Supplementary Table S2

Category	Term	Count	%	PValue	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
UP_KEYWORDS	Transport	76	17.15575621	4.808E-07	437	1980	20568	1.806587615	0.000182687
GOTERM_BP_DIRECT	GO:0043161~proteasome-mediated ubiquitin-dependent protein catabolic process	19	4.288939052	2.84869E-06	418	201	16787	3.796246043	0.005887932
GOTERM_BP_DIRECT	GO:0070979~protein K11-linked ubiquitination	8	1.805869074	3.20595E-06	418	27	16787	11.89934432	0.006623907
GOTERM_CC_DIRECT	GO:0005680~anaphase-promoting complex	7	1.58013544	1.14224E-05	427	23	18202	12.97362794	0.004785935
GOTERM_BP_DIRECT	GO:0051439~regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	7	1.58013544	1.59822E-05	418	23	16787	12.22269607	0.032588619
GOTERM_CC_DIRECT	GO:0005829~cytosol	115	25.95936795	2.08675E-05	427	3397	18202	1.44309037	0.008726134
UP_KEYWORDS	Disease mutation	82	18.51015801	0.000101353	437	2539	20568	1.520063666	0.037783779
GOTERM_BP_DIRECT	GO:0051437~positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	10	2.257336343	0.000108034	418	76	16787	5.2842483	0.200657402
UP_KEYWORDS	Glycoprotein	130	29.34537246	0.000156275	437	4557	20568	1.342687514	0.057660153
INTERPRO	IPR005828:General substrate transporter	7	1.58013544	0.000184695	430	37	18593	8.180452546	0.162800203
UP_SEQ_FEATURE	mutagenesis site	73	16.4785553	0.000198153	435	2191	20063	1.53669295	0.253163454
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	123	27.76523702	0.000282843	435	4234	20063	1.33986448	0.340772884
UP_KEYWORDS	Alternative splicing	261	58.91647856	0.000343625	437	10594	20568	1.159554499	0.122431314
GOTERM_BP_DIRECT	GO:0051436~negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	9	2.031602709	0.000367174	418	71	16787	5.090740616	0.532937107
INTERPRO	IPR020846:Major facilitator superfamily domain	12	2.708803612	0.000385061	430	139	18593	3.732909486	0.309610798
UP_SEQ_FEATURE	topological domain:Cytoplasmic	103	23.25056433	0.000459525	435	3456	20063	1.374580274	0.49187882
UP_KEYWORDS	Membrane	192	43.34085779	0.000467292	437	7420	20568	1.217889679	0.162733154
UP_KEYWORDS	Phosphoprotein	210	47.40406321	0.000491216	437	8250	20568	1.19805284	0.170314097
GOTERM_BP_DIRECT	GO:0006810~transport	21	4.740406321	0.000499408	418	350	16787	2.409617225	0.644962024
UP_KEYWORDS	Growth factor	11	2.483069977	0.000517257	437	132	20568	3.922196796	0.178487718
UP_KEYWORDS	Ion transport	28	6.320541761	0.000589573	437	640	20568	2.059153318	0.200767924
UP_KEYWORDS	Transferase	56	12.64108352	0.000692783	437	1666	20568	1.582062573	0.231526127
GOTERM_BP_DIRECT	GO:0031145~anaphase-promoting complex-dependent catabolic process	9	2.031602709	0.000757962	418	79	16787	4.575222579	0.792339543
UP_SEQ_FEATURE	domain:Laminin G-like 5	4	0.902934537	0.0007663	435	9	20063	20.49859515	0.676706054
GOTERM_BP_DIRECT	GO:0001504~neurotransmitter uptake	4	0.902934537	0.000776561	418	8	16787	20.08014354	0.800199403
