase A anchoring protein Ht31	K.ALQLSNS*PGASSAFLK.A	S983	1.02	0.98	0.999985466	0.80	0.99	0.999977015	1.35	0.97
445815	AKAP2	A-kinase anchor protein 2	R.TLS*MIEEIR.A	S720	1.80	0.95	0.999990428	1.51	0.99	0.999988163	0.93	0.99
445815	AKAP2	A-kinase anchor protein 2	R.DALGDSLQVPVSP*PSSTSSR.C	S152	1.23	1.00	0.888422319	0.94	1.00	0.888518424	1.06	1.00

445815	AKAP2	A-kinase anchor protein 2	R.SVNVS*LTQEELDSGLDELSVR.S	\$465	0.80	0.89	0.999990202	0.72	0.93	0.999990467	1.12	0.82
84335	AKT1S1	Proline-rich AKT1 substrate 1	K.S*LPVSVPVWGFK.E	\$183	1.88	1.00	0.999990221	1.06	1.00	0.999991865	1.04	0.99
54882	ANKHD1	CDNA FLJ14127 fis, clone MAMMA10	K.TVSLPLS*SPNIK.L	\$1669	0.55	0.83	0.999907327	0.79	0.69	0.795270455	2.09	0.99
29123	ANKRD11	ankyrin repeat domain 11	K.FACLS*PGYYSPDYGLPSPK.V	\$1858	1.01	0.88	0.999992410	0.78	0.81	0.999981789	0.26	0.90
23294	ANKS1A	Ankyrin repeat and SAM domain-contain	K.S*PSFASEWDEIEK.I	\$661	1.22	0.99	0.055914758	1.05	1.00	0.999965101	0.97	0.99
23294	ANKS1A	Ankyrin repeat and SAM domain-contain	K.SPS*FASEWDEIEK.I	\$663	1.22	0.99	0.999990250	1.05	1.00	0.999986407	0.97	0.99
55139	ANKZF1	Ankyrin repeat and zinc finger domain-c	R.LAAQLGAPTS*PIPSAIVNTR.R	\$675	0.90	0.98	0.994079033	0.96	0.93	0.992689494	1.76	0.64
9824	ARHGAP11A	Rho GTPase activating protein 11A	K.LASLGDTAS*PLVK.S	\$868	0.27	0.93	0.999964572	0.72	0.72	0.999949795	4.00	0.96
57584	ARHGAP21	Rho GTPase-activating protein 21	K.AQPSSS*EDELNDVFFK.K	\$1432	1.57	0.96	0.994563577	0.81	0.96	0.802401375	0.83	0.96
57636	ARHGAP23	PREDICTED: similar to Rho GTPase ac	R.SAEALPGALVS*PR.F	\$372	0.80	0.88	0.999958987	0.76	0.91	0.999925867	1.29	0.98
23365	ARHGEF12	Rho guanine nucleotide exchange factor	R.TAS*QGQPTDSVIQNSSENIK.A	\$1288	1.16	0.87	0.999986041	1.16	0.99	0.999986947	1.34	0.50
23370	ARHGEF18	CDNA FLJ45102 fis, clone BRAWH303	R.SLS*PILSGR.H	\$980	0.01	0.89	0.999972767	119.23	0.98	0.999970216	0.01	0.50
23370	ARHGEF18	CDNA FLJ45102 fis, clone BRAWH303	R.SLS*PILPGR.H	\$980	1.17	0.89	0.999934375	0.82	0.98	0.999983325	1.34	0.99
9181	ARHGEF2	Guanine nucleotide exchange factor GEF	R.S*LPAGDALYLSFNPPQPSR.G	\$858	2.43	0.93	0.976064188	1.52	0.99	0.943259351	1.14	1.00
9181	ARHGEF2	Guanine nucleotide exchange factor GEF	R.EPALPLEPDSGGNTS*PGVTANGEAR.T	\$668	1.45	0.98	0.999800710	0.96	0.96	0.978639898	1.38	0.97
8289	ARID1A	AT-rich interactive domain-containing pr	R.SNS*VGIQDAFNDGSDSTFQK.R	\$1184	0.88	0.86	0.999981273	0.79	0.97	0.999933221	0.91	0.85
8289	ARID1A	AT-rich interactive domain-containing pr	R.GPS*PSPVGPASVAQSR.S	\$696	0.30	0.69	0.999980554	0.85	0.88	0.999984118	1.34	0.93
55252	ASXL2	Additional sex combs-like protein 2	R.FCLSS*PTEALK.M	\$1154	1.33	0.96	0.999149074	1.09	0.81	0.986198523	0.43	0.93
79915	ATAD5	ATPase family AAA domain-containing	K.SGYIS*ESESENSEISQQVR.F	\$306	1.43	0.99	0.999993091	0.75	0.97	0.999994026	1.14	0.97
11016	ATF7	activating transcription factor 7	K.AAAGPLDMS*LPST*PDIK.I	\$108;T112	1.13	0.95	0.999988957	0.65	0.94	0.999952498	0.55	0.70
11016	ATF7	activating transcription factor 7	K.AAAGPLDMS*LPS*TPDIK.I	\$108;S111	1.02	0.95	0.999985825	0.65	0.94	0.999994771	0.62	0.82
1822	ATN1	Atrophin-1	K.TAS*PPGPPPYGK.R	\$627	1.04	0.91	0.999593240	0.75	0.96	0.999715851	0.48	0.99
6310	ATXN1	Ataxin-1	K.ALSTGLDYS*PPSAPR.S	\$88	3.33	0.83	0.999941607	0.69	0.73	0.999959656	0.78	0.68
6311	ATXN2	Ataxin-2	R.TS*PSGGTWSSVVSQVPR.L	\$666	1.03	1.00	0.999985209	0.75	1.00	0.999825459	1.18	0.94
6311	ATXN2	Ataxin-2	R.TSPS*GGTWSSVVSQVPR.L	\$668	1.26	0.83	0.999958907	0.76	1.00	0.999979976	1.26	0.71
11273	ATXN2L	Ataxin-2-like protein	K.LQPSSS*PENSLDPFPPR.I	\$559	1.12	0.99	0.626382053	0.75	0.99	0.593370203	1.18	0.99
11273	ATXN2L	Ataxin-2-like protein	K.EVDGLLTSEPMGS*PVSSK.T	\$594	0.97	1.00	0.999987722	0.93	1.00	0.999984004	1.21	1.00
11273	ATXN2L	Ataxin-2-like protein	K.GPPQS*PVFEGVYNSR.M	\$111	1.35	1.00	0.999994548	1.03	1.00	0.999994323	1.62	0.98
55971	BAIAP2L1	Brain-specific angiogenesis inhibitor 1-a	K.TPASTPVSGTPQAS*PMIER.S	\$261	1.18	1.00	0.999980696	0.63	1.00	0.999989408	1.35	0.99
55971	BAIAP2L1	Brain-specific angiogenesis inhibitor 1-a	R.SVS*VATGLNMMK.K	\$331	0.97	0.97	0.999992810	0.43	0.95	0.999984192	1.43	0.99
55971	BAIAP2L1	Brain-specific angiogenesis inhibitor 1-a	K.LLEENETEAVTVPTPS*PTPVR.S	\$414	0.68	1.00	0.900039514	0.56	1.00	0.776051326	1.47	0.97
55971	BAIAP2L1	Brain-specific angiogenesis inhibitor 1-a	K.LLEENETEAVTVPTPSPT*PVR.S	T416	0.66	1.00	0.752209327	0.56	1.00	0.768538076	1.71	0.79
55971	BAIAP2L1	Brain-specific angiogenesis inhibitor 1-a	K.TPASTPVSGT*PQAS*PMIER.S	T257,S261	0.46	0.99	0.999994704	0.60	0.99	0.999994502	2.05	0.90
7916	BAT2	Large proline-rich protein BAT2	K.EGPEPPEEVPPPTT*PPVPK.V	T610	1.04	1.00	0.431304307	0.92	1.00	0.397794543	1.32	0.98

7916	BAT2	Large proline-rich protein BAT2	K.EAPPPVLLT*PK.A	T1347	0.80	0.97	0.557756926	1.13	0.92	0.672198906	2.14	0.98
7916	BAT2	Large proline-rich protein BAT2	R.VDLYQQAS*PPDALR.W	S2113	0.76	0.85	0.999986249	1.01	0.93	0.999967729	2.64	0.92
23215	BAT2D1	Putative uncharacterized protein (HBxA)	K.LPDLS*PVENK.E	S2105	0.85	0.91	0.999978281	0.87	0.86	0.999990917	1.19	0.81
11176	BAZ2A	Bromodomain adjacent to zinc finger do	R.AGDPGEMPQS*PTGLGQPK.R	S1370	0.92	0.94	0.999981420	3.77	0.94	0.999974545	0.74	0.97
8412	BCAR3	Breast cancer anti-estrogen resistance pr	R.QNS*PVTQDGIQESPWQDR.H	S83	1.07	0.97	0.998960771	1.06	0.99	0.846061195	1.50	0.94
607	BCL9	B-cell lymphoma 9 protein	R.IPVEGPLS*PSR.G	S687	2.81	0.85	0.999954174	0.60	0.90	0.999984574	1.48	0.52
9774	BCLAF1	Bcl-2-associated transcription factor 1	R.IDIS*PSTLR.K	S658	0.94	1.00	0.999979134	0.79	1.00	0.999991114	0.99	0.78
9774	BCLAF1	Bcl-2-associated transcription factor 1	K.SSATSGDIWPGLSAYDNS*PR.S	S222	0.98	0.94	0.243271029	0.87	0.98	0.845695123	1.33	0.99
23774	BRD1	Bromodomain-containing protein 1	R.IVEYS*PPSAPR.R	S128	1.19	0.90	0.999983223	0.74	0.98	0.999990570	1.11	0.99
9024	BRSK2	CDNA FLJ16763 fis, clone BRAMY301	K.SMEVLSVTDGGS*PVPAR.R	S393	0.50	0.93	0.999931780	0.59	0.75	0.999168651	1.57	0.98
9024	BRSK2	CDNA FLJ16763 fis, clone BRAMY301	R.SIGASSGLSTS*PLSSPR.V	S423	0.70	0.87	0.999950179	0.93	0.90	0.999947228	1.82	0.89
54014	BRWD1	Bromodomain and WD repeat domain-cd	K.IPELVGS*PTQSTSSR.T	S1475	1.30	0.95	0.999063823	0.77	0.97	0.862722797	1.20	0.94
84811	BUD13	BUD13 homolog	K.YEYDPDIS*PPR.K	S325	2.69	0.96	0.999959616	0.52	0.97	0.999966252	0.82	0.99
254427	C10orf47	Protein C10orf47	R.MAGNEALSPTS*PFR.E	S315	1.09	0.81	0.955491317	0.92	0.83	0.997759921	1.19	0.90
221150	C13orf3	Protein C13orf3	R.S*PQLSDFGLER.Y	S159	1.07	0.89	0.999991555	0.88	0.94	0.999983999	3.36	0.50
283489	C13orf8	Zinc finger protein 828	R.KT*SPASLDFPESQK.S	T458	1.44	0.89	0.999959503	0.52	0.87	0.999982887	0.06	0.41
283489	C13orf8	Zinc finger protein 828	K.CDILVQEELLAS*PK.K	S603	1.58	0.94	0.999959077	0.78	0.99	0.999854752	0.81	0.96
283489	C13orf8	Zinc finger protein 828	R.KTS*PASLDFPESQK.S	S459	1.32	0.77	0.999953413	0.73	0.66	0.999920595	1.11	0.79
91748	C14orf43	Uncharacterized protein C14orf43	R.SFELPPYT*PPPILS*PVR.E	T655,S661	1.21	0.92	0.999368900	0.63	0.95	0.989756583	0.42	0.98
90381	C15orf42	Uncharacterized protein C15orf42	R.LLYNS*PEYEASFPR.M	S292	1.27	0.99	0.999993831	0.87	0.98	0.999992786	1.03	0.99
79447	C16orf53	Uncharacterized protein C16orf53	R.DLFSLSDSEDPSPAS*PPLR.S	S237	1.12	0.99	0.999982986	0.84	0.99	0.999971080	1.20	0.95
124944	C17orf49	Uncharacterized potential DNA-binding	K.VYEDSGIPLPAES*PK.K	S96	1.06	0.99	0.389772939	0.81	0.99	0.276237032	1.02	0.97
55421	C17orf85	Uncharacterized protein C17orf85	K.AEAPAGPALGLPS*PEAESGVDR.G	S25	1.28	0.99	0.999988221	0.60	0.98	0.999990272	0.97	0.96
126353	C19orf21	Uncharacterized protein C19orf21	R.ALS*SDSILSPAPDAR.A	S394	2.35	0.98	0.999967195	0.69	1.00	0.999264657	0.90	0.98
126353	C19orf21	Uncharacterized protein C19orf21	R.NALFPEVFS*PTPDENSQNSR.S	S575	1.37	0.92	0.999988704	0.72	0.91	0.999991288	1.14	0.83
126353	C19orf21	Uncharacterized protein C19orf21	R.AST*PDWVSEGPQGLR.R	T377	1.23	0.99	0.988672602	0.60	0.95	0.999939453	1.28	0.86
23272	C3orf63	KIAA1105 protein	R.SSDYQFPSS*PFTDTLK.G	S979	0.65	0.98	0.471038310	0.96	0.97	0.817952976	1.68	0.98
23272	C3orf63	KIAA1105 protein	R.SSDYQFPSSPFT*DTLK.G	T982	0.65	0.98	0.084599289	0.96	0.97	0.173697743	1.93	0.33
54887	C6orf107	UHRF1-binding protein 1	R.TVSQQS*FDGVSLDSSGPEDR.I	S1106	1.05	0.65	0.999963660	1.12	0.75	0.999965583	0.04	0.50
55122	C6orf166	Uncharacterized protein C6orf166	R.TLDFDLLSPAS*PK.R	S21	1.00	0.99	0.924589227	0.94	0.98	0.937920172	1.91	0.99
79886	C9orf82	Uncharacterized protein C9orf82	K.SVNEILGLAESS*PNEPK.A	S312	1.54	0.90	0.996387963	0.78	0.99	0.998549053	0.89	0.90
800	CALD1	Caldesmon	R.S*LAALSQIAYQR.N	S12	0.00	0.90	0.999967213	85.85	0.50	0.999963598	1.96	0.81
23271	CAMSAP1L1	calmodulin regulated spectrin-associated	R.EQQSWVISPPQPS*PQK.Q	S909	1.16	0.70	0.999930391	1.06	0.84	0.999893596	1.72	0.94
23271	CAMSAP1L1	calmodulin regulated spectrin-associated	R.SESVEGFLS*PSR.C	S1292	0.89	0.89	0.999985244	1.16	0.99	0.999985427	2.12	0.99

79092	CARD14	Caspase recruitment domain-containing	R.ANMVS*SCELELQEQLR.T	\$240	1.56	0.97	0.999993945	0.68	0.91	0.999994806	1.18	0.86
23589	CARHSP1	Calcium-regulated heat stable protein 1	R.GNVVPS*PLPTR.R	\$41	1.38	0.99	0.952303172	0.67	1.00	0.977401911	1.31	0.84
831	CAST	calpastatin	R.SES*ELIDELSEDFDR.S	\$366	1.18	0.89	0.999930432	1.08	0.92	0.999984204	2.34	0.99
91603	CCDC16	Zinc finger protein 830	K.EEENADS*DDEGELQDLLSQDWR.V	\$351	1.38	0.98	0.999936951	0.63	0.94	0.999972694	0.92	0.99
8030	CCDC6	Coiled-coil domain-containing protein 6	R.DISMEIDS*PENMMR.H	\$254	1.09	0.98	0.999958968	0.68	0.96	0.999983570	0.98	0.96
8030	CCDC6	Coiled-coil domain-containing protein 6	R.AEQEEEFISNT*LFK.K	T115	1.10	0.87	0.999729488	1.01	0.83	0.909676809	1.10	0.97
8030	CCDC6	Coiled-coil domain-containing protein 6	K.SGGIVIS*PFR.L	\$52	1.41	0.97	0.997988596	0.76	0.97	0.991323542	1.16	0.99
8030	CCDC6	Coiled-coil domain-containing protein 6	K.LDQPVSAPPS*PR.D	\$244	1.85	0.98	0.995566978	0.94	1.00	0.999073191	1.34	0.99
8030	CCDC6	Coiled-coil domain-containing protein 6	K.LDQPVS*APPS*PR.D	\$240,\$244	1.15	0.99	0.999992361	1.05	0.95	0.999992577	1.36	0.85
79080	CCDC86	Coiled-coil domain-containing protein 86	R.LQQGAGLESPQGQPEPGAAS*PQR.Q	\$91	1.06	1.00	0.999982614	0.81	1.00	0.999992705	0.95	1.00
79080	CCDC86	Coiled-coil domain-containing protein 86	R.LQQGAGLES*PQGQPEPGAAS*PQR.Q	\$80,\$91	1.07	0.98	0.999991290	0.72	0.99	0.999993634	2.60	0.94
55704	CCDC88A	Hook-related protein 1	K.SSS*QENLLDEVMS.K	\$1702	3.66	0.84	0.998690718	1.38	0.94	0.868726850	0.74	0.93
9134	CCNE2	G1/S-specific cyclin-E2	K.QQPQPSQTES*PQEAQIIQAK.K	\$21	0.89	0.92	0.931670398	0.90	0.95	0.999750631	0.93	0.98
57018	CCNL1	Cyclin-L1	K.AEEKS*PISINVK.T	\$352	0.99	0.64	0.999942334	0.75	0.82	0.999988554	1.04	0.99
81669	CCNL2	Cyclin-L2	R.GLLPGGTQVLDGTSGFS*PAPK.L	\$330	0.84	0.99	0.999380472	0.77	1.00	0.973316866	0.95	0.98
151195	CCNYL1	CDNA FLJ40432 fis, clone TESTI20392	R.SFS*ADNFIGIQR.S	\$344	1.20	0.98	0.999992170	0.92	0.99	0.999991705	0.96	0.96
10849	CD3EAP	RNA polymerase I-associated factor PAH	K.QEQINTEPLEDTVLS*PTK.K	\$285	0.96	1.00	0.986123800	0.77	1.00	0.989145582	1.17	0.99
983	CDC2	Cell division control protein 2 homolog	K.IGEGT*YGVVYK.A	T14	0.69	0.57	0.999992324	0.94	0.96	0.999993770	1.14	0.97
983	CDC2	Cell division control protein 2 homolog	K.IGEGTY*GVVYK.A	Y15	1.01	0.80	0.255349001	1.41	0.87	0.999890995	1.82	0.71
728642	CDC2L2	Isoform SV6 of PITSLRE serine/threonin	K.AYT*PVVVTQWYR.A	T580	0.85	0.99	0.999735743	0.72	0.94	0.999919361	1.06	1.00
728642	CDC2L2	Isoform SV6 of PITSLRE serine/threonin	R.DLLSDLQDIS*DSER.K	\$271	1.19	0.91	0.999989150	0.83	0.99	0.999927344	1.07	0.95
23580	CDC42EP4	Cdc42 effector protein 4	K.NAMS*LPQLNEK.E	\$118	1.06	0.94	0.999978291	1.07	0.97	0.999970882	0.83	0.99
990	CDC6	Cell division control protein 6 homolog	K.LEPTNVQTVTCS*PR.V	\$45	0.97	0.94	0.883708958	1.25	0.99	0.964002808	2.42	0.99
8317	CDC7	Cell division cycle 7-related protein kina	K.ASCLVQT*PPGQYSGNSFK.K	T503	0.93	0.91	0.999967195	0.87	0.77	0.999827114	2.14	0.82
113130	CDCA5	Sororin	K.SGS*ELPSILPEIWP.K	\$35	0.70	0.99	0.945956633	0.70	0.96	0.668700883	1.71	0.98
55143	CDCA8	Borealin	R.IYNISGNGS*PLADSK.E	\$219	0.64	0.98	0.999949641	0.67	0.99	0.999965222	2.29	0.98
6792	CDKL5	Cyclin-dependent kinase-like 5	R.YFPSSCLDLSNPTSPT*PTR.H	T531	1.35	0.66	0.999958087	0.74	0.73	0.999931290	1.17	0.65
1039	CDR2	Cerebellar degeneration-related protein 2	R.SSS*ETILSSLAGSDIVK.G	\$311	1.26	0.97	0.999749421	0.59	0.98	0.834844016	1.41	0.91
1059	CENPB	Major centromere autoantigen B	R.TPAAPAS*PAAVPSEGGSTTGWR.A	\$156	1.05	0.96	0.999972560	0.94	0.90	0.999991979	0.88	0.99
1060	CENPC1	Centromere protein C 1	R.TIS*PAESTALFQGR.K	\$333	0.97	0.99	0.999985775	0.84	0.95	0.999970985	0.81	0.93
1063	CENPF	Centromere protein F	K.LALS*PLSLGK.E	\$3119	0.64	0.96	0.999983923	0.66	0.99	0.999951216	2.86	0.93
1063	CENPF	Centromere protein F	K.IFTTPLT*PSQYYSGSK.Y	T154	0.63	0.96	0.999967627	0.68	0.90	0.886079369	3.30	0.94
1063	CENPF	Centromere protein F	R.LQLQLDLS*SR.S	\$1747	0.47	0.62	0.999992771	0.67	0.94	0.999991914	3.62	0.74
116985	CENTD2	centaurin delta 2	R.LFPEFDDS*DYDEVPEEGPGAPAR.V	\$249	1.18	0.98	0.882240677	0.79	0.99	0.905325293	1.43	0.96

116987	CENTG2	Centaurin-gamma 2	R.FVLMAT*PNLSR.R	T386	0.73	0.96	0.998667814	0.61	0.91	0.999939738	1.88	0.75
9859	CEP170	KARP-1-binding protein	R.FPTDYASTS*EDEFSGNR.N	S1241	0.92	0.51	0.985572698	0.70	0.50	0.999966154	0.92	0.84
9859	CEP170	KARP-1-binding protein	R.S*ESLDPDSSMDTTLILK.D	S879	1.32	0.96	0.999923644	1.18	0.97	0.999412762	1.23	0.96
9859	CEP170	KARP-1-binding protein	R.SES*LDPDSSMDTTLILK.D	S881	1.23	0.94	0.999985969	1.18	0.97	0.999949051	1.45	0.92
55165	CEP55	Centrosome protein 55	K.S*PTAALNESLVECPK.C	S428	1.61	0.99	0.999972578	0.92	1.00	0.999984838	1.11	0.89
55165	CEP55	Centrosome protein 55	R.YS*TTALLEQLEETTR.E	S96	4.15	0.72	0.999991661	1.54	0.96	0.999994242	1.42	0.99
1107	CHD3	Chromodomain helicase-DNA-binding p	K.METEADAPS*PAPSLGER.L	S1601	7.19	0.72	0.999958451	0.83	0.93	0.999989106	1.14	0.80
55636	CHD7	Chromodomain-helicase-DNA-binding p	R.NIPS*PGQLDPDTR.I	S2559	0.99	0.99	0.651687437	0.83	0.99	0.862087526	1.81	0.99
57680	CHD8	Chromodomain-helicase-DNA-binding p	R.APGYPSS*PVTTASGTTLR.L	S2240	0.98	0.99	0.999924301	0.86	0.98	0.999632786	0.95	0.97
63922	CHTF18	Protein CTF18 homolog	R.VENSPQVDGS*PPGLEGLLGIGEK.G	S1080	1.13	0.81	0.999990677	0.72	0.93	0.999991405	1.41	0.99
23332	CLASP1	CLIP-associating protein 1	R.SRS*DIDVNAASAK.S	S600	1.08	0.94	0.999977849	0.77	0.82	0.999989749	0.79	0.82
23332	CLASP1	CLIP-associating protein 1	R.VLSTS*TDLEAAVADALK.K	S797	1.26	0.99	0.970205799	0.61	0.99	0.449168549	1.03	1.00
23122	CLASP2	CDNA FLJ34132 fis, clone FCBBF3010	R.LGAGALNAGSYAS*LGR.V	S407	0.67	1.00	0.999994275	0.72	1.00	0.999994953	0.93	0.99
23122	CLASP2	CDNA FLJ34132 fis, clone FCBBF3010	R.VLNTGS*DVEEAVADALK.K	S596	1.11	0.99	0.999994480	0.68	1.00	0.999992471	0.98	0.99
23122	CLASP2	CDNA FLJ34132 fis, clone FCBBF3010	R.DYNPYNYSDSIS*PFNK.S	S1029	0.90	0.97	0.999978804	1.33	0.97	0.999972530	1.30	0.99
23122	CLASP2	CDNA FLJ34132 fis, clone FCBBF3010	R.SRS*DIDVNAAGAK.A	S370	1.09	0.99	0.999985493	0.31	0.61	0.999985206	7.49	0.72
63967	CLSPN	Claspin	K.LSEPSLPIEDSQDLYNAS*PEPK.T	S846	0.77	0.93	0.999987280	0.80	0.95	0.999983844	2.54	0.93
8161	COIL	Coilin	K.LLELTSSYS*PDVSDYK.E	S489	1.05	0.80	0.999370678	1.11	0.81	0.999765864	0.70	0.97
79869	CPSF7	Cleavage and polyadenylation specificity	R.DSSDSADGRAT*PSENLPSSAR.V	T203	1.34	0.99	0.999994574	0.98	1.00	0.999990752	2.00	0.99
79869	CPSF7	Cleavage and polyadenylation specificity	R.DSSDSADGRATPS*ENLPSSAR.V	S205	1.34	0.99	0.999989296	0.91	1.00	0.999980638	2.00	0.99
64784	CRTC3	transducer of regulated CREB protein 3	R.LFSLS*NPSLSTTNLSGSPSR.R	S370	1.08	0.98	0.999992352	0.69	0.97	0.999993496	1.07	0.99
1453	CSNK1D	Casein kinase I isoform delta	R.GAPVNISS*SDLTGR.Q	S383	0.70	0.98	0.999900911	0.84	0.93	0.999963723	1.50	0.83
1453	CSNK1D	Casein kinase I isoform delta	R.GAPVNIS*SSDLTGR.Q	S382	0.70	0.98	0.999987195	1.16	0.96	0.999987246	2.59	0.99
1465	CSRPI	Cysteine and glycine-rich protein 1	K.GFGFGQGAGALVHS*E.-	S192	1.48	1.00	0.999994708	1.00	1.00	0.999993501	1.00	1.00
1495	CTNNA1	Catenin alpha-1	R.TPEELDDS*DFETEDFDVR.S	S641	1.20	0.99	0.999994683	0.84	1.00	0.999994425	0.89	0.99
1500	CTNND1	Isoform 1ABC of Catenin delta-1	R.GSLAS*LDSL.R.K	S349	1.62	0.94	0.999990599	0.98	0.99	0.999992763	0.88	0.93
9646	CTR9	RNA polymerase-associated protein CTR	K.GGEFDEFVNDT*DDDLPIK.K	T925	1.00	0.99	0.999822939	0.95	0.97	0.999956480	1.00	1.00
2017	CTTN	cortactin	K.TQTTPVS*PAPQPTEER.L	S405	2.97	0.99	0.992983513	0.76	0.89	0.999896384	0.91	0.85
2017	CTTN	cortactin	K.TQT*PPVS*PAPQPTEER.L	T401,S405	1.48	0.89	0.999993551	0.73	0.97	0.999985648	1.00	0.94
2017	CTTN	cortactin	R.LPSS*PVYEDAASF.K.A	S418	1.48	0.99	0.999537362	0.86	1.00	0.999783312	1.12	0.99
2017	CTTN	cortactin	R.LPS*SPVYEDAASF.K.A	S417	1.41	1.00	0.999889561	0.86	0.94	0.984948863	1.13	0.98
2017	CTTN	cortactin	K.TQT*PPVPAPQPTEER.L	T401	1.47	0.99	0.894107461	0.90	1.00	0.868927652	1.57	1.00
55917	CTTNBP2NL	CTTNBP2 N-terminal-like protein	K.FQSQADQDQASGLQS*PPSR.D	S481	0.77	0.59	0.999970817	0.77	0.92	0.999986724	1.06	0.90
1523	CUTL1	Homeobox protein cut-like 1	R.AYQQKPYPS*PK.T	S1270	1.22	0.97	0.999973440	0.80	0.94	0.999982847	1.31	0.91

55787	CXorf15	Lipopolysaccharide-specific response protein	R.SAVQKPPS*TGSAPIAESVD.-	S517	1.23	0.98	0.999981163	0.68	0.88	0.999990580	1.15	0.97
1601	DAB2	Disabled homolog 2	K.SSPNPFVGS*PPK.G	S401	0.96	0.74	0.995598484	1.00	0.85	0.941002420	1.24	0.98
1616	DAXX	Death domain-associated protein 6	K.DGDKS*PMSSLQISNEK.N	S495	0.37	0.72	0.999976497	1.23	0.84	0.999994581	1.13	0.95
1616	DAXX	Death domain-associated protein 6	K.ELDLS*ELDDPDSAYLQEAR.L	S213	18.16	0.82	0.999957026	0.77	0.98	0.999992140	1.15	0.97
10926	DBF4	DBF4-type zinc finger-containing protein	K.YSVGSLs*PVSASVLK.K	S359	1.52	0.99	0.999993523	0.78	0.99	0.999993994	1.26	0.99
84301	DDI2	Protein DDI1 homolog 2	R.IDFSSIAVPGTSS*PR.Q	S106	0.59	0.97	0.232362963	1.20	0.92	0.093158797	1.28	0.98
9188	DDX21	Nucleolar RNA helicase 2	R.NGIDILVGT*PGR.I	T315	1.07	0.95	0.999957787	0.78	0.92	0.999637818	0.98	0.96
9188	DDX21	Nucleolar RNA helicase 2	K.KKEEPSQNDIS*PK.T	S89	1.15	0.97	0.999988226	0.54	0.98	0.999991663	1.07	0.85
51428	DDX41	Probable ATP-dependent RNA helicase	R.S*EAEDDEDYVYVPLR.Q	S23	0.88	0.95	0.935881980	0.96	0.96	0.680443089	1.05	0.85
83479	DDX59	DEAD box protein 59	K.ADSEPES*PLNASYVYK.E	S160	1.18	0.96	0.993392857	0.90	0.96	0.999979279	1.24	0.76
11083	DIDO1	Death-inducer obliterator 1	R.S*PPEGDTTLFLSR.L	S1040	1.31	0.99	0.999993830	0.78	1.00	0.999993895	1.07	0.65
11083	DIDO1	Death-inducer obliterator 1	R.YLSVPPS*PNISTSES.R.S	S1030	1.39	0.90	0.996793846	1.01	0.58	0.994056874	1.34	0.94
222229	DKFZp434K1	Hypothetical protein DKFZp434K1815	R.ACAS*PSAQVEGSPVAGSDGSQPAVK.L	S251	1.21	0.94	0.999986265	0.93	1.00	0.999990825	0.87	0.95
222229	DKFZp434K1	Hypothetical protein DKFZp434K1815	R.ACASPS*AQVEGSPVAGSDGSQPAVK.L	S253	1.21	0.94	0.999981336	0.93	1.00	0.999988182	0.88	1.00
55355	DKFZp76E1	hypothetical protein LOC55355	R.GGPAS*PGGLQGLETR.R	S203	0.99	0.96	0.999989842	0.81	0.99	0.999993302	2.00	0.99
9231	DLG5	Disks large homolog 5	R.ATHGSNS*LPSSAR.L	S1254	1.34	0.77	0.999966827	0.76	0.86	0.999979037	0.71	0.55
1786	DNMT1	DNA (cytosine-5)-methyltransferase 1	K.EADDDEEVDDNIPEMPS*PK.K	S714	1.31	1.00	0.491293216	0.78	1.00	0.456808160	1.09	0.99
30836	DNTTIP2	Deoxynucleotidyltransferase terminal-int	R.QILIACS*PVSSVR.K	S117	1.15	0.98	0.990424013	0.65	0.99	0.999982084	1.66	0.98
57572	DOCK6	Dedicator of cytokinesis protein 6	K.SIS*SSNPDLAVAPGSDDEVS.R.I	S882	1.26	0.99	0.969174180	1.03	0.99	0.992545584	2.34	0.99
57572	DOCK6	Dedicator of cytokinesis protein 6	K.SISSS*NPDLAVAPGSDDEVS.R.I	S884	1.26	0.99	0.831118581	1.03	0.99	0.959225205	2.34	0.99
85440	DOCK7	Dedicator of cytokinesis protein 7	R.S*PSGSAFGSQENLR.W	S1430	0.56	0.96	0.999978073	15.24	0.81	0.999973660	0.70	0.82
85440	DOCK7	Dedicator of cytokinesis protein 7	R.SLSNS*NPDISGTPSPDDEVR.S	S900	1.55	0.98	0.999971437	0.57	1.00	0.999987652	0.98	0.95
85440	DOCK7	Dedicator of cytokinesis protein 7	K.AAPWGSNPS*PSAESTQAMDR.S	S946	1.03	0.91	0.999920201	1.07	0.92	0.999853111	1.16	0.95
85440	DOCK7	Dedicator of cytokinesis protein 7	R.SLS*NSNPDISGTPSPDDEVR.S	S898	1.19	0.95	0.999987366	1.14	1.00	0.999979137	1.67	0.99
1808	DPYSL2	Dihydropyrimidinase-related protein 2	R.GLYDGPVCEVSVT*PK.T	T509	1.34	1.00	0.999323776	0.68	1.00	0.896644317	1.79	0.85
1809	DPYSL3	Dihydropyrimidinase-related protein 3	R.GMYDGPVFDLTT*PK.G	T509	1.07	0.99	0.999967064	0.77	0.94	0.999968354	1.25	0.98
1832	DSP	Isoform DPH of Desmoplakin	K.GLPSPYNMSSAPGS*R.S	S2825	1.25	0.99	0.999899765	0.94	0.99	0.999626134	1.19	1.00
1832	DSP	Isoform DPH of Desmoplakin	R.SSSFS*DTLEESSPIAIFDTENLEK.I	S2610	1.09	1.00	0.999672882	0.96	1.00	0.997049554	1.25	1.00
51514	DTL	RA-regulated nuclear matrix-associated p	R.TPSSS*PPIT*PPAETK.I	S512;T516	1.11	0.96	0.995668460	1.03	0.96	0.999789722	0.70	0.73
51143	DYNC1LI1	Cytoplasmic dynein 1 light intermediate	R.DFQEYVEPEGDFPAS*PQR.R	S207	1.04	0.98	0.999915236	0.61	0.94	0.999912019	1.20	0.68
1859	DYRK1A	Isoform Long of Dual specificity tyrosine	R.IYQY*IQSR.F	Y321	1.15	0.95	0.763723515	0.77	1.00	0.576783538	0.84	0.90
1936	EEF1D	Elongation factor 1-delta	R.ATAPQTQHVS*PMR.Q	S133	1.29	0.84	0.999982451	0.66	1.00	0.999952611	0.80	0.72
1956	EGFR	Epidermal growth factor receptor precursor	R.ELVEPLT*PSGEAPNQUALLR.I	T693	0.97	1.00	0.997490644	0.65	0.98	0.999907960	0.53	0.99
728350	EIF2S2	Eukaryotic translation initiation factor 2	K.IESDVQEPT*EPEDDLDIMLGNK.K	T111	1.46	1.00	0.999993678	0.73	0.99	0.999992793	0.85	0.99