GOTERM_MF_DIRECT	GO:0031625~ubiquitin protein ligase binding	18	4.063205418	0.000953045	414	284	16313	2.497397428	0.465003712
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	90	20.31602709	0.001109897	427	2785	18202	1.377553723	0.372753349
UP_SEQ_FEATURE	metal ion-binding site:Calcium	8	1.805869074	0.001380431	435	77	20063	4.791879385	0.869290677
UP_SEQ_FEATURE	domain:Laminin G-like 6	3	0.677200903	0.001380539	435	3	20063	46.12183908	0.869311591
UP_KEYWORDS	Acetylation	98	22.12189616	0.001428358	437	3432	20568	1.343969532	0.41909259
SMART	SM00194:PTPc	6	1.354401806	0.001483889	233	37	10071	7.00916367	0.262451314
UP_KEYWORDS	Ligand-gated ion channel	8	1.805869074	0.001538854	437	80	20568	4.706636156	0.443013846
GOTERM_BP_DIRECT	GO:0007589~body fluid secretion	4	0.902934537	0.001603465	418	10	16787	16.06411483	0.964086782
INTERPRO	IPR000242:Protein-tyrosine phosphatase, receptor/non-receptor type	6	1.354401806	0.0017123	430	38	18593	6.827294982	0.807689635
UP_KEYWORDS	Ubl conjugation	57	12.86681716	0.001808295	437	1778	20568	1.508876608	0.497306318
GOTERM_BP_DIRECT	GO:0097112~gamma-aminobutyric acid receptor clustering	3	0.677200903	0.001816403	418	3	16787	40.16028708	0.976920889
BBID	94.E2F_transcriptional_activity_cell_cycle	4	0.902934537	0.00183103	17	7	388	13.04201681	0.037755673
INTERPRO	IPR016130:Protein-tyrosine phosphatase, active site	8	1.805869074	0.001842782	430	76	18593	4.551529988	0.830413358
GOTERM_BP_DIRECT	GO:0007165~signal transduction	46	10.38374718	0.00205562	418	1163	16787	1.588455035	0.985957766
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	51	11.51241535	0.002323359	427	1417	18202	1.534233852	0.623540964
UP_SEQ_FEATURE	active site:Phosphocysteine intermediate	8	1.805869074	0.002614003	435	86	20063	4.290403635	0.978836307
UP_KEYWORDS	Ubl conjugation pathway	27	6.094808126	0.002810099	437	678	20568	1.874324133	0.65676533
SMART	SM00404:PTPc_motif	7	1.58013544	0.003182216	233	63	10071	4.802575107	0.479723305
INTERPRO	IPR003595:Protein-tyrosine phosphatase, catalytic	7	1.58013544	0.003263997	430	63	18593	4.804392765	0.956937399
UP_SEQ_FEATURE	short sequence motif:Nuclear localization signal	17	3.837471783	0.003545391	435	344	20063	2.279276931	0.994655254
GOTERM_BP_DIRECT	GO:0007091~metaphase/anaphase transition of mitotic cell cycle	3	0.677200903	0.003573049	418	4	16787	30.12021531	0.999400968
GOTERM_BP_DIRECT	GO:0030534~adult behavior	5	1.128668172	0.003637878	418	26	16787	7.723132131	0.999476552
SMART	SM00294:4.1m	4	0.902934537	0.003639952	233	14	10071	12.34947885	0.526475441
INTERPRO	IPR003585:Neurexin/syndecan/glycophorin C	4	0.902934537	0.00367374	430	14	18593	12.35415282	0.971005406
UP_SEQ_FEATURE	domain:Laminin G-like 4	4	0.902934537	0.003768661	435	15	20063	12.29915709	0.996157854
GOTERM_CC_DIRECT	GO:0098793~presynapse	7	1.58013544	0.004090493	427	65	18202	4.590668348	0.821207684
UP_KEYWORDS	Nucleotide-binding	55	12.41534989	0.005167076	437	1787	20568	1.448600943	0.860344848