1975	EIF4B	eukaryotic translation initiation factor 4B	K.SPPY*TAFLGNLPYDVTEESIK.E	Y96	1.28	1.00	0.999907829	0.82	1.00	0.999896842	0.71	1.00
1975	EIF4B	eukaryotic translation initiation factor 4B	K.S*PPYTAFLGNLPYDVTEESIK.E	S93	1.33	1.00	0.998045148	0.78	1.00	0.999876800	1.06	1.00
1981	EIF4G1	eukaryotic translation initiation factor 4 g	R.EAALPPVS*PLK.A	S1232	1.14	0.99	0.126681719	0.98	0.99	0.104953334	0.95	1.00
1982	EIF4G2	eukaryotic translation initiation factor 4 g	R.TQT*PLGQTPQLGLK.T	T470	0.81	0.99	0.990039072	0.78	1.00	0.991840098	1.86	0.98
8672	EIF4G3	Eukaryotic translation initiation factor 4 g	R.S*PVPAQAIAITVPK.T	S495	0.97	0.98	0.999987540	0.86	0.98	0.999990532	1.16	0.92
2058	EPRS	glutamyl-prolyl tRNA synthetase	K.EYIPGQPPLSQSSDSS*PTR.N	S886	1.22	1.00	0.722626803	0.65	1.00	0.846213532	0.92	0.69
157570	ESCO2	Establishment of cohesion 1 homolog 2	R.VLSEPIGPES*PSSTECPR.A	S512	1.25	0.99	0.999953854	0.72	0.97	0.999946467	0.78	0.99
2117	ETV3	ETS translocation variant 3	R.SSGVVPQS*APPVPTASSR.F	S139	0.78	0.88	0.999989561	8.07	0.73	0.991899607	1.07	0.99
9156	EXO1	Exonuclease 1	R.S*AELSEDDLLSQYLSLFTK.K	S422	1.18	0.85	0.999956572	0.83	0.78	0.997125345	1.23	0.99
2146	EZH2	enhancer of zeste 2	K.ESSIHAPAPAEDVDT*PPR.K	T487	2.12	0.95	0.653929630	0.99	0.92	0.891400693	1.19	0.98
645272	FAM21A	Family with sequence similarity 21, mem	K.GLFS*DEEDSEDLFSSQSASK.L	S433	1.24	0.94	0.999988971	0.70	0.98	0.999993151	0.67	0.89
253725	FAM21C	Protein FAM21C	K.GLFS*DEEDSEDLFSSQSASNLK.G	S539	1.14	0.98	0.999992229	0.79	0.97	0.999992630	0.99	0.99
85369	FAM40A	Protein FAM40A	R.AAS*PPASASDLIEQQQK.R	S335	1.13	0.96	0.999839264	1.17	0.95	0.999988550	1.00	0.95
51307	FAM53C	Protein FAM53C	R.SLS*VPVDLSR.W	S122	1.18	1.00	0.994413619	0.74	1.00	0.995983222	0.95	0.89
51307	FAM53C	Protein FAM53C	R.FSLS*PSLGPQASR.F	S234	1.33	0.99	0.999981677	1.06	1.00	0.999988062	1.06	0.99
79567	FAM65A	Protein FAM65A	R.FSTYSQS*PPDTPSLR.E	S351	1.21	0.99	0.999962703	0.74	0.99	0.999987651	0.75	0.99
55177	FAM82C	Cerebral protein-10	R.SQS*LPNSLDYTQTSDPGR.H	S46	1.18	1.00	0.999991595	0.78	1.00	0.999957939	1.41	0.97
644815	FAM83G	Protein FAM83G	R.S*IPQLDLGWPDITAIYR.G	S127	1.30	0.95	0.998105896	0.76	0.94	0.996778767	0.94	0.99
10160	FARP1	FERM, RhoGEF and pleckstrin domain-	K.SSSPAPEFLASS*PPDNK.S	S872	0.93	0.97	0.983067002	0.96	0.87	0.998694151	1.12	0.97
10160	FARP1	FERM, RhoGEF and pleckstrin domain-	R.LGAPENSGIST*LER.G	T24	0.73	1.00	0.882275385	0.88	1.00	0.068473809	1.25	1.00
81608	FIP1L1	Pre-mRNA 3'-end-processing factor FIP1	K.AEFTS*PPSLFK.T	S259	0.81	0.92	0.727713563	0.68	0.97	0.505684782	2.11	0.93
400793	FLJ13137	Uncharacterized protein FLJ13137	R.TSS*LDNEGPHPDLLSFE.-	S258	1.48	1.00	0.999949034	1.00	1.00	0.999623001	1.00	1.00
2303	FOXC2	Forkhead box protein C2	K.VETLS*PESALQGS*PR.S	S232,S240	1.20	0.97	0.999993327	1.21	0.76	0.999984277	0.98	0.95
2303	FOXC2	Forkhead box protein C2	K.SEAAS*PALPVITK.V	S219	0.99	0.99	0.999993030	0.84	1.00	0.999992265	1.42	1.00
2303	FOXC2	Forkhead box protein C2	K.VETLS*PESALQGS*PR.S	S240	1.30	0.99	0.999967621	1.02	0.95	0.999945990	1.56	0.98
2303	FOXC2	Forkhead box protein C2	K.VETLS*PESALQGS*PR.S	S232	1.33	0.97	0.999988535	0.74	0.96	0.999993249	1.94	0.83
221937	FOKK1	forkhead box K1	R.EGS*PIPHDPEFGSK.L	S445	1.39	0.89	0.980353898	0.96	0.98	0.973235056	1.08	0.90
24140	FTSJ1	FtsJ homolog 1	K.YTPPTQPPIS*PPYQEAETLK.R	S271	1.21	0.97	0.984841466	0.97	0.98	0.859198954	1.81	0.68
10146	G3BP1	Ras-GTPase-activating protein-binding p	R.YQDEVFVGDFVTEPQEES*EEEVEEPEER.Q	S149	1.23	0.98	0.999955304	0.90	0.99	0.709769526	0.98	1.00
10146	G3BP1	Ras-GTPase-activating protein-binding p	K.SS*SPAPADIAQTQVEDLR.T	S231	1.28	1.00	0.863819774	0.79	1.00	0.951852601	0.99	0.92
10146	G3BP1	Ras-GTPase-activating protein-binding p	K.SS*PAPADIAQTQVEDLR.T	S232	1.26	1.00	0.879615060	0.79	1.00	0.992145299	0.99	0.98
9908	G3BP2	Ras-GTPase-activating protein-binding p	K.STT*PPPAEPVSLPQEPPK.A	T227	1.32	0.99	0.860134137	0.78	0.98	0.905690966	1.03	0.91
26130	GAPVD1	GTPase-activating protein and VPS9 dor	R.LQELESCSGLGS*TSDDTDVR.E	S746	1.18	1.00	0.999986984	0.93	1.00	0.999994478	0.60	0.66
26130	GAPVD1	GTPase-activating protein and VPS9 dor	R.SRS*SDIVSSVR.R	S902	1.07	0.78	0.999975565	0.87	0.14	0.999959785	0.99	0.82

253959	GARNL1	GTPase-activating Rap/Ran-GAP domain	R.SSS*TSIDILEPFTVER.A	S797	1.84	0.99	0.896583399	0.86	1.00	0.982275564	0.99	0.94
10634	GAS2L1	GAS2-like protein 1	R.VSS*PSPPELGTTPASIFR.T	S490	1.00	0.98	0.970254569	0.98	0.98	0.963096189	1.18	0.98
10634	GAS2L1	GAS2-like protein 1	R.VSSPS*PELGTTPASIFR.T	S492	1.12	0.95	0.997835863	1.15	0.95	0.994368412	1.39	0.93
283431	GAS2L3	Growth arrest-specific protein 2-like 3	K.SALNLNQPVSVSSVS*PVK.A	S570	0.85	0.97	0.997957496	0.87	0.98	0.999964937	3.45	0.94
57459	GATAD2B	Transcriptional repressor p66 beta	R.LTPSPDIIVLS*DNEASSPR.S	S129	3.10	0.90	0.999990020	0.71	0.95	0.999975424	18.61	0.20
2673	GFPT1	glucosamine-fructose-6-phosphate aminid	R.VDS*TTCLFPVEEK.A	S261	1.37	1.00	0.999895196	0.75	1.00	0.999881694	0.77	0.99
28964	GIT1	ARF GTPase-activating protein GIT1	K.SLS*SPTDNLELSLR.S	S361	1.33	0.99	0.999976348	0.82	1.00	0.999989737	0.06	0.60
28964	GIT1	ARF GTPase-activating protein GIT1	K.S*LSSPTDNLELSLR.S	S359	1.33	0.99	0.999954688	0.91	0.90	0.999940067	0.24	0.93
28964	GIT1	ARF GTPase-activating protein GIT1	R.S*MDSSDLSGDGAVTLQEYLELK.K	S410	1.63	0.94	0.968107564	0.86	0.95	0.999965159	1.30	0.93
28964	GIT1	ARF GTPase-activating protein GIT1	K.SLSS*PTDNLELSLR.S	S362	1.35	0.99	0.645483589	0.80	1.00	0.413618364	1.32	0.99
28964	GIT1	ARF GTPase-activating protein GIT1	K.GVSASAVPFTPSS*PLLSCSQEGSR.H	S571	0.62	0.93	0.588126063	0.94	0.95	0.633738067	2.12	0.70
113263	GLCCI1	Glucocorticoid-induced transcript 1 prot	R.VPCNVEGIS*PELEK.V	S303	0.71	0.83	0.999986689	1.01	0.96	0.999993440	0.76	0.99
113263	GLCCI1	Glucocorticoid-induced transcript 1 prot	R.TSS*LDTITGPLYLTGQWPR.D	S172	1.75	0.96	0.982771698	0.67	0.97	0.815851317	1.12	1.00
57476	GRAMD1B	GRAM domain-containing protein 1B	K.SQSWYNVLS*PTYK.Q	S88	0.54	0.69	0.999961743	0.54	0.86	0.999934193	3.43	0.97
339970	GRINL1A	Glutamate receptor-like protein 1A	R.VSS*QAEDTSSSFNDLNFIDR.L	S179	1.14	0.98	0.999335838	1.26	1.00	0.999931256	1.26	0.95
339970	GRINL1A	Glutamate receptor-like protein 1A	R.VS*SQAEDTSSSFNDLNFIDR.L	S178	1.14	0.98	0.967895493	1.14	0.99	0.901727000	1.78	0.86
2870	GRK6	G protein-coupled receptor kinase 6	K.DVLDIEQFST*VK.G	T485	0.85	0.99	0.999945471	0.70	1.00	0.999975587	0.68	0.98
2870	GRK6	G protein-coupled receptor kinase 6	K.DVLDIEQFS*TVK.G	S484	0.85	0.99	0.999988701	0.70	1.00	0.999983071	0.68	1.00
2909	GRLF1	Glucocorticoid receptor DNA-binding fa	R.TSFSVGS*DDELGPIR.K	S1179	1.07	1.00	0.999993383	0.90	0.99	0.999993761	0.87	1.00
2909	GRLF1	Glucocorticoid receptor DNA-binding fa	R.AGSPLCNS*NLQDSEEDIEPSYSLFR.E	S980	1.08	0.99	0.999911495	1.01	0.98	0.999231005	0.88	0.88
2909	GRLF1	Glucocorticoid receptor DNA-binding fa	R.AGS*PLCNSNLQDSEEDIEPSYSLFR.E	S975	1.08	0.95	0.976254759	1.01	0.98	0.984428836	0.91	0.92
2969	GTF2I	General transcription factor II-I	R.T*NTPVKEDWNVR.I	T556	2.12	0.52	0.999943676	0.82	0.79	0.999894565	1.54	1.00
2969	GTF2I	General transcription factor II-I	R.TNT*PVKEDWNVR.I	T558	1.56	0.97	0.999957349	0.82	0.79	0.999980597	1.56	1.00
2969	GTF2I	General transcription factor II-I	R.SILS*PGGSCGPIK.V	S210	0.67	1.00	0.999992052	0.68	1.00	0.999991355	1.72	1.00
51512	GTSE1	G2 and S phase-expressed protein 1	R.VPQALNFS*PEESDSTFSK.S	S592	0.78	0.99	0.999994804	0.58	0.96	0.999990248	2.63	0.99
51512	GTSE1	G2 and S phase-expressed protein 1	R.ETYYLSDS*PLLGPPVGEPR.L	S152	0.57	0.97	0.952967866	0.66	0.98	0.991774060	3.79	0.97
10767	HBS1L	HBS1-like protein	R.LSS*TDSLESLLSK.N	S786	0.77	0.85	0.999153091	0.79	0.92	0.987601702	0.37	0.59
51564	HDAC7A	Histone deacetylase	R.AQS*SPAAPASLSAPEPASQAR.V	S486	1.01	0.96	0.999923262	0.83	0.99	0.999981535	0.54	0.95
92797	HELB	helicase (DNA) B	K.LSSSGAPPADFPS*PR.K	S967	0.65	0.86	0.999975206	1.14	0.92	0.999944293	0.98	0.93
124790	HEXIM2	Hexamethylene bis-acetamide-inducible	R.TQS*PGGCSAEAVLAR.K	S76	0.73	0.57	0.999988688	0.08	0.50	0.999908073	1.47	0.83
10363	HMG20A	High mobility group protein 20A	R.DSNAPKS*PLTGYVR.F	S105	1.44	0.84	0.999942713	0.54	0.97	0.999992987	1.11	0.88
3157	HMGCS1	Hydroxymethylglutaryl-CoA synthase, cy	R.LPATAAEPEAAVIS*NGEH.-	S516	1.48	1.00	0.999990878	1.00	1.00	0.999987907	1.00	1.00
3161	HMMR	Hyaluronan-mediated motility receptor	R.FNDPSGCAPS*PGAYDVK.T	S20	0.45	0.98	0.999986890	1.05	0.71	0.999985812	3.86	0.96
51155	HN1	hematological and neurological expres	K.MASNIFGT*PEENQASWAK.S	T54	0.79	0.98	0.999988443	0.84	0.94	0.999975671	2.20	0.97

90861	HN1L	Hematological and neurological expres	K.TSDIFGS*PVTATSR.L	S97	0.66	0.92	0.999992721	0.80	0.98	0.999989227	2.48	0.94
3181	HNRPA2B1	Isoform A2 of Heterogeneous nuclear rib	R.NMGGPYGGGNYGPGGSGGS*GGYGGR.S	S344	0.80	0.97	0.999993454	0.82	0.99	0.999992404	1.43	0.77
3181	HNRPA2B1	Isoform A2 of Heterogeneous nuclear rib	R.GFGDGYNGYGGGPGGNGFGGS*PGYGGC	S259	0.72	1.00	0.999994439	0.79	1.00	0.999993739	1.67	1.00
220988	HNRPA3	Heterogeneous nuclear ribonucleoprotein	R.SSGSPY*GGGYGSGGGSGGYGSR.R	Y360	0.94	0.99	0.999991564	0.87	0.97	0.999957327	1.07	0.50
220988	HNRPA3	Heterogeneous nuclear ribonucleoprotein	R.SSGS*PYGGGYGSGGGSGGYGSR.R	S358	1.17	0.99	0.999987260	0.79	1.00	0.999982472	3.08	0.97
3190	HNRPK	Heterogeneous nuclear ribonucleoprotein	K.IILDISES*PIK.G	S216	1.18	0.98	0.999942778	0.65	0.99	0.999927932	0.95	1.00
3190	HNRPK	Heterogeneous nuclear ribonucleoprotein	R.GSY*GDLGGPIITTQVTIPK.D	Y380	0.59	1.00	0.999995115	0.82	1.00	0.999993563	1.74	0.99
3190	HNRPK	Heterogeneous nuclear ribonucleoprotein	R.GS*YDGLGGPIITTQVTIPK.D	S379	0.59	0.96	0.530906814	0.89	1.00	0.478114581	1.92	0.84
3192	HNRPU	heterogeneous nuclear ribonucleoprotein	R.NFILDQT*NVSAAAQR.R	T581	0.93	0.82	0.999940283	0.95	0.89	0.999663015	1.22	0.81
11100	HNRPUL1	Heterogeneous nuclear ribonucleoprotein	R.NYILDQTNVYGS*AQR.R	S512	1.29	0.97	0.999992378	0.81	0.98	0.999994567	0.79	0.99
3315	HSPB1	Heat-shock protein beta-1	R.GPS*WDPFR.D	S15	1.69	0.91	0.999565038	0.33	0.90	0.999970521	0.13	0.93
25998	IBTK	inhibitor of Bruton's tyrosine kinase	R.SDSS*GGYNLSDIIQSPSSTGLLK.S	S993	1.28	0.96	0.999991649	0.81	0.94	0.999976083	0.66	0.95
10644	IGF2BP2	Insulin-like growth factor 2 mRNA-bindin	K.ISYIPDEEVSS*PSPQR.A	S162	0.99	0.94	0.923606824	0.79	0.99	0.939948358	1.06	0.91
3609	ILF3	Interleukin enhancer-binding factor 3	K.LFPDT*PLALDANK.K	T592	0.64	0.96	0.667880000	0.73	0.95	0.627434961	1.37	0.80
3609	ILF3	Interleukin enhancer-binding factor 3	K.VLAGETLS*VNDPPDVLDR.Q	S190	0.99	0.85	0.998765996	0.71	0.94	0.999298899	2.44	0.84
3619	INCENP	inner centromere protein antigens 135/15	R.TSSAVWNS*PPLQGAR.V	S904	1.03	0.85	0.999894369	1.02	0.95	0.852488925	0.35	0.65
3619	INCENP	inner centromere protein antigens 135/15	R.IAQVS*PGPR.D	S263	0.90	0.95	0.999976603	0.85	0.98	0.999989735	1.68	0.94
3619	INCENP	inner centromere protein antigens 135/15	R.DSPAFPDS*PWR.E	S275	0.91	0.79	0.938705273	0.70	0.94	0.447478947	3.58	0.99
9922	IQSEC1	IQ motif and Sec7 domain-containing pr	R.NS*WSPAFSNDVIR.K	S512	0.71	0.88	0.999983971	0.97	0.92	0.999994275	1.08	0.97
8660	IRS2	Insulin receptor substrate 2 insertion mut	R.SDDYMPMS*PASVSAPK.Q	S679	1.42	0.92	0.998453151	1.03	0.97	0.999925331	1.19	0.84
8660	IRS2	Insulin receptor substrate 2 insertion mut	K.S*PGEYINIDFGEPGAR.L	S915	1.15	0.62	0.999992135	0.80	0.99	0.999988886	1.35	0.99
8660	IRS2	Insulin receptor substrate 2 insertion mut	K.SSEGGVGVGPGGDEPPTS*PR.Q	S1203	1.43	0.72	0.950543217	0.77	0.96	0.999349886	1.35	0.83
3707	ITPKB	Inositol-trisphosphate 3-kinase B	R.AVLS*PGSVFSPGR.G	S43	1.07	0.87	0.999975890	0.79	0.91	0.999991420	1.32	0.81
6453	ITSN1	Intersectin-1	R.SAFPTATATGSSPS*PVLGQGEK.V	S904	1.05	0.99	0.999939122	0.89	0.99	0.999968267	0.92	0.96
284252	KCTD1	BTB/POZ domain-containing protein KC	R.S*PASPLNNQGIPTAQLTK.S	S9	1.08	0.95	0.993696646	0.75	0.96	0.998853310	1.14	0.78
10657	KHDRBS1	KH domain-containing, RNA-binding, si	R.SGS*MDPSGAHPSVR.Q	S20	0.71	0.75	0.999985791	0.79	0.70	0.999993721	0.95	0.97
10657	KHDRBS1	KH domain-containing, RNA-binding, si	R.S*GSMPSGAHPSVR.Q	S18	0.60	0.82	0.999939423	0.79	0.73	0.999989573	1.03	0.88
23248	KIAA0460	Uncharacterized protein KIAA0460	K.ASIGQS*PGLPSTTFK.L	S614	0.79	0.99	0.999975563	0.87	0.99	0.999987725	0.71	0.98
23248	KIAA0460	Uncharacterized protein KIAA0460	K.SFNYS*PNSSTSEVSSTSASK.A	S593	1.00	1.00	0.999991536	0.89	1.00	0.999988374	0.75	0.98
9847	KIAA0528	Uncharacterized protein KIAA0528	K.LSSPAAFLPACNS*PSK.E	S260	1.25	0.98	0.858420321	0.78	0.99	0.819090785	1.05	0.99
23255	KIAA0802	Uncharacterized protein KIAA0802	K.SLYGDVDS*PLPTGEAGPPSTR.E	S540	1.24	0.99	0.999981299	1.19	1.00	0.999975182	1.65	0.99
731210	KIAA0819	Uncharacterized protein KIAA0819	R.LGS*PLAVDEALR.R	S283	1.35	0.93	0.999990021	0.88	0.95	0.999820874	0.96	0.99
23379	KIAA0947	Uncharacterized protein KIAA0947	R.VPGEDGTLPTQGS*PLR.T	S255	1.45	0.62	0.999991202	0.85	0.66	0.999961403	1.40	0.80
23379	KIAA0947	Uncharacterized protein KIAA0947	R.SCSSPAVSAVSQLPLS*PK.E	S1903	2.58	0.70	0.998464168	0.57	0.86	0.999855677	6.29	0.83

284058	KIAA1267	Uncharacterized protein KIAA1267	R.ETEAAPTS*PIVPLK.S	S1082	1.31	0.99	0.998376032	0.67	0.99	0.824805754	0.60	0.99
57521	KIAA1303	Regulatory-associated protein of mTOR	R.VLDTSSLTQSAPAS*PTNK.G	S863	1.25	0.99	0.999963381	1.01	1.00	0.999971661	1.63	0.88
25962	KIAA1429	Protein virilizer homolog	R.SFLSEPS*SPGR.T	S1578	0.88	0.90	0.999851389	1.28	0.83	0.999917195	1.12	0.90
57624	KIAA1486	Uncharacterized protein KIAA1486	R.SAST*SGVPPPSVTPLR.Q	T647	0.72	0.96	0.972623958	2.48	0.51	0.986635358	1.17	0.89
57648	KIAA1522	Uncharacterized protein KIAA1522	R.GS*PSGGSTAEASDTLSIR.S	S404	1.14	0.96	0.999954557	0.73	0.82	0.999926798	0.89	0.91
57648	KIAA1522	Uncharacterized protein KIAA1522	R.TLS*PSSGYSSQSGTPTLPPK.G	S520	0.90	0.86	0.998893204	0.64	0.51	0.998670298	0.98	0.21
57648	KIAA1522	Uncharacterized protein KIAA1522	R.TLSPSSGYSSQS*GPTLPPK.G	S529	0.85	0.85	0.999871123	0.75	0.49	0.908135766	0.99	0.63
57648	KIAA1522	Uncharacterized protein KIAA1522	K.GLAGPPAS*PGK.A	S545	0.91	0.96	0.999758849	0.82	0.92	0.999924204	1.21	0.92
80728	KIAA1688	Uncharacterized protein KIAA1688	R.AELPGSSS*PLLAQPR.K	S286	0.84	0.95	0.260267115	0.87	0.80	0.804411417	1.58	0.96
10749	KIF1C	Kinesin-like protein KIF1C	R.YPPYTT*PPR.M	T1083	0.99	0.94	0.999189149	0.76	0.91	0.986746562	1.30	0.90
9493	KIF23	kinesin family member 23	R.SNS*CSSISVASCISEWEQK.I	S716	1.00	0.95	0.999988746	0.95	0.92	0.999987379	1.13	0.99
55083	KIF26B	Kinesin family member 26B	R.LIPALSLDTSS*PVR.K	S1958	0.71	0.81	0.991659605	1.29	0.94	0.548656472	6.23	0.96
24137	KIF4A	Chromosome-associated kinesin KIF4A	R.ALASNTSFFSGCS*PIEEEAH.-	S1225	1.48	1.00	0.999955613	1.00	1.00	0.999960022	1.00	1.00
3831	KLC1	Isoform N of Kinesin light chain 1	R.ASS*LNVLNVGGK.A	S543	3.67	0.88	0.999929628	0.69	1.00	0.939621616	1.00	0.98
3831	KLC1	Isoform N of Kinesin light chain 1	R.ALSAS*HTDLAH.-	S574	1.48	1.00	0.999992400	1.00	1.00	0.999975432	1.00	1.00
89953	KLC4	Kinesin light chain 4	R.AAS*LNVLNQPAAAPLQVSR.G	S590	0.95	1.00	0.999981239	0.78	1.00	0.999990433	1.17	1.00
3838	KPNA2	Importin subunit alpha-2	R.NVSSFDDATS*PLQENR.N	S62	0.63	0.99	0.950883795	0.66	0.99	0.852077608	2.62	0.94
3839	KPNA3	Importin alpha-3 subunit	R.NVPQEESEDS*DVDADFK.A	S60	1.28	0.96	0.963081783	0.91	0.97	0.987347369	1.31	0.96
65095	KRI1	Protein KRI1 homolog	R.AFVEDS*EDEDGAGEGGSSLLQK.R	S177	1.50	0.89	0.999985678	0.51	0.93	0.999991953	1.62	0.69
23367	LARP1	La-related protein 1	R.S*LPTTVPEPSPNYR.N	S766	1.51	0.99	0.728511430	1.31	1.00	0.747865503	0.58	0.78
23367	LARP1	La-related protein 1	K.GLSAS*LPDLSENWIEVK.K	S548	0.99	0.98	0.999994289	1.17	1.00	0.999993823	1.13	0.99
23367	LARP1	La-related protein 1	R.SLPTTVPEPSPNYR.N	Y776	1.25	0.99	0.998593015	0.67	1.00	0.677034360	1.26	1.00
23367	LARP1	La-related protein 1	R.SLPTTVPEPSPNYR.N	S774	0.67	1.00	0.517894187	0.66	1.00	0.475227482	1.30	0.99
23367	LARP1	La-related protein 1	R.AVT*PVPTKTEEVSNLK.T	T526	0.78	0.99	0.999993001	1.01	0.99	0.999991255	1.30	0.97
23367	LARP1	La-related protein 1	K.NTFTAWS*DEESDYEIDDR.D	S627	1.13	0.98	0.999992400	0.94	0.98	0.999994603	1.33	0.97
23367	LARP1	La-related protein 1	R.S*LPTTVPEPSPNYR.N	S766,S774	1.20	0.99	0.923136598	1.46	0.58	0.775963526	1.59	0.87
113251	LARP4	La-related protein 4	K.EQYVPPRS*PK.-	S721	1.24	0.71	0.999975037	0.85	0.84	0.998538853	1.45	0.68
113251	LARP4	La-related protein 4	R.ASTAS*PCNNNINAATAVALQEPR.K	S596	1.02	0.94	0.999969178	0.88	0.99	0.999985592	1.55	0.98
81887	LASIL	LAS1-like protein	R.MEVGPFSTGQES*PTAENAR.L	S617	1.23	0.59	0.999973403	3.73	0.63	0.999990662	4.65	0.70
3927	LASPI	LIM and SH3 domain protein 1	K.GFSVVADT*PELQR.I	T104	0.44	0.99	0.999879283	0.44	0.96	0.998605989	0.58	0.97
23592	LEMD3	LEM domain-containing protein 3	K.VLLGFSSDES*DVEASPR.D	S144	1.27	0.83	0.999911031	0.80	0.95	0.999981269	0.47	0.72
23592	LEMD3	LEM domain-containing protein 3	K.APPAPLAASEVTNSNS*AER.R	S187	0.65	0.99	0.999994246	0.62	0.98	0.999994536	2.91	0.96
51474	LIMA1	LIM domain and actin-binding protein 1	R.ETPHS*PGVEDAPIAK.V	S490	1.01	0.99	0.841417540	0.83	1.00	0.954565751	0.90	0.98
51474	LIMA1	LIM domain and actin-binding protein 1	R.ET*PHSPGVEDAPIAK.V	T487	1.03	0.92	0.999958435	0.68	0.72	0.953088997	0.90	0.98

22998	LIMCH1	LIM and calponin homology domains-co	K.S*PEPEATLTFPFLDK.M	\$718	1.41	0.98	0.999981834	0.75	1.00	0.999982795	1.00	1.00
22998	LIMCH1	LIM and calponin homology domains-co	R.CS*PTVAFVEFPSSPQLK.N	\$670	5.24	0.90	0.999910072	0.70	0.99	0.987985204	3.19	0.76
4000	LMNA	Lamin-A/C	R.SVGGG*GGGSGFDNLVTR.S	\$632	0.60	0.70	0.999988135	3.23	0.92	0.999974451	0.33	0.84
4000	LMNA	Lamin-A/C	R.SGAQASSTPLS*PTR.I	\$22	1.36	0.97	0.990737843	0.77	0.99	0.999753169	1.11	0.80
4000	LMNA	Lamin-A/C	R.S*VGGSGGGSGFDNLVTR.S	\$628	0.46	0.99	0.999994272	0.93	0.99	0.999995195	3.15	0.98
4000	LMNA	Lamin-A/C	R.SVGGSGGGG*FGDNLVTR.S	\$636	0.37	0.86	0.999992393	3.23	0.92	0.999989862	4.07	0.90
4008	LMO7	LIM domain only protein 7	R.S*WASPVYTEADGTFSR.L	\$342	2.94	0.86	0.999991455	1.51	0.97	0.999993117	0.91	0.99
4008	LMO7	LIM domain only protein 7	R.LPS*PTSPFSSLSQDQAATSK.A	\$654	1.42	0.88	0.999750676	0.95	0.95	0.999701626	1.75	0.55
4008	LMO7	LIM domain only protein 7	R.LPSPTS*PFSSLSQDQAATSK.A	\$657	1.31	0.90	0.999807000	1.11	0.95	0.999964991	2.25	0.77
144097	LOC144097	Uncharacterized protein LOC144097	R.AES*PSPAPPPGLR.G	\$308	1.41	0.72	0.999970788	0.49	0.90	0.999980200	1.01	0.98
146909	LOC146909	kinesin family member 18B	K.LQVYEGGGQPPPQDLPGS*PK.S	\$404	1.04	0.99	0.628473053	0.81	0.99	0.935559876	1.46	0.98
553158	LOC553158	Rho-GTPase-activating protein 8	K.FMS*SPSLSDLGK.R	\$10	1.09	0.91	0.999991297	0.38	0.77	0.999990602	0.86	0.96
728849	LOC728849	PREDICTED: similar to transcriptional r	K.LTPVLSL*NSPIK.G	\$597	0.98	0.95	0.784754466	1.40	0.95	0.996937345	1.07	0.98
728849	LOC728849	PREDICTED: similar to transcriptional r	K.LTPVLSNS*PIK.G	\$599	1.05	0.96	0.300105014	1.40	0.95	0.276171838	1.07	0.98
84859	LRCH3	Leucine-rich repeats and calponin homol	R.WS*GNEPTDEFSDLPLR.V	\$324	1.02	0.86	0.999989361	0.86	0.95	0.999982793	1.35	0.88
55604	LRRC16	leucine rich repeat containing 16	K.S*NDSGEEAEKEFIV.-	\$1357	1.10	0.98	0.998775625	1.11	0.98	0.998671864	1.18	0.96
57470	LRRC47	Leucine-rich repeat-containing protein 47	K.EEGS*LSDTEADAVSQQLPDTTNPAGK	\$518	1.27	0.99	0.179445633	0.83	1.00	0.999991616	0.95	0.94
57470	LRRC47	Leucine-rich repeat-containing protein 47	K.EEGSL*DTEADAVSQQLPDTTNPAGK	\$520	1.27	0.99	0.999984813	0.83	1.00	0.999982633	0.98	0.88
124801	LSM12	Protein LSM12 homolog	R.TET*PPPLASLVSK.L	T75	1.07	1.00	0.999820787	0.88	0.99	0.999986826	1.33	0.99
51599	LSR	Lipolysis-stimulated lipoprotein receptor	K.NLALS*RESLVV.-	\$643	2.79	0.88	0.997056127	0.78	0.97	0.813213763	0.75	0.95
51599	LSR	Lipolysis-stimulated lipoprotein receptor	R.S*VDALDDLTPPSTAESGSR.S	\$493	2.29	0.98	0.999953949	0.86	0.97	0.621165962	0.97	0.87
8379	MAD1L1	Mitotic spindle assembly checkpoint pro	R.AILGSYDSELTPAEYS*PQLTR.R	\$428	1.13	0.96	0.932999191	1.05	0.93	0.891250634	0.90	0.99
8567	MADD	MAP-kinase activating death domain-co	R.GT*LSDSEIETNSATSTIFGK.A	T1237	1.14	0.99	0.999980383	0.87	0.99	0.999990363	1.10	0.99
8567	MADD	MAP-kinase activating death domain-co	R.GTSL*DSEIETNSATSTIFGK.A	\$1239	1.23	0.99	0.999991173	0.87	0.99	0.999987469	1.20	0.89
4131	MAP1B	microtubule-associated protein 1B	K.AAEAGGAEQYGFLLT*PTK.Q	T1067	1.14	0.99	0.998891513	0.95	0.98	0.784313218	2.46	0.97
4133	MAP2	Microtubule-associated protein 2	K.SGTSTPTTPGSTAITPGT*PPSYSSR.T	T1605	1.62	1.00	0.789929499	0.66	1.00	0.890667076	1.41	0.98
4296	MAP3K11	Mitogen-activated protein kinase kinase	R.NVFEVGPGRD*PTFPR.F	\$524	0.23	0.90	0.998310461	0.84	0.76	0.999932742	1.54	0.75
6885	MAP3K7	Isoform 1C of Mitogen-activated protein	R.S*IQDLTVTGTEPGQVSSR.S	\$439	2.88	0.95	0.866024538	0.49	0.86	0.631629141	1.07	0.98
9053	MAP7	Microtubule-associated protein 7	R.LSSS*SATLLNSPDR.A	\$202	1.97	0.77	0.999733504	1.13	0.92	0.999844669	1.90	0.99
9053	MAP7	Microtubule-associated protein 7	K.STAALSGEAASCS*PIIMPYK.A	\$254	0.35	0.97	0.846713281	0.60	0.95	0.988599431	3.92	0.97
9053	MAP7	Microtubule-associated protein 7	K.LFVT*PPEGSSR.R	T277	0.79	0.99	0.999967822	0.72	1.00	0.999986158	3.94	1.00
9053	MAP7	Microtubule-associated protein 7	R.LQLS*PWESSVNR.L	\$219	0.63	0.98	0.999992668	0.66	1.00	0.999993448	4.98	0.80
55700	MAP7D1	Arginine/proline rich coiled-coil 1	R.LSASTASELS*PK.S	\$460	0.61	0.81	0.998636083	1.01	0.90	0.999970749	13.61	0.83
79649	MAP7D3	MAP7 domain-containing protein 3	K.NCPPS*PLPLISK.Q	\$524	0.14	0.72	0.999809333	1.47	0.83	0.999977580	0.97	0.85

2011	MARK2	MAP/microtubule affinity-regulating kin	K.VPAS*PLPGLER.K	\$456	0.81	1.00	0.999992394	0.64	1.00	0.999993213	1.48	0.98
4140	MARK3	MAP/microtubule affinity-regulating kin	R.TPVAS*THSISSAATPDR.I	\$563	1.01	0.56	0.999992464	0.84	0.56	0.999976769	0.70	0.59
4140	MARK3	MAP/microtubule affinity-regulating kin	K.GIAPAS*PMLGNASNPNA.A	\$492	0.78	0.91	0.989421791	0.87	0.97	0.999869132	1.56	0.96
23139	MAST2	Microtubule-associated serine/threonine-	R.NQSLGQS*APSLTAGLK.E	\$148	1.16	0.97	0.999989574	1.05	0.98	0.999994098	1.39	0.92
23139	MAST2	Microtubule-associated serine/threonine-	K.EQDVVTGVS*PLLFR.K	\$66	0.73	0.98	0.995214324	0.60	0.92	0.999927726	1.42	0.98
23139	MAST2	Microtubule-associated serine/threonine-	R.SWVIGS*PEILR.K	\$900	0.93	0.91	0.999960556	0.77	0.97	0.998381687	1.43	0.98
84930	MASTL	Microtubule-associated serine/threonine-	R.DYLSSS*FLCSDDDR.A	\$552	0.42	0.74	0.983708689	1.63	0.69	0.786672841	4.24	0.78
23263	MCF2L	MCF.2 cell line derived transforming seq	R.ALEQSQLPLPAPTSTS*PSR.G	\$974	1.59	0.99	0.514237843	0.83	1.00	0.672338784	1.65	0.98
8888	MCM3AP	MCM3 minichromosome maintenance d	R.SESTDLSGGLS*PSEVTAIQCK.N	\$430	1.00	0.98	0.999989151	0.70	0.97	0.999989624	1.62	0.98
10445	MCRS1	Microspherule protein 1	K.GDQVLNFS*DAEDLIDDSK.L	\$282	1.19	0.99	0.999993005	0.78	1.00	0.999994701	0.89	0.99
4204	MECP2	Methyl CpG binding protein 2	K.AETSESGSAPAVPEASAS*PK.Q	\$80	1.20	0.93	0.918552744	0.89	0.84	0.279678653	0.74	0.07
4208	MEF2C	Myocyte-specific enhancer factor 2C	R.NS*PGLLVSPGNLNK.N	\$222	1.04	0.94	0.999964760	1.43	0.99	0.999979195	2.79	0.99
4209	MEF2D	Isoform MEF2DA'B of Myocyte-specific	R.LLS*PQQPALQR.N	\$180	1.10	0.97	0.999983623	0.79	0.99	0.999978956	3.19	0.99
4236	MFAP1	Microfibrillar-associated protein 1	K.IVEPEVVGESDS*EVEGDAWR.M	\$118	1.14	0.98	0.999987552	0.69	0.98	0.999364141	1.01	0.97
4236	MFAP1	Microfibrillar-associated protein 1	R.SLAALDALNT*DDENDEEEYEAWK.V	T267	0.98	0.99	0.999993347	0.80	1.00	0.999991160	1.08	0.99
23269	MGA	PREDICTED: similar to MAX-interactin	K.GLPFYAGLS*PAGK.L	\$1457	0.88	0.74	0.984180624	0.71	0.94	0.999827739	0.74	0.78
23269	MGA	PREDICTED: similar to MAX-interactin	K.SILPYPVS*PK.Q	\$924	1.27	0.92	0.169166492	0.79	0.98	0.068329420	0.75	0.93
85377	MICALL1	Molecule interacting with Rab13	R.SPVSPGS*SSPQLQVK.S	\$619	1.05	0.98	0.999567774	0.75	0.98	0.999896120	1.01	0.98
85377	MICALL1	Molecule interacting with Rab13	R.VEQMPQAS*PGLAPR.T	\$578	0.95	0.98	0.999980233	0.73	0.96	0.999988812	1.13	0.99
4288	MKI67	antigen identified by monoclonal antibod	K.IPCES*PPELVDDTTASTK.R	\$2708	1.42	0.75	0.999982776	0.35	0.90	0.999986587	2.59	0.74
4288	MKI67	antigen identified by monoclonal antibod	K.DINTFLGT*PVQK.L	T1801	0.48	0.96	0.999927506	0.66	0.97	0.999091347	3.53	0.98
4288	MKI67	antigen identified by monoclonal antibod	K.LDLLGNLPGS*K.R	\$1937	0.58	0.95	0.999964107	0.65	0.96	0.999963830	4.13	0.93
4297	MLL	Isoform 14P-18B of Zinc finger protein F	R.NSSTPGLQVPVS*PTVPIQNQK.Y	\$3036	1.13	0.97	0.999975896	0.85	0.99	0.999979339	0.39	0.97
8777	MPDZ	Multiple PDZ domain protein	R.GSLPQLVS*PIVSR.S	\$230	1.00	0.99	0.974043384	0.51	0.98	0.965364368	0.40	0.86
8777	MPDZ	Multiple PDZ domain protein	R.TAPTALGITLSS*PTSTPELR.V	\$354	0.61	0.90	0.999604070	1.84	0.76	0.152103210	1.19	0.95
143098	MPP7	MAGUK p55 subfamily member 7	R.S*QESDGVVEYIFISK.H	\$409	0.78	0.95	0.999994218	1.00	0.86	0.999992365	0.75	0.44
103910	MRLC2	Myosin regulatory light chain	R.ATS*NVFAMFDQSQIQEFK.E	\$19	0.38	0.99	0.998388309	1.28	0.98	0.999154623	1.30	0.99
9112	MTA1	Metastasis-associated protein MTA1	K.VAPVINNGSPT*ILGK.R	T578	0.75	0.99	0.988184286	0.88	0.99	0.836392626	1.66	0.89
9112	MTA1	Metastasis-associated protein MTA1	K.VAPVINNGS*PTILGK.R	\$576	0.75	0.99	0.907643023	0.88	0.99	0.578549805	1.81	0.80
27085	MTBP	Mdm2, transformed 3T3 cell double min	K.TFVLTPELS*PGK.L	\$639	1.29	0.84	0.999587824	0.96	0.94	0.999946544	1.67	0.95
8898	MTMR2	Myotubularin-related protein 2	K.SASVVSSDSISTSADNFS*PDLR.V	\$58	0.94	0.99	0.999989601	0.71	0.99	0.999991941	0.98	0.98
57509	MTUS1	mitochondrial tumor suppressor 1	R.NSGSFPSPSIS*PR.-	\$1268	1.36	0.77	0.999739516	0.94	0.89	0.999200576	1.58	0.96
23077	MYCBP2	Probable ubiquitin ligase protein MYCB	R.VNS*GDTEVGSSLLR.H	\$3467	2.36	0.63	0.999548873	0.25	0.81	0.999657965	1.94	0.88
4673	NAP1L1	Nucleosome assembly protein 1-like 1	R.LDGLVETPTGYIES*LPR.V	\$69	1.34	0.94	0.999977720	0.81	0.93	0.999965520	0.84	0.96