UP_KEYWORDS	Hydrolase	52	11.73814898	0.005255583	437	1669	20568	1.466417496	0.864987519
INTERPRO	IPR005829:Sugar transporter, conserved site	5	1.128668172	0.0053704	430	31	18593	6.97411853	0.994373387
SMART	SM00831:SM00831	4	0.902934537	0.005412881	233	16	10071	10.80579399	0.671314763
INTERPRO	IPR023298:P-type ATPase, transmembrane domain	4	0.902934537	0.005461824	430	16	18593	10.80988372	0.994849574
UP_KEYWORDS	Angiogenesis	9	2.031602709	0.005462365	437	126	20568	3.361882968	0.87524316
GOTERM_BP_DIRECT	GO:0015695~organic cation transport	4	0.902934537	0.005543643	418	15	16787	10.70940989	0.99999011
GOTERM_MF_DIRECT	GO:0097109~neuroligin family protein binding	3	0.677200903	0.006078276	414	5	16313	23.64202899	0.981675505
KEGG_PATHWAY	hsa04110:Cell cycle	11	2.483069977	0.006184439	222	124	6910	2.761188608	0.771556586
INTERPRO	IPR006068:Cation-transporting P-type ATPase, C-terminal	4	0.902934537	0.006519935	430	17	18593	10.17400821	0.998150267
UP_KEYWORDS	Disulfide bond	93	20.99322799	0.006675555	437	3394	20568	1.289679324	0.92154387
GOTERM_CC_DIRECT	GO:0016020~membrane	70	15.8013544	0.00677677	427	2201	18202	1.355717595	0.942497756
KEGG_PATHWAY	hsa05218:Melanoma	8	1.805869074	0.007285578	222	71	6910	3.507169141	0.824534851
INTERPRO	IPR004014:Cation-transporting P-type ATPase, N-terminal	4	0.902934537	0.007691627	430	18	18593	9.60878553	0.999405594
GOTERM_MF_DIRECT	GO:0022857~transmembrane transporter activity	6	1.354401806	0.007757488	414	49	16313	4.824903875	0.993956388
KEGG_PATHWAY	hsa05166:HTLV-I infection	17	3.837471783	0.007811076	222	256	6910	2.066969313	0.845310367
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	11	2.483069977	0.008309516	414	162	16313	2.67553826	0.99580481
GOTERM_BP_DIRECT	GO:0030168~platelet activation	9	2.031602709	0.008373881	418	116	16787	3.115884343	0.999999973
GOTERM_MF_DIRECT	GO:0005001~transmembrane receptor protein tyrosine phosphatase activity	4	0.902934537	0.008412087	414	17	16313	9.271383916	0.996080026
GOTERM_BP_DIRECT	GO:0007269~neurotransmitter secretion	6	1.354401806	0.008493135	418	51	16787	4.724739657	0.999999979
UP_SEQ_FEATURE	domain:Laminin G-like 3	4	0.902934537	0.008716487	435	20	20063	9.224367816	0.999997491
UP_SEQ_FEATURE	disulfide bond	82	18.51015801	0.009855423	435	2917	20063	1.296534386	0.999999539
GOTERM_BP_DIRECT	GO:0007050~cell cycle arrest	10	2.257336343	0.009901327	418	144	16787	2.788908825	0.999999999
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	18	4.063205418	0.010649461	418	367	16787	1.969714353	1
UP_SEQ_FEATURE	metal ion-binding site:Calcium; via carbonyl oxygen	5	1.128668172	0.010674906	435	40	20063	5.765229885	0.999999864
UP_KEYWORDS	Transcription	68	15.34988713	0.010767927	437	2395	20568	1.336330934	0.983657754
UP_KEYWORDS	Metal-binding	97	21.89616253	0.011201506	437	3637	20568	1.255275521	0.986165527