4673	NAP1L1	Nucleosome assembly protein 1-like 1	R.LDGLVET*PTGYIESLPR.V	T62	0.95	1.00	0.999993445	0.76	1.00	0.999969311	1.04	1.00
89796	NAV1	neuron navigator 1	K.GQLTNIVS*PTAATTPR.I	S1000	0.97	0.95	0.999958530	0.76	0.98	0.999989282	1.55	0.84
89797	NAV2	neuron navigator 2	K.YPDVAS*PTLR.R	S1319	1.01	0.91	0.999986288	0.82	0.96	0.999992880	2.00	1.00
23310	NCAPD3	Condensin-2 complex subunit D3	R.SLGVLPFTLNSGS*PEK.T	S1384	0.78	0.97	0.973512642	0.84	0.99	0.935185698	1.32	1.00
4691	NCL	nucleolin	K.KVVVS*PTK.K	S67	1.22	0.95	0.999991179	0.78	0.98	0.999987530	1.04	0.98
4691	NCL	nucleolin	K.KVVVSPT*K.K	T69	1.19	0.88	0.999922725	0.76	0.96	0.999962481	1.33	0.69
4691	NCL	nucleolin	K.GGFVDFNS*EEDAK.A	S619	0.84	0.78	0.999978917	0.79	0.81	0.999975358	1.34	0.97
4691	NCL	nucleolin	K.VAVAT*PAKK.A	T76	0.60	0.96	0.999984179	0.77	0.92	0.999989440	2.45	0.97
4691	NCL	nucleolin	K.ALVAT*PGKK.G	T121	0.70	1.00	0.999973549	0.74	1.00	0.999989777	2.83	0.96
8202	NCOA3	Nuclear receptor coactivator 3	R.AVS*LDSPVSVGSSPPVK.N	S857	1.11	0.99	0.999988204	0.57	0.86	0.999875107	0.78	0.94
9611	NCOR1	Nuclear receptor corepressor 1	R.S*PGSISYLPSTFK.L	S2184	1.20	0.99	0.999985413	0.81	0.99	0.999991760	0.80	0.98
9612	NCOR2	Isoform TRAC-1 of Nuclear receptor corepressor 2	K.S*PGNTSQPPAFFSK.L	S2261	1.00	0.91	0.999963807	0.90	0.98	0.999940639	1.10	1.00
23327	NEDD4L	E3 ubiquitin-protein ligase NEDD4-like 1	R.S*LSSPTVTLAPLEGAK.D	S446	0.92	1.00	0.999983218	1.04	1.00	0.999993511	1.22	0.92
91754	NEK9	Serine/threonine-protein kinase Nek9	R.SST*VTEAPIAVVTSR.T	T333	1.01	0.40	0.999978728	0.96	0.98	0.999981949	0.86	0.96
91624	NEXN	Nexilin	K.TIS*QEFLTPGK.L	S365	1.11	0.99	0.999982518	0.86	1.00	0.999976554	1.05	0.98
4763	NF1	Neurofibromin	R.SNSGLATYS*PPMGPVSR.K	S864	1.01	0.90	0.999969254	0.91	0.96	0.999993366	1.36	0.95
4763	NF1	Neurofibromin	K.GSEGYLAATYPTVGQTS*PR.A	S2515	1.13	0.96	0.721490902	0.87	0.99	0.735296445	1.58	0.97
4772	NFATC1	Isoform A-beta of Nuclear factor of activated T-cells 1	R.LGLGACTLLGS*PR.H	S233	1.27	0.66	0.999983287	0.90	0.85	0.999988568	0.81	0.94
84901	NFATC2IP	NFATC2-interacting protein	R.GAADEVEVEPEPPGPVAS*R.D	S84	1.61	0.90	0.998994072	0.62	0.76	0.999670362	0.59	0.61
4774	NFIA	Nuclear factor 1	K.SVEDEMDS*PGEEPFTGQGR.S	S287	1.16	0.98	0.999988840	0.98	0.98	0.999982838	1.23	0.93
4782	NFIC	Nuclear factor 1 C-type	R.NWTEDMEGGISS*PVK.K	S323	0.73	0.98	0.999934975	1.33	0.91	0.999773404	0.42	0.99
4782	NFIC	Nuclear factor 1 C-type	K.SPFNSPS*PQDSPR.L	S339	1.14	0.80	0.999979807	0.89	0.98	0.999964675	0.74	0.99
4784	NFIX	Nuclear factor 1 X-type	K.SIDDS*EMESPVDVVFYPGTGR.S	S284	1.29	0.90	0.992633496	0.88	0.91	0.855474766	0.44	0.96
4784	NFIX	Nuclear factor 1 X-type	K.S*IDDSEMESPVDDVVFYPGTGR.S	S280	1.29	0.90	0.983038735	0.86	0.98	0.690961146	0.44	0.96
124245	NHN1	Zinc finger CCCH domain-containing protein 1	K.LGVSVS*PSR.A	S534	1.47	0.90	0.999949704	0.74	0.98	0.999988867	0.90	0.99
57224	NHSL1	PREDICTED: similar to NHS-like 1	R.S*LIYDTLVR.R	S190	0.89	0.88	0.999969964	0.93	1.00	0.999969903	1.28	0.98
57224	NHSL1	PREDICTED: similar to NHS-like 1	K.SGSS*PSQSPCSDLLEPWLP.R.S	S723	1.10	0.89	0.999884556	0.97	0.97	0.966894976	1.41	0.97
25836	NIPBL	Nipped-B-like protein	K.AITSLGGGS*PK.N	S2658	1.27	0.93	0.999983572	0.86	0.99	0.999989141	0.98	0.98
25836	NIPBL	Nipped-B-like protein	R.DVPPDILLDS*PER.K	S318	1.18	0.96	0.853200894	0.69	0.86	0.951871235	1.08	0.78
25836	NIPBL	Nipped-B-like protein	K.AAMYDIHSSPS*KDSTK.L	S352	0.89	0.79	0.999945598	0.88	0.95	0.844181497	1.08	0.81
79576	NKAP	NF-kappa-B-activating protein	R.IGELGAPEVWGLS*PK.N	S149	1.14	0.93	0.969983572	0.80	0.98	0.763534665	0.93	0.99
4820	NKTR	NK-tumor recognition protein	R.LDT*PDINIVLK.Q	T1155	0.64	0.95	0.999989469	0.91	0.92	0.999988912	0.96	0.91
9221	NOLC1	Nucleolar phosphoprotein p130	R.GGSISVQVNSIKFDS*E.-	S698	1.15	0.65	0.999993699	0.86	1.00	0.999982906	0.76	0.97
51070	NOSIP	Nitric oxide synthase interacting protein	K.ALSGTS*PDDVQPGPSVGPSPK.D	S138	2.01	0.73	0.304627857	0.51	0.90	0.997502963	1.49	0.98

51070	NOSIP	Nitric oxide synthase interacting protein	K.ALS*GTSPDDVQPGPSVGPSPK.D	S135	2.01	0.73	0.984076146	0.51	0.90	0.610461438	2.67	0.94
64710	NUCKS1	Nuclear ubiquitous casein and cyclin-dep	K.ATVTPS*PVKGGK.G	S181	1.29	1.00	0.999988439	0.83	0.99	0.999988299	0.86	0.99
64710	NUCKS1	Nuclear ubiquitous casein and cyclin-dep	K.VVDYSQFQES*DDADEDYGR.D	S19	1.13	1.00	0.999993435	0.84	1.00	0.999994753	0.98	0.99
57532	NUFIP2	Nuclear fragile X mental retardation-inte	R.NDS*WGSFDLR.A	S652	1.39	1.00	0.999990418	0.86	1.00	0.999987595	0.71	1.00
57532	NUFIP2	Nuclear fragile X mental retardation-inte	R.TS*PQVLGSILK.S	S572	0.98	0.99	0.999951197	0.89	1.00	0.998161616	0.99	0.90
57532	NUFIP2	Nuclear fragile X mental retardation-inte	K.DYEIESQNPLAS*PTNTLLGSAK.E	S629	1.12	1.00	0.999992922	1.06	1.00	0.999989480	1.22	1.00
57532	NUFIP2	Nuclear fragile X mental retardation-inte	K.DYEIESQNPLASPT*NTLLGSAK.E	T631	1.18	0.88	0.999977919	1.06	1.00	0.999984437	1.22	1.00
4926	NUMA1	Nuclear mitotic apparatus protein 1	R.TQPDGTSVPGEPAS*PISQR.L	S1757	0.75	1.00	0.998532401	0.61	0.98	0.990547502	1.92	1.00
57122	NUP107	Nuclear pore complex protein Nup107	R.SGFGEISS*PVIR.E	S11	0.40	0.93	0.999921316	0.31	0.56	0.999902052	2.28	0.98
9972	NUP153	Nuclear pore complex protein Nup153	K.NTSLPLWS*PEAER.S	S209	0.64	0.97	0.943575944	0.79	0.90	0.685415473	1.00	0.82
129401	NUP35	nucleoporin 35kDa isoform b	R.SIYDDISS*PGLGSTPLTSR.R	S100	0.82	0.99	0.996452798	0.75	0.99	0.966954592	2.81	0.98
129401	NUP35	nucleoporin 35kDa isoform b	R.SIYDDISS*PGLGST*PLTSR.R	S100,T106	0.36	0.74	0.816627185	0.91	0.86	0.424668493	4.64	0.81
4927	NUP88	Nuclear pore complex protein Nup88	R.FFTSS*TSLTLK.H	S168	1.17	0.85	0.729127051	0.64	0.66	0.531729116	0.91	0.73
4928	NUP98	nucleoporin 98kD isoform 4	K.NLNNSNLFS*PVNR.D	S612	0.89	0.98	0.999987365	0.79	0.99	0.999987547	1.08	0.92
4928	NUP98	nucleoporin 98kD isoform 4	K.NLNNS*NLFSPVNR.D	S608	0.31	0.68	0.999963863	0.87	0.99	0.999956431	1.14	0.95
5007	OSBP	Oxysterol-binding protein 1	R.TGS*NISGASSDISLDEQYK.H	S379	1.00	1.00	0.999986854	0.74	1.00	0.999978059	0.60	0.93
5007	OSBP	Oxysterol-binding protein 1	R.T*GSNISGASSDISLDEQYK.H	T377	1.00	1.00	0.999972529	0.74	1.00	0.999962699	0.69	0.80
5007	OSBP	Oxysterol-binding protein 1	R.TGSNIS*GASSDISLDEQYK.H	S382	1.24	0.95	0.999989459	0.88	0.97	0.999991230	2.12	0.63
114885	OSBPL11	Oxysterol-binding protein-related protein	R.SFSLASSNS*PISQR.R	S181	0.37	0.98	0.999929958	0.72	1.00	0.999649537	1.16	0.79
26031	OSBPL3	Isoform 1c of Oxysterol-binding protein-	K.QLMEQDASS*PSAQVIGLK.N	S372	0.56	0.96	0.998652141	1.01	0.97	0.998014724	1.26	0.78
55593	OTUD5	OTU domain containing 5	R.ATS*PLVSLYPALECR.A	S508	1.18	1.00	0.329977414	0.65	1.00	0.466719295	1.09	1.00
29763	PACSIN3	Protein kinase C and casein kinase subst	R.ALYDYAGQEADELS*FR.A	S383	1.11	0.88	0.999991806	0.60	0.94	0.999983786	5.63	0.86
5058	PAK1	Serine/threonine-protein kinase PAK 1	R.DVATSPISPENTNT*PPDALTR.N	T230	1.20	0.92	0.176295880	0.90	0.94	0.999835604	0.98	0.87
5062	PAK2	Serine/threonine-protein kinase PAK 2	K.YLS*FTPPEK.D	S141	1.65	0.99	0.999982969	1.05	1.00	0.999984543	1.08	1.00
10298	PAK4	Serine/threonine-protein kinase PAK 4	K.S*LVGTPYWMAPELISR.L	S474	1.30	0.94	0.999982714	0.79	0.99	0.999990474	1.26	0.97
23022	PALLD	palladin	K.TTSVSLTIGSS*PK.T	S401	8.40	0.90	0.999149028	0.65	0.72	0.987809922	2.82	0.87
64895	PAPOLG	Poly(A) polymerase gamma	K.S*VDAIGGESMPIPTIDTSR.K	S688	1.98	0.90	0.989709967	0.78	0.87	0.999471612	0.32	0.53
64895	PAPOLG	Poly(A) polymerase gamma	K.TVS*PPTVCTIPTVGR.N	S599	0.83	0.88	0.999989398	0.75	0.93	0.999978524	0.91	0.72
56288	PARD3	Partitioning-defective 3 homolog	K.AAIDSADCSLS*PDVDPVLAQRE	S809	1.58	0.93	0.999991233	0.59	0.96	0.999991542	0.49	0.97
56288	PARD3	Partitioning-defective 3 homolog	R.FS*PDSQYIDNR.S	S383	1.16	0.81	0.999951822	2.98	0.73	0.999903241	1.38	0.71
117583	PARD3B	Partitioning-defective 3 homolog B	K.SSS*LESLQTAVAEVR.K	S746	1.11	0.94	0.999956438	0.80	0.98	0.998693734	0.89	0.94
51585	PCF11	pre-mRNA cleavage complex II protein H	R.IDT*PPACTEESIATPSEIK.T	T1530	1.40	0.98	0.083277758	0.74	0.99	0.986099615	0.77	0.96
5128	PCTK2	Serine/threonine-protein kinase PCTAIR	K.LQINS*PPFDQPMR.R	S165	0.91	0.82	0.999947848	3.62	0.58	0.999780547	1.34	0.68
11333	PDAP1	28 kDa heat- and acid-stable phosphopro	R.QYTS*PEEIDAQLQAEK.Q	S19	0.92	0.98	0.999010006	0.83	0.97	0.708245132	1.25	0.80

5139	PDE3A	cGMP-inhibited 3',5'-cyclic phosphodiesterase 3	R.VNPVTSLSSENYTCS*DSEESSEK.D	\$408	6.94	0.87	0.953571704	0.74	0.89	0.999249091	0.99	0.77
5139	PDE3A	cGMP-inhibited 3',5'-cyclic phosphodiesterase 3	K.IS*PLSSPCSSPLQGTPASSLVSK.I	\$520	1.07	0.98	0.999961835	0.92	0.99	0.999980574	1.13	0.94
10130	PDIA6	Protein disulfide-isomerase A6 precursor	R.DGELPVEDDDIDLSD*DVLEDDLKDEL.-	\$428	1.22	1.00	0.423256681	0.89	1.00	0.999872447	0.86	0.99
5170	PDPK1	3-phosphoinositide-dependent protein kinase-1	R.ANS*FVGTAQYVSPPELLTEK.S	\$241	1.41	0.96	0.999792397	0.70	0.98	0.999644164	1.07	0.98
5208	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-bisphosphate phosphatase	R.NS*FTPLSSSNTIR.R	\$466	1.70	0.95	0.999976693	1.13	0.98	0.999962790	1.05	0.96
65979	PHACTR4	Phosphatase and actin regulator 4	R.S*LPITIEMLK.V	\$464	0.81	0.92	0.999791635	1.54	0.97	0.999953080	0.80	0.98
9767	PHF16	PHD finger protein 16	K.GVQVPAS*PDTVPQPSLR.I	\$85	1.43	0.99	0.998910432	1.08	0.92	0.999965607	1.03	0.95
5253	PHF2	PHD finger protein 2	K.DSDYVYPSLES*DEDNPIFK.S	\$882	1.20	0.99	0.999124693	0.73	0.97	0.988056835	0.74	0.99
23469	PHF3	PHD finger protein 3	K.SFS*LDEPPLFIPDNIATIR.R	\$682	1.01	0.67	0.999893698	1.07	0.93	0.412990687	2.19	0.99
7262	PHLDA2	Pleckstrin homology-like domain family	R.LSLFPAS*PR.A	\$42	0.75	0.97	0.366502220	0.86	0.98	0.630493849	4.35	0.90
23187	PHLDB1	Pleckstrin homology-like domain family	R.LS*PAYSLGSLTGASPCQSPCVQR.K	\$539	1.82	0.95	0.999636104	1.02	0.88	0.999978146	0.72	0.98
23187	PHLDB1	Pleckstrin homology-like domain family	R.ELPPLS*PSLSR.R	\$461	0.86	0.99	0.116067100	0.68	0.99	0.382731606	0.84	0.98
23187	PHLDB1	Pleckstrin homology-like domain family	K.SALLTQNGTGS*LPR.N	\$1017	0.74	0.92	0.999979206	0.89	0.94	0.999968637	1.26	0.99
90102	PHLDB2	Pleckstrin homology-like domain family	K.TSASEGNPYVSSSTLSVPAS*PR.V	\$334	0.93	1.00	0.962536743	0.69	0.98	0.802313142	0.15	0.99
90102	PHLDB2	Pleckstrin homology-like domain family	R.NFS*CGSVEFDEADLES.LR.Q	\$384	0.85	0.92	0.999986464	0.66	0.64	0.999990377	0.91	0.96
90102	PHLDB2	Pleckstrin homology-like domain family	K.EGLYLSDT*LPR.K	\$898	0.40	0.95	0.992878981	0.64	0.92	0.999976955	1.52	0.99
5585	PKN1	protein kinase N1	R.TDVSNFDEEFTGEAPTLA*PPR.D	\$916	0.99	0.96	0.999982881	0.94	0.96	0.999955390	1.02	0.97
11187	PKP3	PREDICTED: similar to Plakophilin-3	R.LSS*GFDDIDLPSAVK.Y	\$314	1.08	0.97	0.999923232	1.08	0.99	0.986693769	0.38	0.98
11187	PKP3	PREDICTED: similar to Plakophilin-3	R.LS*SGFDDIDLPSAVK.Y	\$313	1.08	0.92	0.999975156	1.08	0.99	0.999992639	0.38	0.98
11187	PKP3	PREDICTED: similar to Plakophilin-3	R.AGGLDWPEATEVS*PSR.T	\$238	0.84	0.99	0.999986957	1.08	0.99	0.999923472	1.63	1.00
5339	PLEC1	plectin 1 isoform 11	R.TSS*EDNLYLAVLR.A	\$22	1.37	0.96	0.970876638	0.67	0.98	0.998084383	1.53	0.97
59339	PLEKHA2	Pleckstrin homology domain-containing	K.APS*VASSWQPWTPVPQAGEK.L	\$349	0.90	0.58	0.999946707	0.62	0.78	0.999815668	0.37	0.98
54477	PLEKHA5	Pleckstrin homology domain-containing	R.S*VPAGLTLQSVSPQSLQGK.T	\$596	1.63	0.96	0.996561228	1.79	0.96	0.964920061	0.83	0.95
54477	PLEKHA5	Pleckstrin homology domain-containing	K.S*PTPESSTIASYVTLR.K	\$855	1.02	0.93	0.999985901	0.80	0.93	0.999976904	1.26	0.95
54477	PLEKHA5	Pleckstrin homology domain-containing	K.GLNVIGASDQSPQSLQ*PSNLR.D	\$937	4.25	0.88	0.999984615	0.73	0.96	0.999993467	1.29	0.96
54477	PLEKHA5	Pleckstrin homology domain-containing	K.GLNVIGASDQS*PLQSPSNLR.D	\$933	0.76	0.92	0.999337362	1.17	0.98	0.999506662	1.29	0.81
54477	PLEKHA5	Pleckstrin homology domain-containing	R.GVISYQT*LPR.N	\$438	0.56	1.00	0.993443420	0.77	1.00	0.999711832	1.35	0.96
54477	PLEKHA5	Pleckstrin homology domain-containing	R.TNS*MQQLEQWIK.I	\$410	0.84	0.97	0.999990997	1.46	0.98	0.999990842	1.57	0.97
54477	PLEKHA5	Pleckstrin homology domain-containing	K.GLNVIGASDQS*PLQSPSNLR.D	\$933;\$937	0.38	0.97	0.999966671	0.31	0.95	0.999988754	2.23	0.78
54477	PLEKHA5	Pleckstrin homology domain-containing	R.SVPAGLTLQSVS*PQSLQGK.T	\$607	0.66	0.98	0.998569311	0.88	0.99	0.997927426	3.05	0.96
26030	PLEKHG3	pleckstrin homology domain containing	K.GPLS*PFNSR.A	\$76	0.60	0.86	0.999987179	0.70	0.93	0.999990759	1.11	0.99
84271	POLDIP3	Polymerase delta-interacting protein 3	R.SS*PAAFINPPIGTVTPALK.L	\$127	0.79	0.87	0.999487022	0.77	0.98	0.999772087	0.65	0.68
5430	POLR2A	DNA-directed RNA polymerase II largest subunit	K.YSPTSPTYSPYS*PK.Y	\$1899	1.14	0.94	0.972436349	0.78	0.99	0.990249889	0.44	0.65
5430	POLR2A	DNA-directed RNA polymerase II largest subunit	K.YTPTSPSYSPS*SPEYTPSPK.Y	\$1849	1.14	1.00	0.999936680	0.71	0.98	0.995446114	0.46	0.92

5430	POLR2A	DNA-directed RNA polymerase II largest subunit	K.YSPTSPTYSPVYTP*SPK.Y	T1905	1.13	1.00	0.034726445	0.80	1.00	0.973181271	0.55	0.95
5430	POLR2A	DNA-directed RNA polymerase II largest subunit	K.YSPTSPTYSP*SPVYTPSPK.Y	T1898	1.07	0.83	0.978163588	0.68	0.96	0.998189208	0.55	0.98
5469	PPARB	Peroxisome proliferator-activated receptor gamma	R.SQT*PPGVATPPPIK.I	T1051	1.38	1.00	0.984795641	0.69	1.00	0.999825225	0.53	0.97
5469	PPARB	Peroxisome proliferator-activated receptor gamma	K.LPSTSDDCPAIGT*PLR.D	T805	0.56	0.90	0.999989483	2.89	0.81	0.999993563	0.94	0.98
5469	PPARB	Peroxisome proliferator-activated receptor gamma	K.SPAYTPQNLD*EESGSSIAEK.S	S1463	1.18	0.99	0.999993181	0.74	0.91	0.999984484	1.05	0.73
5469	PPARB	Peroxisome proliferator-activated receptor gamma	K.DNPAQDFSTLYGSS*PLER.Q	S664	0.93	0.87	0.999777344	0.70	0.76	0.648828381	1.59	0.93
8500	PPFIA1	Protein tyrosine phosphatase receptor type 1	R.GLAAGSAET*LPANFR.V	T1159	0.61	0.99	0.997703329	0.65	0.96	0.966211501	0.89	0.99
8541	PPFIA3	Protein tyrosine phosphatase receptor type 3	R.GEGPAIPGDT*PPPTPR.S	T714	1.15	0.97	0.711403477	0.76	0.97	0.890508979	0.83	0.95
8496	PPFIBP1	Liprin-beta-1	R.SQS*TFNPDMMSEPEFK.R	S601	0.89	0.96	0.999963184	0.54	0.98	0.999550482	1.08	0.71
8496	PPFIBP1	Liprin-beta-1	R.NSPFQIPPS*PDSK.K	S579	1.22	0.88	0.985257382	0.50	0.88	0.551220856	1.11	0.86
4659	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	K.T*GSYGALAEITASK.E	T443	0.31	0.95	0.999992568	0.68	0.98	0.999990536	1.40	0.97
4659	PPP1R12A	Protein phosphatase 1 regulatory subunit 12A	K.TGS*YGALAEITASK.E	S445	0.31	0.95	0.999991082	0.68	0.98	0.999992788	1.69	0.97
5546	PRCC	papillary renal cell carcinoma translocation	K.QITQEEDS*DEEVAPENFFSLPEK.A	S267	1.21	0.99	0.970990575	0.89	1.00	0.984237011	0.92	0.99
7799	PRDM2	PR domain zinc finger protein 2	R.ETVS*PPCFDEYK.M	S595	1.18	0.99	0.983037767	0.80	0.99	0.972928282	0.90	0.94
5565	PRKAB2	5'-AMP-activated protein kinase subunit 2	R.DLSS*SPPGPGYQEMYAFR.S	S183	1.48	0.94	0.686341057	0.70	0.99	0.951196766	0.85	0.62
5565	PRKAB2	5'-AMP-activated protein kinase subunit 2	R.DLSS*SPPGPGYQEMYAFR.S	S184	1.49	0.95	0.997889377	0.64	0.95	0.859891529	0.96	0.98
5565	PRKAB2	5'-AMP-activated protein kinase subunit 2	K.IMVGS*TDDPSVFLPSDK.L	S39	1.03	0.90	0.999991115	0.87	0.83	0.999991937	1.06	0.88
5568	PRKACG	Protein kinase, cAMP-dependent, catalytic	R.T*WTLCTPEYLPEIILSK.G	T192	1.06	1.00	0.999966574	0.86	1.00	0.999863681	1.06	1.00
5568	PRKACG	Protein kinase, cAMP-dependent, catalytic	R.TWT*LCGTPEYLPEIILSK.G	T194	1.06	0.98	0.999727542	0.74	0.99	0.999993162	1.16	1.00
5580	PRKCD	protein kinase C, delta	R.AST*FCGTPDYIAPEILQGLK.Y	T507	0.98	0.99	0.937290092	0.79	1.00	0.771751517	0.67	1.00
5580	PRKCD	protein kinase C, delta	R.S*DSASSEPVGIYQGFEEK.K	S302		0.96	0.999638947		0.96	0.999644510		0.85
25865	PRKD2	Serine/threonine-protein kinase D2	R.LGTSES*LPCTAEELSR.S	S214	0.69	0.95	0.999984777	0.48	0.88	0.999989837	0.28	0.78
25865	PRKD2	Serine/threonine-protein kinase D2	R.S*VVGTPAYLAPEVLLNQGYNR.S	S710	0.67	0.98	0.896339161	0.75	0.95	0.986529846	0.54	0.98
23683	PRKD3	Serine/threonine-protein kinase D3	R.S*VVGTPAYLAPEVLR.S	S735	0.60	1.00	0.999975000	0.86	0.99	0.993160246	0.37	0.98
23683	PRKD3	Serine/threonine-protein kinase D3	K.TIS*PSTSNNIPLMR.V	S391	1.42	1.00	0.999452891	0.71	1.00	0.999978528	0.94	0.99
23683	PRKD3	Serine/threonine-protein kinase D3	R.LS*NGSFSAPSLTNSR.G	S41	1.57	0.99	0.999986386	0.72	1.00	0.999939073	1.38	0.83
23683	PRKD3	Serine/threonine-protein kinase D3	K.SVLPTAIPAVLPAAS*PCS*SPK.T	S27;S30	0.86	0.97	0.958826484	0.86	1.00	0.941569947	1.39	0.87
23683	PRKD3	Serine/threonine-protein kinase D3	K.SVLPTAIPAVLPAASPCS*S*PK.T	S30;S31	0.90	0.97	0.971821116	0.85	1.00	0.951602419	1.41	0.87
23683	PRKD3	Serine/threonine-protein kinase D3	K.SVLPTAIPAVLPAAS*PCSS*PK.T	S27;S31	0.90	0.97	0.997370818	0.86	1.00	0.877737289	1.64	0.88
79899	PROTOR-2	Protein observed with Rictor-2	R.FMS*SPVLSLPR.F	S28	0.96	0.93	0.999985841	1.26	0.96	0.999990591	0.97	0.81
5747	PTK2	PTK2 protein tyrosine kinase 2	K.LQPQEIS*PPPTANLDR.S	S910	1.40	0.98	0.694792570	1.19	0.98	0.999860625	1.97	0.95
51495	PTPLAD1	Protein tyrosine phosphatase-like protein 1	R.WLDES*DAEMELR.A	S114	1.21	0.98	0.999993584	0.82	0.99	0.999992238	1.00	0.98
5782	PTPN12	Tyrosine-protein phosphatase non-receptor type 12	K.DVDVSEDS*PPPLPER.T	S673	1.33	0.93	0.999899019	0.78	0.97	0.999899613	1.21	0.92
80223	RAB11FIP1	Rab11 family-interacting protein 1	R.QGSS*LNLFEDVQITEPEAESK.S	S501	1.68	0.97	0.988724382	0.67	0.92	0.993077485	0.91	0.98

26056	RAB11FIP5	Rab11 family-interacting protein 5	R.SNS*SSEAVLQGEELSAQAK.V	\$395	0.70	0.89	0.999910368	1.53	0.94	0.997676552	0.62	0.90
117177	RAB3IP	RAB3A-interacting protein	K.TLVLSSTPTS*PTQEPLGGK.T	\$265	1.51	0.88	0.992649374	0.81	0.93	0.995945281	0.74	0.83
29127	RACGAP1	Rac GTPase-activating protein 1	R.S*IGSAVDQGNESIVAK.T	\$203	0.89	0.99	0.999995043	1.02	0.99	0.999994555	1.53	0.96
10111	RAD50	DNA repair protein RAD50	R.VFQT*EAELQEVISDLQSK.L	T690	1.20	0.97	0.999147288	0.64	0.97	0.999970539	3.56	0.99
5894	RAF1	RAF proto-oncogene serine/threonine-pr	K.DAVFDGSSCIS*PTIVQQFGYQR.R	\$29	1.04	0.94	0.999990264	1.22	0.95	0.999981943	0.84	1.00
10743	RAI1	Retinoic acid-induced protein 1	K.GAGGS*PVGVEEGLVNVGTGQK.L	T1374	1.14	0.97	0.999993294	0.76	0.99	0.999993382	0.94	0.99
5903	RANBP2	Ran-binding protein 2	K.SVFGT*PTLETANK.N	T1144	0.42	0.80	0.999511304	0.90	0.58	0.998871178	1.77	0.74
8498	RANBP3	Ran-binding protein 3	R.T*SSLTQFPPSQSEER.S	T124	1.25	0.72	0.444753977	1.26	0.69	0.784404456	0.12	0.81
8498	RANBP3	Ran-binding protein 3	R.TSS*LTQFPPSQSEER.S	\$126	1.27	0.80	0.898850726	1.29	0.54	0.998237983	0.74	0.74
8498	RANBP3	Ran-binding protein 3	R.TS*SLTQFPPSQSEER.S	\$125	1.25	0.76	0.696823852	1.11	0.40	0.646489213	0.92	0.80
5909	RAP1GAP	RAP1, GTPase activating protein 1	R.SFT*FGAYGGVDK.S	T9	0.46	0.74	0.999990469	1.74	0.88	0.999987637	1.51	0.81
51735	RAPGEF6	Rap guanine nucleotide exchange factor	K.GLIVYCVTS*PK.K	\$1494	1.23	0.97	0.999959471	1.14	0.96	0.999906140	1.14	0.98
65059	RAPH1	Isoform RMO1abc of Ras-associated and	R.SQS*IVSSFSEAWK.R	\$623	1.24	0.98	0.999987190	0.81	0.97	0.998191182	0.92	0.98
9462	RASAL2	RAS protein activator like 2 isoform 2	R.TVS*VPSEGFPEYPPGATK.L	\$116	1.08	0.94	0.999983139	0.96	0.94	0.999107037	0.86	0.98
9462	RASAL2	RAS protein activator like 2 isoform 2	K.ASIDSS*LENLSTASSR.S	\$803	2.85	0.63	0.996474164	1.28	0.99	0.999159301	1.20	0.85
9462	RASAL2	RAS protein activator like 2 isoform 2	K.SLTNPT*PIQQQLR.R	T620	1.24	0.91	0.999955006	1.54	0.75	0.999988086	5.37	0.96
125950	RAVER1	Ribonucleoprotein PTB-binding 1	R.LLS*PLSSAR.L	\$567	0.92	0.90	0.999966918	0.73	0.98	0.999980243	1.01	0.96
5925	RB1	Retinoblastoma-associated protein	K.TAVIPINGS*PR.T	\$249	0.07	0.90	0.999892335	21.19	0.50	0.889332321	3.58	0.82
5930	RBBP6	Retinoblastoma-binding protein 6	K.VTGTEGSSSTLVDTSTSTGGS*PVR.K	\$1277	1.04	1.00	0.999950491	0.76	0.98	0.999984160	1.00	0.97
64783	RBM15	Putative RNA-binding protein 15	R.SLS*PGGAALGYR.D	\$294	1.03	1.00	0.999987330	0.90	1.00	0.999988283	1.15	0.99
64783	RBM15	Putative RNA-binding protein 15	R.LHSYSS*PSTK.N	\$128	1.15	0.95	0.938809644	0.91	0.64	0.897864857	1.44	0.84
29890	RBM15B	RNA binding motif protein 15B	R.TFLEGDWTS*PSK.S	\$225	0.90	1.00	0.188931402	0.84	1.00	0.395575504	0.98	1.00
29890	RBM15B	RNA binding motif protein 15B	R.SLS*PVAAPPLR.E	\$267	1.38	0.98	0.999988513	0.69	0.99	0.999970046	1.02	0.98
155435	RBM33	RNA-binding protein 33	R.AADEDWDS*ELEDLLGEDLLSGK.K	\$41	1.24	0.99	0.999991456	0.90	1.00	0.999993290	0.82	0.99
10181	RBM5	RNA-binding protein 5	R.GLVAAYSGDS*DNEELVER.L	\$624	1.21	1.00	0.999993172	0.81	1.00	0.999993900	0.97	0.98
27316	RBMX	Heterogeneous nuclear ribonucleoprotein	R.DVYLS*PRDDGYSTK.D	\$208	0.66	0.89	0.999986447	1.31	0.78	0.999993682	1.08	0.99
27316	RBMX	Heterogeneous nuclear ribonucleoprotein	R.GFAFVTES*PADA.K	\$58	0.77	0.98	0.999984092	0.70	0.97	0.999861059	1.09	0.98
27316	RBMX	Heterogeneous nuclear ribonucleoprotein	K.VEQATKPS*FESGR.R	\$88	0.53	0.87	0.999964934	0.83	0.79	0.999895613	1.43	0.91
7936	RDBP	Negative elongation factor E	R.SLS*EQPVMdTATATEQAK.Q	\$51	1.33	1.00	0.999994117	0.40	1.00	0.999994581	0.53	0.91
7936	RDBP	Negative elongation factor E	K.SVWGS LAVQNS*PK.G	\$353	0.66	0.97	0.994816981	0.84	1.00	0.998719160	1.67	1.00
7936	RDBP	Negative elongation factor E	K.S*LYESFVSSDR.L	\$131	0.80	0.99	0.999982867	0.89	1.00	0.999979861	1.83	0.97
5981	RFC1	Replication factor C subunit 1	R.IIYDS*DS*ESEETLQVK.N	\$69;\$71	1.08	0.85	0.999962466	0.86	0.98	0.999981376	1.12	0.99
64864	RFXDC2	Regulatory factor X domain-containing p	R.NLS*GSTLYPVSNIPIR.S	\$1081	1.06	0.98	0.999811855	0.83	0.98	0.999965139	0.72	0.99
64864	RFXDC2	Regulatory factor X domain-containing p	R.SPTTVLFTSS*PIK.T	\$358	2.20	0.71	0.998253961	0.79	0.76	0.997670419	0.94	0.97