GOTERM_BP_DIRECT	GO:0035335~peptidyl-tyrosine dephosphorylation	8	1.805869074	0.011681661	418	99	16787	3.245275724	1
INTERPRO	IPR000387:Protein-tyrosine/Dual specificity phosphatase	7	1.58013544	0.011692541	430	82	18593	3.691179807	0.999987805
GOTERM_BP_DIRECT	GO:0050798~activated T cell proliferation	3	0.677200903	0.011901113	418	7	16787	17.21155161	1
GOTERM_BP_DIRECT	GO:0006469~negative regulation of protein kinase activity	8	1.805869074	0.012301407	418	100	16787	3.212822967	1
GOTERM_MF_DIRECT	GO:0015101~organic cation transmembrane transporter activity	3	0.677200903	0.012342236	414	7	16313	16.88716356	0.999710364
UP_KEYWORDS	Transcription regulation	66	14.89841986	0.012576115	437	2328	20568	1.334355611	0.991845848
GOTERM_BP_DIRECT	GO:0006470~protein dephosphorylation	9	2.031602709	0.012812125	418	125	16787	2.89154067	1
UP_SEQ_FEATURE	topological domain:Extracellular	78	17.60722348	0.013013224	435	2787	20063	1.290815733	0.999999996
GOTERM_BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	6	1.354401806	0.013422708	418	57	16787	4.22739864	1
GOTERM_MF_DIRECT	GO:0004725~protein tyrosine phosphatase activity	8	1.805869074	0.013530029	414	100	16313	3.152270531	0.999868472
GOTERM_CC_DIRECT	GO:0016323~basolateral plasma membrane	11	2.483069977	0.014214489	427	190	18202	2.467915691	0.997553074
GOTERM_BP_DIRECT	GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process	10	2.257336343	0.0143124	418	153	16787	2.624855365	1
UP_KEYWORDS	DNA-binding	59	13.31828442	0.014500832	437	2055	20568	1.351296998	0.996115102
GOTERM_BP_DIRECT	GO:0006511~ubiquitin-dependent protein catabolic process	11	2.483069977	0.015731688	418	182	16787	2.427270098	1
UP_SEQ_FEATURE	sequence variant	292	65.91422122	0.01582866	435	12443	20063	1.082341639	1
GOTERM_BP_DIRECT	GO:0021987~cerebral cortex development	6	1.354401806	0.016489199	418	60	16787	4.016028708	1
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	83	18.73589165	0.016601055	427	2799	18202	1.264056333	0.999115923
GOTERM_BP_DIRECT	GO:0030163~protein catabolic process	5	1.128668172	0.016948971	418	40	16787	5.020035885	1
UP_KEYWORDS	Biological rhythms	8	1.805869074	0.017272885	437	125	20568	3.01224714	0.998667961
UP_KEYWORDS	Chloride	6	1.354401806	0.018345178	437	72	20568	3.922196796	0.999120278
GOTERM_BP_DIRECT	GO:0048468~cell development	5	1.128668172	0.018422939	418	41	16787	4.897595986	1
GOTERM_MF_DIRECT	GO:0048306~calcium-dependent protein binding	6	1.354401806	0.018944833	414	61	16313	3.875742457	0.999996445
BBID	26.cyclin-CDK_complexes	4	0.902934537	0.019379468	17	15	388	6.08627451	0.336989162
GOTERM_BP_DIRECT	GO:0030071~regulation of mitotic metaphase/anaphase transition	3	0.677200903	0.019742403	418	9	16787	13.38676236	1
GOTERM_BP_DIRECT	GO:0031053~primary miRNA processing	3	0.677200903	0.019742403	418	9	16787	13.38676236	1
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	68	15.34988713	0.020717516	414	2074	16313	1.291914152	0.999998914
KEGG_PATHWAY	hsa04914:Progesterone-mediated oocyte maturation	8	1.805869074	0.020888157	222	87	6910	2.862172517	0.993422084
UP_KEYWORDS	Polymorphism	277	62.5282167	0.022892628	437	12042	20568	1.082659205	0.999849315
UP_KEYWORDS	Protein phosphatase	8	1.805869074	0.023388673	437	133	20568	2.831059342	0.999875758
GOTERM_CC_DIRECT	GO:0009986~cell surface	22	4.966139955	0.023513596	427	560	18202	1.674657076	0.999954312
GOTERM_CC_DIRECT	GO:0005741~mitochondrial outer membrane	9	2.031602709	0.025016441	427	150	18202	2.55765808	0.999976074
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	12	2.708803612	0.02532561	418	225	16787	2.141881978	1
GOTERM_BP_DIRECT	GO:0040014~regulation of multicellular organism growth	4	0.902934537	0.025910291	418	26	16787	6.178505705	1
INTERPRO	IPR011161:MHC class I-like antigen recognition	4	0.902934537	0.026068236	430	28	18593	6.177076412	1
GOTERM_CC_DIRECT	GO:0016605~PML body	7	1.58013544	0.02637143	427	97	18202	3.076221058	0.999986659
UP_SEQ_FEATURE	domain:Laminin G-like 2	4	0.902934537	0.026490187	435	30	20063	6.149578544	1
UP_SEQ_FEATURE	domain:Laminin G-like 1	4	0.902934537	0.026490187	435	30	20063	6.149578544	1
UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase 1	3	0.677200903	0.026697043	435	12	20063	11.53045977	1
UP_SEQ_FEATURE	domain:Laminin G-like	3	0.677200903	0.026697043	435	12	20063	11.53045977	1
UP_SEQ_FEATURE	domain:Tyrosine-protein phosphatase 2	3	0.677200903	0.026697043	435	12	20063	11.53045977	1
GOTERM_BP_DIRECT	GO:0019882~antigen processing and presentation	5	1.128668172	0.02696795	418	46	16787	4.365248596	1
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	6	1.354401806	0.027232269	414	67	16313	3.528661043	0.999999986
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	18	4.063205418	0.027679928	418	409	16787	1.767445397	1
GOTERM_CC_DIRECT	GO:0031410~cytoplasmic vesicle	9	2.031602709	0.028675147	427	154	18202	2.491225402	0.999995067
GOTERM_BP_DIRECT	GO:0045860~positive regulation of protein kinase activity	5	1.128668172	0.028917447	418	47	16787	4.272370966	1
GOTERM_BP_DIRECT	GO:0009636~response to toxic substance	7	1.58013544	0.029629503	418	94	16787	2.990659676	1
KEGG_PATHWAY	hsa04120:Ubiquitin mediated proteolysis	10	2.257336343	0.031116191	222	137	6910	2.271980009	0.999459664
GOTERM_BP_DIRECT	GO:0071805~potassium ion transmembrane transport	8	1.805869074	0.031371919	418	121	16787	2.655225592	1
KEGG_PATHWAY	hsa05223:Non-small cell lung cancer	6	1.354401806	0.032589592	222	56	6910	3.334942085	0.999623851
UP_KEYWORDS	Symport	7	1.58013544	0.033313092	437	113	20568	2.915615318	0.999997438
UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	20	4.514672686	0.033583426	435	554	20063	1.665048342	1
UP_KEYWORDS	Calcium	28	6.320541761	0.034092816	437	876	20568	1.504404251	0.999998114

Supplementary Table S2 (continued)

UP_SEQ_FEATURE	propeptide:Removed in mature form	11	2.483069977	0.034312296	435	237	20063	2.140676075	1