22999	RIMS1	Regulating synaptic membrane exocytosis	R.ASQSS*LESSTGPPCIR.S	S1680	0.76	0.74	0.996788908	1.28	0.94	0.985353394	1.36	0.99
6015	RING1	Polycomb complex protein RING1	R.TPQEAIMDGTIEIAVS*PR.S	S38	1.12	0.99	0.999993479	0.83	0.99	0.999993179	1.30	0.96
7737	RNF113A	RING finger protein 113A	R.YGVYEDENYEVGS*DDEEIPFK.C	S253	1.29	1.00	0.999994712	0.80	1.00	0.999994731	0.74	1.00
254225	RNF169	RING finger protein 169	R.VLS*PLIIK.S	S403	1.25	0.97	0.999968044	0.84	0.93	0.999069763	0.90	0.98
56254	RNF20	Ubiquitin-protein ligase BRE1A	K.ALVVPEPEPDS*NSQER.K	S138	1.09	0.95	0.998503257	0.61	0.93	0.998012299	0.62	0.50
8986	RPS6KA4	Ribosomal protein S6 kinase alpha-4	R.LEPVYSPPGS*PPPGDPR.I	S347	1.24	0.97	0.999983304	0.96	0.97	0.999970662	1.40	0.96
64121	RRAGC	Ras-related GTP-binding protein C	K.MSPNETLFLEST*NK.I	T96	1.56	0.92	0.999987363	0.68	0.98	0.999967483	0.88	0.99
6239	RREB1	RAS-responsive element-binding protein	R.ANS*GGVDLDSSGEFASIEK.M	S1167	1.02	0.99	0.999992503	1.13	0.98	0.999984812	0.70	0.91
23076	RRP1B	Ribosomal RNA processing protein 1 homolog	K.VGDGDL*AEIIPENEVSLR.R	S245	0.94	0.99	0.999980087	0.73	0.99	0.999984475	1.08	1.00
51773	RSF1	Remodeling and spacing factor 1	K.VGS*PLDYSLVDLPSTNGQS*PGK.A	S1349;S1365	1.37	0.86	0.999846605	0.89	0.91	0.999989709	0.90	0.92
51773	RSF1	Remodeling and spacing factor 1	K.VGS*PLDYSLVDLPSTNGQSPGK.A	S1349	1.21	0.88	0.999958863	0.89	0.94	0.999823087	1.32	0.87
26156	RSL1D1	Ribosomal L1 domain-containing protein	K.ATNES*EDEIPLVPIGK.K	S361	0.94	0.97	0.876693412	0.83	1.00	0.871597619	0.96	0.98
6294	SAFB	Scaffold attachment factor B1	R.SVVS*FDKVK.E	S604	0.25	0.52	0.999991719	0.26	0.63	0.999988378	1.02	0.58
9667	SAFB2	Scaffold attachment factor B2	K.VTPDIEES*LLEPENEK.I	S207	0.45	0.97	0.843886980	0.82	0.91	0.941381302	2.08	0.72
9667	SAFB2	Scaffold attachment factor B2	K.NTLETS*SLNFK.V	S194	1.05	0.83	0.999882082	0.71	0.86	0.999949545	3.22	0.95
29115	SAP30BP	SAP30-binding protein	K.GGLVS*DAYGEDDFSR.L	S43	1.08	0.99	0.999993906	0.77	0.97	0.999994352	0.87	0.98
23328	SASH1	SAM and SH3 domain-containing protein	R.TCS*FGGFDLNR.S	S407	0.71	0.78	0.999974915	1.05	0.88	0.999990335	0.73	0.34
6305	SBF1	SET-binding factor 1	R.LGLGT*LSSLSR.A	T1137	1.29	0.93	0.999992043	0.91	0.99	0.999993875	1.42	0.99
6322	SCML1	sex comb on midleg-like 1 isoform a	K.NEVYETFSYPESYS*PTLPVSR.R	S17	0.42	0.89	0.994219022	3.44	0.50	0.995958005	0.82	0.95
10389	SCML2	Sex comb on midleg-like 2	R.SVPGTTSPLVGDIS*PK.S	S590	1.34	0.99	0.922536237	0.80	0.99	0.937239557	1.06	0.99
10801	SEPT9	Septin-9	R.S*FEVEEVETPNSTPPR.R	S30	1.00	0.99	0.986535214	0.92	0.96	0.998100455	1.31	0.98
26135	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	R.TDKS*SASAPDVDDPEAFPALA.-	S391	0.92	1.00	0.999966203	1.56	0.95	0.999889714	0.52	0.96
26135	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	R.TDKS*ASAPDVDDPEAFPALA.-	S392	0.92	1.00	0.999400610	1.02	1.00	0.999828899	0.54	0.99
26135	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	R.T*DKSSASAPDVDDPEAFPALA.-	T388	0.92	1.00	0.371728692	1.02	1.00	0.975602546	0.54	0.99
26135	SERBP1	Plasminogen activator inhibitor 1 RNA-binding protein	R.FDQLFDES*DPFEVLK.A	S25	0.61	0.93	0.999992652	3.40	0.63	0.999992547	0.93	1.00
29072	SETD2	Histone-lysine N-methyltransferase SETD2	K.MEIGDTLSTAEESS*PPK.S	S131	1.22	0.97	0.999844858	0.84	0.93	0.993465171	0.95	0.89
29072	SETD2	Histone-lysine N-methyltransferase SETD2	R.QQEELPIYSS*DFEDVPNK.S	S1207	1.43	0.97	0.816365276	0.81	0.98	0.942611666	1.34	0.84
7536	SF1	Splicing factor 1	K.YACGLWGLS*PASR.K	S463	0.61	0.74	0.999980263	0.60	0.95	0.999982631	2.92	0.96
9169	SFRS2IP	SFRS2-interacting protein	K.LESS*EGEIIQTVDR.Q	S299	2.12	0.87	0.999506868	0.65	0.94	0.972150396	1.89	0.58
79834	SGK269	Tyrosine-protein kinase SGK269	K.TDQEAPNASQPT*PPPLPK.K	T1151	1.05	0.94	0.999868892	0.89	0.93	0.999940166	1.84	0.89
63898	SH2D4A	SH2 domain-containing protein 4A	R.TLS*SSAQEDIR.W	S315	0.78	0.97	0.999991430	0.53	0.98	0.999991708	0.36	0.75
23677	SH3BP4	SH3 domain-binding protein 4	R.SYS*LSELSVLQAK.S	S246	1.32	0.99	0.999993291	0.99	0.99	0.999991709	0.93	0.99
30011	SH3KBP1	SH3-domain kinase binding protein 1	R.S*IEVENDFLPVEK.T	S193	3.02	0.95	0.999980752	0.98	0.98	0.999975721	1.02	0.96
57619	SHROOM3	Protein Shroom3	R.EDS*LPEESSAPDFANLK.H	S1440	0.96	0.88	0.999106993	1.34	0.98	0.996804823	0.71	0.83

26037	SIPAIL1	Signal-induced proliferation-associated 1	K.LIDLLES*PTPESQK.S	S1549	0.49	0.98	0.999989805	35.32	0.50	0.999985031	0.61	0.98
26037	SIPAIL1	Signal-induced proliferation-associated 1	R.FLMPEAYPS*SPR.K	S161	0.66	0.87	0.999828016	0.96	0.93	0.999611591	2.34	0.86
6499	SKIV2L	superkiller viralicidic activity 2-like hom	R.ASS*LEDLVLK.E	S256	0.92	0.97	0.917923373	0.85	0.99	0.985753566	0.93	0.95
22950	SLC4A1AP	Kanadapтин	K.NWEDEDFYDS*DDDTFLDR.T	S466	1.12	0.97	0.999969095	0.82	0.99	0.999987110	1.02	0.99
9497	SLC4A7	Sodium bicarbonate cotransporter 3	R.NGILASPQS*APGNLNSK.S	S382	1.92	0.99	0.999977716	0.26	0.96	0.999976238	0.42	0.97
84138	SLC7A6OS	Solute carrier family 7, member 6 opposi	K.TSDPDVILCNS*VELIR.E	S168	0.99	0.82	0.999987972	1.08	0.82	0.999045635	0.75	0.60
6601	SMARCC2	SWI/SNF-related matrix-associated actin	K.DMDEPS*PVPNVEEVLTPK.T	S347	1.12	0.98	0.825359339	0.85	0.98	0.994121856	0.91	0.92
10051	SMC4	Structural maintenance of chromosomes	R.TES*PATAAETASEELDNR.S	S41	1.52	0.57	0.999979560	0.77	0.95	0.999986213	0.81	0.67
6607	SMN2	Isoform SMN-delta7 of Survival motor n	R.GTGQS*DDSDIWD TALIK.A	S28	0.98	0.96	0.999977796	0.92	0.86	0.999985953	0.80	0.96
10285	SMNDC1	Survival of motor neuron-related-splicing	R.SIFAS*PESVTGK.V	S201	0.56	0.77	0.999438490	0.73	0.96	0.999991855	2.88	0.92
23557	SNAPAP	SNARE-associated protein Snapin	R.AMLDSGIYPPGS*PGK.-	S133	1.19	0.53	0.997650501	0.84	0.87	0.988788030	1.51	0.75
6645	SNTB2	Beta-2-syntrophin	R.S*PSLGSDLTFATR.T	S393	1.75	0.98	0.999969238	0.62	0.99	0.999964814	0.76	0.98
6645	SNTB2	Beta-2-syntrophin	R.GPAGEAGAS*PPVR.R	S110	1.48	0.71	0.999979103	1.43	0.64	0.999978035	1.03	0.93
6651	SON	Isoform J of SON protein	K.ESDQTLAALLS*PK.E	S1697	0.73	0.93	0.999884854	0.96	0.93	0.999928413	0.77	0.94
8470	SORBS2	Sorbin and SH3 domain-containing prote	R.LGEVTGSPS*PPPR.S	S260	0.94	0.67	0.999504604	0.87	0.90	0.999967842	1.47	0.92
10174	SORBS3	Sorbin and SH3 domain-containing prote	R.LCDDGSQLPTS*PR.L	S530	1.04	1.00	0.228669387	0.69	1.00	0.903605017	1.12	1.00
10174	SORBS3	Sorbin and SH3 domain-containing prote	R.SPADPTDLGGQTS*PR.R	S563	1.10	0.93	0.999907663	0.83	0.99	0.998802841	1.16	0.99
10174	SORBS3	Sorbin and SH3 domain-containing prote	R.LCDDGSQLPT*SPR.L	T529	1.04	0.97	0.999737990	0.70	0.98	0.982559571	1.94	0.98
9825	SPATA2	Spermatogenesis-associated protein 2	R.S*VDAYDSYWESR.K	S253	0.63	0.94	0.999968327	0.84	0.94	0.999972057	0.69	0.74
56907	SPIRE1	Protein spire homolog 1	K.FLPISST*PQPER.R	T350	1.52	0.83	0.982400742	0.67	0.94	0.999946338	1.17	0.94
23350	SR140	U2-associated protein SR140	K.LYSILQGDS*PTK.W	S485	1.06	0.95	0.999737989	0.89	1.00	0.999772501	0.95	0.99
153443	SRFBP1	serum response factor binding protein 1	K.AVTIANS*PSKPSEK.D	S203	1.25	0.94	0.999975403	0.79	0.90	0.999978558	0.92	0.97
10250	SRRM1	Serine/arginine repetitive matrix protein	R.APQTSSS*PPPVR.R	S696	1.65	0.88	0.931161073	0.52	0.79	0.997712757	0.81	0.93
23524	SRRM2	Serine/arginine repetitive matrix protein	R.MAPALSGANLTS*PR.V	S2382	0.62	0.98	0.999772353	2.41	0.95	0.999985471	0.42	0.76
23524	SRRM2	Serine/arginine repetitive matrix protein	R.TPAAAAAMNLAS*PR.T	S2271	0.76	0.98	0.999993521	0.85	1.00	0.999990133	0.77	0.99
23524	SRRM2	Serine/arginine repetitive matrix protein	K.AGMSSNQSISS*PVLDAVPR.T	S1404	0.92	0.98	0.948723761	0.83	0.99	0.649326175	1.03	0.94
23524	SRRM2	Serine/arginine repetitive matrix protein	R.T*PTAPAVNLAGAR.T	T2289	0.74	0.93	0.999972160	0.76	0.97	0.999937195	1.04	0.96
23524	SRRM2	Serine/arginine repetitive matrix protein	R.ENSEFGS*PLEFR.N	S1329	0.93	0.98	0.977705817	0.85	0.99	0.996903316	1.05	0.99
23524	SRRM2	Serine/arginine repetitive matrix protein	K.MALPPQEDATAS*PPR.Q	S1179	0.95	0.98	0.963540445	0.81	0.98	0.856500557	1.09	0.95
23524	SRRM2	Serine/arginine repetitive matrix protein	K.SST*PPGESYFGVSSQLK.G	T1043	1.84	0.64	0.730919611	0.11	0.86	0.724268684	1.56	1.00
23524	SRRM2	Serine/arginine repetitive matrix protein	R.SSTGPEPPAPT*PLLAER.H	T367	0.59	0.80	0.997583046	1.24	0.95	0.999973253	2.16	0.97
23524	SRRM2	Serine/arginine repetitive matrix protein	K.EQNSALPTSS*QDEELMEVVEK.S	S1233	1.04	0.99	0.623045364	0.83	0.98	0.873826908	3.52	0.66
23648	SSBP3	Single-stranded DNA-binding protein 3	K.NS*PNNISGISNPPGTPR.D	S324	0.46	0.96	0.999952951	8.87	0.60	0.999954619	0.96	0.93
23648	SSBP3	Single-stranded DNA-binding protein 3	K.NSPNNISGISNPPGT*PR.D	T337	3.37	0.97	0.996743695	0.78	0.92	0.998157156	0.99	0.90

170463	SSBP4	single stranded DNA binding protein 4 isoform 1	K.SS*PGAVAGLSNAPGTPR.D	S320	0.11	0.90	0.999959963	1.56	0.94	0.999986373	0.97	0.99
6744	SSFA2	Sperm specific antigen 2	R.SQS*LPTTLLSPVR.V	S739	1.14	0.95	0.999799591	0.59	0.97	0.999982050	1.07	0.96
117178	SSX2IP	Afadin- and alpha-actinin-binding protein 2	R.VDDSTGTVIS*DVEEDAGELSR.E	S312	1.77	0.95	0.999984987	0.72	0.91	0.999993209	0.36	0.98
27067	STAU2	Double-stranded RNA-binding protein S	K.VISGTTLGYL*PK.D	S408	0.51	0.98	0.999891666	0.71	0.96	0.999976407	1.64	0.91
3925	STMN1	Stathmin	R.ASGQAFELIL*PR.S	S25	0.98	0.99	0.999980847	0.87	1.00	0.999969191	0.73	0.98
3925	STMN1	Stathmin	R.AS*GQAFELIL*PR.S	S16,S25	1.10	0.96	0.999987599	1.32	0.99	0.999993197	0.92	0.96
3925	STMN1	Stathmin	R.AS*GQAFELILSPR.S	S16	1.52	0.96	0.999988375	1.36	0.99	0.999992252	1.53	1.00
3925	STMN1	Stathmin	K.ESVPEFPL*PPK.K	S38	1.44	0.64	0.965950125	0.76	1.00	0.918738514	1.56	1.00
6829	SUPT5H	Transcription elongation factor SPT5	R.DVTNFTVGGFAPMS*PR.I	S666	1.00	1.00	0.953567989	0.84	1.00	0.973324514	1.34	0.97
23512	SUZ12	Polycomb protein SUZ12	K.ASMSEFLES*EDGEVEQQR.T	S546	1.09	0.98	0.999993599	0.88	0.98	0.999994096	1.06	0.99
6840	SVIL	Supervillin	R.YQT*QPVTLGEVEQVQSGK.L	T852	0.61	0.98	0.997211920	0.89	0.98	0.999991705	1.57	0.92
11346	SYNPO	Synaptopodin	K.VAS*EEEEVPLVVYLK.E	S263	1.05	0.96	0.999990155	0.71	0.98	0.999989945	0.82	0.98
11346	SYNPO	Synaptopodin	K.S*PGILGYNICPR.G	S871	0.96	0.94	0.999981724	0.85	0.99	0.999971389	0.88	0.96
11346	SYNPO	Synaptopodin	R.CPS*PTMSLPSSWK.Y	S510	1.15	0.86	0.999944119	0.84	0.97	0.999903330	0.93	0.35
11346	SYNPO	Synaptopodin	R.S*PPSYSVLYPSSDPK.S	S336	0.86	1.00	0.999988908	0.84	1.00	0.999993107	8.72	0.83
10460	TACC3	Transforming acidic coiled-coil-containing protein 3	K.NTENCDFLFS*PPEVTGR.S	S25	0.59	0.68	0.999981909	0.73	0.81	0.999977373	1.36	0.61
26115	TANC2	Tetratricopeptide repeat, ankyrin repeat domain 2	R.SCEDELSPVS*PTQGGYPSEPTR.S	S1701	1.23	1.00	0.999992850	0.69	0.99	0.999993169	1.03	0.98
26115	TANC2	Tetratricopeptide repeat, ankyrin repeat domain 2	K.DCSYGAVTS*PTSTLESR.D	S43	1.25	1.00	0.904646089	0.68	1.00	0.639484021	1.13	1.00
9882	TBC1D4	TBC1 domain family, member 4	R.SLTSS*LENIFSR.G	S570	1.86	0.99	0.961109388	1.14	0.99	0.891126920	1.39	0.98
9882	TBC1D4	TBC1 domain family, member 4	R.S*LTSSLENIFSR.G	S566	0.80	0.92	0.999986436	1.03	0.78	0.999953740	1.52	0.99
6942	TCF20	Transcription factor 20	R.SVICDIS*PLR.Q	S871	0.80	0.88	0.999603363	0.74	0.96	0.999948931	1.81	0.98
6949	TCOF1	Treacle protein	K.TSQVGAASAPAKES*PR.K	S446	1.38	0.98	0.999992117	0.76	0.98	0.999991852	0.93	0.69
6949	TCOF1	Treacle protein	K.LDSS*PSVSSTLAAK.D	S1228	1.08	0.92	0.854880225	0.71	0.73	0.999984020	0.97	0.53
7014	TERF2	Telomeric repeat-binding factor 2	K.DLVLPQTALPAS*PALK.N	S323	0.95	0.99	0.996432333	0.83	1.00	0.999818788	2.07	1.00
54386	TERF2IP	Telomeric repeat-binding factor 2-interacting protein 1	K.YLLGDAPVS*PSSQK.L	S203	0.92	1.00	0.999600206	0.87	1.00	0.999983038	1.07	1.00
7023	TFAP4	Transcription factor AP-4	R.FIQELSGSS*PK.R	S124	1.11	0.93	0.998667348	0.80	0.99	0.999864173	0.64	0.92
24144	TFIP11	Tuftelin-interacting protein 11	R.TTQSMQDFPVVDS*EEEAEFFQK.E	S210	1.31	0.98	0.999889197	0.87	0.94	0.999928806	0.53	0.57
29844	TFPT	TCF3 fusion partner	R.AGNALT*PELAPVQIK.V	T207	0.64	0.91	0.999979216	0.96	0.91	0.999834399	1.18	0.93
9967	THRAP3	Thyroid hormone receptor-associated protein 3	R.IDIS*PSTFR.K	S682	0.89	1.00	0.999991429	0.84	1.00	0.999990832	0.98	0.99
9862	THRAP4	Thyroid hormone receptor-associated protein 4	R.LLS*SNEDDANILSSPTDR.S	S862	1.02	0.99	0.999993169	0.87	0.98	0.999989654	0.43	0.99
93643	TJAP1	Tight junction-associated protein 1	R.KDS*LTQAQEQGNLLN.-	S545	1.25	0.64	0.999936970	1.11	0.99	0.999973591	0.35	0.75
93643	TJAP1	Tight junction-associated protein 1	R.GS*PEEELPLPAFEK.L	S300	1.04	0.99	0.999990203	0.84	0.97	0.999986463	1.27	0.99
7082	TJP1	Tight junction protein ZO-1	R.LSYLSAPGSEYSMYSTDS*R.H	S837	0.86	0.90	0.998018769	0.94	0.89	0.991250740	0.98	0.90
7082	TJP1	Tight junction protein ZO-1	R.LEEPTPAPSTSYS*PQADSLR.T	S968	1.01	1.00	0.999994413	0.67	0.99	0.999992179	2.21	0.94