UP_KEYWORDS	Nucleus	129	29.11963883	0.034359583	437	5234	20568	1.160023049	0.999998302
GOTERM_BP_DIRECT	GO:0090399~replicative senescence	3	0.677200903	0.034462734	418	12	16787	10.04007177	1
UP_SEQ_FEATURE	signal peptide	88	19.86455982	0.035042376	435	3346	20063	1.213007125	1
UP_KEYWORDS	Cell cycle	22	4.966139955	0.035358839	437	646	20568	1.602879186	0.999998854
GOTERM_CC_DIRECT	GO:0045121~membrane raft	11	2.483069977	0.0356119	427	221	18202	2.121737472	0.999999757
UP_KEYWORDS	Host-virus interaction	15	3.386004515	0.036054838	437	385	20568	1.833754346	0.999999129
GOTERM_BP_DIRECT	GO:0016032~viral process	15	3.386004515	0.036107639	418	329	16787	1.831016128	1
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	7	1.58013544	0.036845452	418	99	16787	2.839616258	1
GOTERM_BP_DIRECT	GO:0097193~intrinsic apoptotic signaling pathway	4	0.902934537	0.037636429	418	30	16787	5.354704944	1
KEGG_PATHWAY	hsa04071:Sphingolipid signaling pathway	9	2.031602709	0.037991198	222	120	6910	2.334459459	0.999900777
UP_KEYWORDS	Synapse	14	3.16027088	0.038436602	437	353	20568	1.866654566	0.99999966
GOTERM_BP_DIRECT	GO:0000209~protein polyubiquitination	10	2.257336343	0.039463631	418	183	16787	2.194551207	1
GOTERM_MF_DIRECT	GO:0015293~symporter activity	5	1.128668172	0.039799573	414	51	16313	3.863076632	1
GOTERM_CC_DIRECT	GO:0000139~Golgi membrane	22	4.966139955	0.03986995	427	591	18202	1.586815503	0.999999962
INTERPRO	IPR017948:Transforming growth factor beta, conserved site	4	0.902934537	0.039921953	430	33	18593	5.241155743	1
INTERPRO	IPR015615:Transforming growth factor-beta-related	4	0.902934537	0.039921953	430	33	18593	5.241155743	1
UP_KEYWORDS	Secreted	53	11.96388262	0.040065138	437	1918	20568	1.300582462	0.999999821
GOTERM_BP_DIRECT	GO:0071625~vocalization behavior	3	0.677200903	0.04007134	418	13	16787	9.267758557	1
GOTERM_BP_DIRECT	GO:0021846~cell proliferation in forebrain	3	0.677200903	0.04007134	418	13	16787	9.267758557	1
GOTERM_BP_DIRECT	GO:1900025~negative regulation of substrate adhesion-dependent cell spreading	3	0.677200903	0.04007134	418	13	16787	9.267758557	1
UP_KEYWORDS	Isopeptide bond	34	7.674943567	0.040220681	437	1131	20568	1.414903884	0.999999832
UP_KEYWORDS	Wnt signaling pathway	9	2.031602709	0.040699216	437	182	20568	2.32745744	0.999999861
UP_SEQ_FEATURE	domain:ARID	3	0.677200903	0.040704878	435	15	20063	9.224367816	1
UP_SEQ_FEATURE	region of interest:Coenzyme A binding	3	0.677200903	0.040704878	435	15	20063	9.224367816	1
KEGG_PATHWAY	hsa05219:Bladder cancer	5	1.128668172	0.040951172	222	41	6910	3.79586904	0.999952347
GOTERM_MF_DIRECT	GO:0022891~substrate-specific transmembrane transporter activity	3	0.677200903	0.041479246	414	13	16313	9.093088071	1
UP_KEYWORDS	Ion channel	14	3.16027088	0.042067028	437	357	20568	1.845739669	0.999999919
UP_SEQ_FEATURE	chain:Choline/ethanolamine kinase	2	0.451467269	0.042796837	435	2	20063	46.12183908	1