9414	TJP2	Tight junction protein 2 (zona occludens)	K.VQVAALQAS*PPLDQDDR.A	S130	1.34	0.94	0.999981441	0.73	0.94	0.999984226	0.73	0.94
7090	TLE3	Transducin-like enhancer protein 3	K.DAPTS*PASVASSSTPSSK.T	S286	1.33	0.98	0.305815821	0.80	0.98	0.858830448	1.34	0.53
7090	TLE3	Transducin-like enhancer protein 3	R.NDAPTPGTSTT*PGLR.S	T334	1.97	0.79	0.895111658	1.01	0.95	0.999765544	3.21	0.97
7090	TLE3	Transducin-like enhancer protein 3	R.NDAPT*PGTSTTPGLR.S	T328	2.34	0.79	0.996827028	1.08	0.83	0.999938089	3.54	0.95
7091	TLE4	transducin-like enhancer protein 4	K.DAPIS*PASIASSSTPSSK.S	S292	1.41	0.92	0.996362277	0.64	0.95	0.999990458	0.85	0.96
9874	TLK1	Serine/threonine-protein kinase tousled-1	K.ISDYFEYQGGNGSS*PVR.G	S159	1.26	0.99	0.488900078	0.76	0.99	0.638388095	0.92	1.00
9874	TLK1	Serine/threonine-protein kinase tousled-1	R.SNSS*GNLHMAGLTASPTPPSSSIITY.-	S744	1.48	1.00	0.998979694	1.00	1.00	0.908704243	1.00	0.95
11011	TLK2	Serine/threonine-protein kinase tousled-1	K.ISDYFEFAGGSAPGTS*PGR.S	S99	1.26	0.94	0.996267715	0.68	0.90	0.955826868	0.78	0.98
7112	TMPO	Lamina-associated polypeptide 2 isoform	R.SHISDQS*PLSSK.R	S351	0.39	0.65	0.999907221	1.34	0.63	0.999982723	1.14	0.86
7112	TMPO	Lamina-associated polypeptide 2 isoform	R.SST*PLTISSSAENTR.Q	T160	0.77	0.98	0.411186215	0.48	0.98	0.980469759	1.19	1.00
7112	TMPO	Lamina-associated polypeptide 2 isoform	K.FQETEFLS*PPR.K	S424	0.65	0.97	0.999990546	0.65	0.99	0.999989603	3.51	0.95
10318	TNIP1	TNFAIP3-interacting protein 1	K.YLQDQLS*PLTR.Q	S403	1.03	0.93	0.999952806	3.25	0.79	0.999977808	0.84	0.74
85456	TNKS1BP1	182 kDa tankyrase 1-binding protein	K.SSGSEGSS*PNWLQALK.L	S1715	0.62	0.66	0.935820361	0.73	0.79	0.999256375	2.11	0.83
26058	TNRC15	PERQ amino acid-rich with GYF domain	R.ALSSGGISITS*PPLS*PALPK.Y	S26;S30	0.74	0.90	0.999973584	1.26	0.99	0.999965483	1.14	0.77
7145	TNS1	Tensin-1	K.EAFEEMEGTSPSS*PPPSGVR.S	S963	1.05	0.99	0.638716209	0.80	0.99	0.867128867	0.81	0.99
7145	TNS1	Tensin-1	R.T*PTQPLLESGFR.S	T1105	1.37	0.93	0.999940941	0.83	0.75	0.999942475	0.91	0.99
7145	TNS1	Tensin-1	R.TVGTNTPPS*PGFGR.R	S1192	1.17	0.99	0.999990780	0.83	0.99	0.999462487	0.97	1.00
7145	TNS1	Tensin-1	K.VATTPGS*PSLGR.H	S1269	0.06	0.90	0.814038868	0.83	0.99	0.874852044	0.99	1.00
7145	TNS1	Tensin-1	R.SQS*FSEAEPQLPPAPVR.G	S621	0.76	0.97	0.958802262	0.90	0.98	0.976150648	1.67	0.86
7145	TNS1	Tensin-1	R.S*QSFSEAEPQLPPAPVR.G	S619	0.74	0.97	0.973322315	0.90	0.98	0.965416373	1.68	0.75
7153	TOP2A	DNA topoisomerase 2-alpha	K.SVVS*DLEADDVK.G	S1377	1.10	0.96	0.999990098	0.78	0.98	0.999991257	1.27	0.98
7153	TOP2A	DNA topoisomerase 2-alpha	K.TQMAEVLPS*PR.G	S1213	1.01	0.94	0.999944838	0.68	0.99	0.989497071	3.04	1.00
7155	TOP2B	Isoform Beta-1 of DNA topoisomerase 2	K.VVEAVNSDS*DSEFGIPK.K	S1524	1.78	0.91	0.999986159	1.05	0.98	0.999987163	0.86	0.98
7158	TP53BP1	Tumor suppressor p53-binding protein 1	K.NS*PEDLGLSLTGDSCK.L	S500	1.23	0.96	0.999990978	0.86	0.97	0.999983126	1.13	0.90
7158	TP53BP1	Tumor suppressor p53-binding protein 1	R.EQYGLGPYEAVT*PLTK.A	T1609	0.78	0.67	0.241585794	0.48	0.79	0.967349223	1.24	0.45
7158	TP53BP1	Tumor suppressor p53-binding protein 1	R.STPFIVPSS*PTEQEGR.Q	S380	1.22	1.00	0.595865799	0.76	1.00	0.924223842	1.25	0.99
7158	TP53BP1	Tumor suppressor p53-binding protein 1	R.ETAVPGPLGIEDISPNS*PDDK.S	S1430	0.97	0.92	0.998274534	0.78	0.96	0.997834907	2.20	0.94
7172	TPMT	Thiopurine S-methyltransferase	R.TSLDIEEYS*DTEVQK.N	S14	1.06	0.87	0.999943091	0.16	0.50	0.999983400	1.35	0.90
22974	TPX2	Hepatocellular carcinoma-associated anti	K.SSDQPLTVPVS*PK.F	S738	0.92	0.96	0.995987486	0.79	1.00	0.747042283	1.92	0.99
22974	TPX2	Hepatocellular carcinoma-associated anti	K.SVAEGLSGS*LVQEPFLATEK.R	S654	0.50	0.99	0.999991906	0.58	0.91	0.999992491	3.05	0.99
9618	TRAF4	TNF receptor-associated factor 4	R.GS*LDESSLGFGYPK.F	S426	1.28	0.99	0.999992267	1.66	1.00	0.999993289	1.68	0.75
10906	TRAFD1	TRAF-type zinc finger domain-containin	R.ALPSLNTGSSS*PR.G	S327	1.12	0.92	0.878206811	0.83	0.98	0.911643033	1.02	0.98
91107	TRIM47	Tripartite motif-containing protein 47	R.GGIPAS*PIDPFQSR.L	S588	1.42	0.93	0.975302387	0.94	0.89	0.972114498	0.34	0.88
7204	TRIO	Triple functional domain protein	R.AGAAS*PLNSPLSSAVPSLGK.E	S2396	1.01	0.97	0.999867918	1.10	0.96	0.999978795	0.89	0.91

9320	TRIP12	Thyroid receptor-interacting protein 12	R.SES*PPAELPSLR.R	\$312	1.21	1.00	0.999557838	0.78	1.00	0.999843822	0.99	1.00
7227	TRPS1	zinc finger transcription factor TRPS1	K.TDLLVNDNPDAPLS*PELQDFK.C	\$216	1.26	0.89	0.999982691	1.07	0.84	0.999912237	0.80	0.97
7272	TTK	Dual specificity protein kinase TTK	R.VPVNLLNS*PDCDVK.T	\$281	0.95	0.95	0.999986211	0.70	0.92	0.999992533	2.49	0.90
26043	UBXD7	UBX domain-containing protein 7	R.SESLIDASEDS*QLEAAIR.A	\$288	0.61	0.94	0.999987311	0.56	0.96	0.999959201	3.37	0.98
7353	UFD1L	ubiquitin fusion degradation 1-like isoform 1	R.FVAFSGEGQS*LR.K	\$299	1.08	0.91	0.999970185	0.78	0.94	0.999889178	0.29	0.93
8408	ULK1	Serine/threonine-protein kinase ULK1	K.TPS*SQNLLALLAR.Q	\$638	1.05	0.83	0.999946441	0.46	0.68	0.999834663	2.08	0.97
7374	UNG	Uracil-DNA glycosylase	K.TLYSFFSPS*PAR.K	\$14	0.62	0.86	0.999672474	0.76	0.90	0.973724578	1.55	0.98
85451	UNK	RING finger protein unkempt homolog	R.NSSLGSPSNLCGS*PPGSIR.K	\$385	1.50	0.98	0.999978072	0.80	0.98	0.998891160	1.38	0.98
5976	UPF1	Regulator of nonsense transcripts 1	K.SQIDVALS*QDSTYQGER.A	\$1107	0.98	0.90	0.999993043	1.11	0.86	0.999994737	0.99	0.94
7398	USP1	Ubiquitin carboxyl-terminal hydrolase 1	R.ASEIDQVVPAQSS*PINCEK.R	\$67	1.11	1.00	0.956345228	0.87	0.99	0.460260982	1.43	0.97
9100	USP10	Ubiquitin carboxyl-terminal hydrolase 10	K.YSPPAIS*PLVSEK.Q	\$370	0.96	0.97	0.772531727	1.16	0.95	0.951904381	1.57	0.72
23358	USP24	Ubiquitin carboxyl-terminal hydrolase 24	R.TIS*AQDTLAYATALLNEK.E	\$1811	0.95	0.99	0.999993308	0.87	0.99	0.999971836	1.40	1.00
84132	USP42	Ubiquitin specific protease 42	R.DSALAEAPEGLS*PAPPAR.S	\$856	0.39	0.94	0.999982689	0.70	0.94	0.998223893	0.94	0.96
9712	USP6NL	USP6 N-terminal-like protein	R.IEVLPVDTGAGGYSGNSGS*PK.N	\$716	0.93	1.00	0.997488056	0.98	0.99	0.996370554	1.31	0.99
7410	VAV2	VAV2 guanine nucleotide exchange factor 2	K.FTS*PADLDASGAGPGPK.M	\$566	3.38	0.98	0.999277590	0.36	0.77	0.995671629	2.07	0.72
51231	VRK3	Serine/threonine-protein kinase VRK3	R.LSLFSDGDSS*ESEDTLSSSER.S	\$83	2.44	0.55	0.990952923	0.65	0.88	0.998869053	4.26	0.66
23063	WAPAL	Wings apart-like protein homolog	K.VEEESTGDPFGFDS*DDESLPVSSK.N	\$77	1.27	0.99	0.999183011	0.88	1.00	0.326206353	0.88	0.83
54521	WDR44	WD repeat-containing protein 44	K.LTQTS*STEQLNVLETETEVLNK.E	\$161	1.37	0.99	0.561340764	1.14	0.99	0.458854479	1.42	0.98
54521	WDR44	WD repeat-containing protein 44	K.LTQTSS*TEQLNVLETETEVLNK.E	\$162	1.38	0.99	0.744621029	1.17	0.99	0.737538574	1.52	0.98
284403	WDR62	WD repeat-containing protein 62	R.S*ISLGDSEGPVATLAQPLR.R	\$1226	1.38	0.99	0.999984375	0.80	0.99	0.999963905	1.13	1.00
284403	WDR62	WD repeat-containing protein 62	R.SIS*LGDSEGPVATLAQPLR.R	\$1228	1.38	0.99	0.999992459	0.81	0.98	0.999991627	1.32	0.98
55135	WDR79	WD repeat protein 79	R.EGDPVLSLSTPLETEFGS*PSELS*PR.I	\$85,S90	1.28	0.92	0.999965376	0.77	0.98	0.999990045	1.00	0.96
55135	WDR79	WD repeat protein 79	R.VFPEPTES*GDEGEELGLPLLSTR.H	\$491	1.36	0.99	0.999994589	0.76	0.99	0.999993204	1.02	0.98
55135	WDR79	WD repeat protein 79	R.EGDPVLSLSTPLETEFGS*PSELS*PR.I	\$85	1.88	0.81	0.095202506	0.56	0.93	0.999980373	1.31	0.98
7468	WHSC1	Wolf-Hirschhorn syndrome candidate 1 protein	K.SSSPS*ASLTENELLWEPTPVK.L	\$620	1.02	0.75	0.999972663	0.73	0.95	0.937917113	1.09	0.77
58525	WIZ	Widely-interspaced zinc finger-containing protein	K.TPLALAGS*PTPK.N	\$996	0.98	0.69	0.999959843	0.66	0.56	0.999944672	0.99	0.99
7515	XRCC1	X-ray repair cross-complementing protein 1	R.AIGSTSKPQES*PK.G	\$241	1.05	0.90	0.999891154	0.72	0.88	0.999966274	1.61	0.97
55689	YEATS2	YEATS domain-containing protein 2	K.IVPQSQVNPES*PGK.S	\$447	1.85	0.72	0.972054458	0.84	0.96	0.993394208	0.71	0.83
79693	YRDC	YrdC domain-containing protein, mitochondrial	R.LPGSGAVQAAS*PER.A	\$60	0.86	0.89	0.999970760	0.54	0.90	0.999978094	1.32	0.98
91746	YTHDC1	YTH domain-containing protein 1	R.GIS*PIVFDR.S	\$308	0.79	0.99	0.999988983	0.83	0.99	0.999985756	1.09	1.00
55249	YY1AP1	YY1 associated protein	K.LEPQELS*PLSATVFPK.V	\$711	0.78	0.93	0.998471747	1.07	0.95	0.997698624	1.14	0.97
51341	ZBTB7A	Zinc finger and BTB domain-containing protein 7A	R.GGAPDPSPGATATPGAPAQPS*SPDAR.R	\$525	1.40	0.98	0.032066059	0.74	0.99	0.999981385	1.18	0.98
51341	ZBTB7A	Zinc finger and BTB domain-containing protein 7A	R.GGAPDPSPGATATPGAPAQPS*PDAR.R	\$526	1.40	0.98	0.999526626	0.74	0.99	0.998800867	1.18	0.98
730411	ZBTB8	BTB/POZ and zinc-finger domain-containing protein 8	R.SSFYSGGWQEGSSS*PR.S	\$161	1.16	0.93	0.999979829	0.88	0.96	0.998129677	1.59	0.69

23091	ZC3H13	Zinc finger CCCH domain-containing pr	K.TSAVSS*PLLDQQR.N	\$242	0.72	0.89	0.999226884	1.79	0.90	0.999932735	0.28	0.66
23091	ZC3H13	Zinc finger CCCH domain-containing pr	R.SLS*PSHLTEDR.Q	\$877	1.23	0.94	0.999977266	0.83	0.85	0.999978476	1.81	0.87
56829	ZC3HAV1	Zinc finger CCCH type antiviral protein	R.AS*LEDAPVDDLTR.K	\$284	1.28	0.99	0.999986937	1.08	0.99	0.999990605	1.29	0.93
56829	ZC3HAV1	Zinc finger CCCH type antiviral protein	R.SS*LGLSQTPEAVTTR.K	\$387	1.40	0.94	0.999990851	1.01	1.00	0.999973719	1.60	1.00
56829	ZC3HAV1	Zinc finger CCCH type antiviral protein	K.TVFS*PTLPAAR.S	\$378	0.85	1.00	0.999987265	0.51	1.00	0.999984057	1.63	0.76
56829	ZC3HAV1	Zinc finger CCCH type antiviral protein	R.VALVND*LSDVTSTSSR.V	\$492	0.97	0.95	0.999989848	0.43	0.85	0.999925319	2.79	0.81
51530	ZC3HC1	Zinc finger C3HC-type protein 1	R.SMGTDTPGLEVPSS*PLR.K	\$396	1.16	0.98	0.989218295	0.92	0.95	0.906126987	0.95	0.99
51530	ZC3HC1	Zinc finger C3HC-type protein 1	R.LPLVPES*PR.R	\$321	1.30	0.97	0.999935053	0.81	0.97	0.998707334	1.22	0.98
25921	ZDHHC5	Probable palmitoyltransferase ZDHHC5	R.GDS*LKEPTSIAESSR.H	\$380	1.14	0.90	0.999933289	0.68	0.95	0.999977875	0.94	0.98
25921	ZDHHC5	Probable palmitoyltransferase ZDHHC5	R.GVGS*PEPGPTAPYLGR.S	\$621	0.99	0.99	0.999967703	0.42	1.00	0.999982427	1.58	0.74
9839	ZEB2	Zinc finger E-box-binding homeobox 2	R.AYLSITPQGYSDSEER.E	\$1122	1.07	0.23	0.999552571	2.00	0.77	0.999587206	1.45	0.88
23613	ZMYND8	Protein kinase C-binding protein 1	K.ELSESVQQSTPVPPLIS*PK.R	\$547	1.47	0.99	0.999908138	0.81	1.00	0.999908183	0.81	0.97
49854	ZNF295	Zinc finger protein 295	K.IQPLEPDS*PTGLSENTPATEK.L	\$1003	1.44	0.99	0.998930452	0.86	1.00	0.998851881	0.70	0.96
49854	ZNF295	Zinc finger protein 295	R.S*LSMDSQVPVYSPSIDLK.S	\$343	1.17	0.95	0.995855529	0.78	0.98	0.969222151	0.74	0.99
24149	ZNF318	Zinc finger protein 318	R.YISQEEGPLS*PFLGQLDEDYR.T	\$214	1.37	0.87	0.999991535	0.63	0.94	0.999968444	0.78	0.98
58499	ZNF462	zinc finger protein 462	K.LANDFPLDLS*PVK.K	\$688	1.35	0.94	0.974248008	0.71	0.93	0.999915348	1.28	0.94
9640	ZNF592	Zinc finger protein 592	K.GSPSVAASS*PPAIPK.V	\$368	7.99	0.90	0.999854755	0.77	0.91	0.999953104	1.13	0.93
23060	ZNF609	zinc finger protein 609	R.FCDS*PTSDEMNR.N	\$358	1.36	0.82	0.999891848	0.67	0.93	0.999988745	0.58	0.63
23060	ZNF609	zinc finger protein 609	K.IYSFTDNAPS*PSIGGSSR.L	\$804	0.89	0.95	0.999374031	0.81	0.96	0.999718944	1.51	0.98
23060	ZNF609	zinc finger protein 609	K.APS*LTDLVK.S	\$1055	1.38	0.78	0.999793481	0.69	0.95	0.999985279	1.56	0.97
7791	ZYX	Zyxin	R.S*PGAPPLTLK.E	\$344	0.85	0.99	0.999986099	0.73	0.98	0.999973187	1.76	0.99

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