UP_SEQ_FEATURE	zinc finger region:SIAH-type	2	0.451467269	0.042796837	435	2	20063	46.12183908	1
UP_SEQ_FEATURE	chain:Carnitine O-palmitoyltransferase 1, muscle isoform	2	0.451467269	0.042796837	435	2	20063	46.12183908	1
GOTERM_MF_DIRECT	GO:0016829~lyase activity	4	0.902934537	0.042903108	414	31	16313	5.084307309	1
GOTERM_CC_DIRECT	GO:0019898~extrinsic component of membrane	6	1.354401806	0.043228366	427	82	18202	3.119095219	0.999999991
UP_SEQ_FEATURE	metal ion-binding site:Magnesium	7	1.58013544	0.043249252	435	118	20063	2.736041301	1
UP_KEYWORDS	ATP-binding	40	9.029345372	0.044221193	437	1391	20568	1.353453963	0.999999966
GOTERM_BP_DIRECT	GO:0014066~regulation of phosphatidylinositol 3-kinase signaling	6	1.354401806	0.044605543	418	78	16787	3.089252852	1
GOTERM_BP_DIRECT	GO:0071560~cellular response to transforming growth factor beta stimulus	5	1.128668172	0.044863726	418	54	16787	3.7185451	1
GOTERM_MF_DIRECT	GO:0051087~chaperone binding	6	1.354401806	0.045547339	414	77	16313	3.070393375	1
SMART	SM00501:BRIGHT	3	0.677200903	0.045554977	233	15	10071	8.644635193	0.999929378
INTERPRO	IPR027158:Neurexin-1-alpha	2	0.451467269	0.045615239	430	2	18593	43.23953488	1
INTERPRO	IPR001606:ARID/BRIGHT DNA-binding domain	3	0.677200903	0.045741612	430	15	18593	8.647906977	1
UP_SEQ_FEATURE	binding site:Chloride	3	0.677200903	0.045867778	435	16	20063	8.647844828	1
UP_KEYWORDS	Extracellular matrix	11	2.483069977	0.047205829	437	256	20568	2.022382723	0.99999999
UP_SEQ_FEATURE	short sequence motif:Cell attachment site	6	1.354401806	0.047517735	435	91	20063	3.041000379	1
GOTERM_MF_DIRECT	GO:0019789~SUMO transferase activity	3	0.677200903	0.047598557	414	14	16313	8.443581781	1
UP_KEYWORDS	Methylation	15	3.386004515	0.047691901	437	401	20568	1.760587091	0.999999991
GOTERM_BP_DIRECT	GO:2001244~positive regulation of intrinsic apoptotic signaling pathway	4	0.902934537	0.047919285	418	33	16787	4.867913586	1
GOTERM_BP_DIRECT	GO:0007411~axon guidance	9	2.031602709	0.048013866	418	161	16787	2.244984992	1
INTERPRO	IPR008250:P-type ATPase, A domain	4	0.902934537	0.049692625	430	36	18593	4.804392765	1
INTERPRO	IPR023299:P-type ATPase, cytoplasmic domain N	4	0.902934537	0.049692625	430	36	18593	4.804392765	1
INTERPRO	IPR018303:P-type ATPase, phosphorylation site	4	0.902934537	0.049692625	430	36	18593	4.804392765	1
INTERPRO	IPR001757:Cation-transporting P-type ATPase	4	0.902934537	0.049692625	430	36	18593	4.804392765	1
GOTERM_MF_DIRECT	GO:0044547~DNA topoisomerase binding	2	0.451467269	0.049995014	414	2	16313	39.40338164	1
GOTERM_MF_DIRECT	GO:0061630~ubiquitin protein ligase activity	10	2.257336343	0.050019765	414	188	16313	2.095924555	1
GOTERM_MF_DIRECT	GO:0005178~integrin binding	7	1.58013544	0.050540614	414	105	16313	2.62689211	1
GOTERM_BP_DIRECT	GO:0051301~cell division	15	3.386004515	0.051553653	418	346	16787	1.741052908	1
UP_SEQ_FEATURE	zinc finger region:C2H2-type 18	5	1.128668172	0.052136981	435	65	20063	3.547833775	1
UP_KEYWORDS	Mitogen	4	0.902934537	0.052472766	437	40	20568	4.706636156	0.999999999
SMART	SM00204:TGFB	4	0.902934537	0.052828859	233	37	10071	4.67277578	0.999985283
UP_KEYWORDS	Chromosomal rearrangement	13	2.934537246	0.053867519	437	334	20568	1.831924252	0.999999999
UP_SEQ_FEATURE	active site:4-aspartylphosphate intermediate	4	0.902934537	0.055114161	435	40	20063	4.612183908	1
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	111	25.05643341	0.056020216	427	4095	18202	1.155474346	1
KEGG_PATHWAY	hsa05214:Glioma	6	1.354401806	0.056133589	222	65	6910	2.873180873	0.999998932
INTERPRO	IPR001839:Transforming growth factor-beta, C-terminal	4	0.902934537	0.05679143	430	38	18593	4.551529988	1
GOTERM_BP_DIRECT	GO:0006366~transcription from RNA polymerase II promoter	20	4.514672686	0.058445806	418	517	16787	1.553589442	1
GOTERM_BP_DIRECT	GO:0007158~neuron cell-cell adhesion	3	0.677200903	0.058723742	418	16	16787	7.530053828	1
GOTERM_BP_DIRECT	GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	3	0.677200903	0.058723742	418	16	16787	7.530053828	1
GOTERM_BP_DIRECT	GO:0007017~microtubule-based process	4	0.902934537	0.059427646	418	36	16787	4.46225412	1
BIOCARTA	h_tcraPathway:Lck and Fyn tyrosine kinases in initiation of TCR Activation	3	0.677200903	0.059523289	61	11	1625	7.265275708	0.999825388
KEGG_PATHWAY	hsa04114:Oocyte meiosis	8	1.805869074	0.059603649	222	109	6910	2.284486321	0.999999555
UP_KEYWORDS	Congenital myasthenic syndrome	3	0.677200903	0.060464123	437	19	20568	7.431530772	1
UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	21	4.740406321	0.061688986	435	636	20063	1.522890913	1
GOTERM_MF_DIRECT	GO:0005249~voltage-gated potassium channel activity	5	1.128668172	0.062097713	414	59	16313	3.339269631	1
UP_KEYWORDS	Li-Fraumeni syndrome	2	0.451467269	0.062258357	437	3	20568	31.37757437	1
KEGG_PATHWAY	hsa04115:p53 signaling pathway	6	1.354401806	0.062414607	222	67	6910	2.78741428	0.999999782
GOTERM_CC_DIRECT	GO:0043231~intracellular membrane-bounded organelle	20	4.514672686	0.063449259	427	555	18202	1.536130979	1
UP_SEQ_FEATURE	region of interest:SBD	2	0.451467269	0.063504986	435	3	20063	30.74789272	1
UP_SEQ_FEATURE	repeat:PC 4	2	0.451467269	0.063504986	435	3	20063	30.74789272	1
UP_SEQ_FEATURE	DNA-binding region:CUT 1	2	0.451467269	0.063504986	435	3	20063	30.74789272	1
UP_SEQ_FEATURE	region of interest:G-domain	2	0.451467269	0.063504986	435	3	20063	30.74789272	1
UP_SEQ_FEATURE	repeat:PC 1	2	0.451467269	0.063504986	435	3	20063	30.74789272	1
UP_SEQ_FEATURE	repeat:PC 2	2	0.451467269	0.063504986	435	3	20063	30.74789272	1
UP_SEQ_FEATURE	DNA-binding region:CUT 2	2	0.451467269	0.063504986	435	3	20063	30.74789272	1
UP_SEQ_FEATURE	repeat:PC 3	2	0.451467269	0.063504986	435	3	20063	30.74789272	1
COG_ONTOLOGY	Posttranslational modification, protein turnover, chaperones	6	1.354401806	0.064941486	43	106	2026	2.666959193	0.60939028
UP_KEYWORDS	Cell division	14	3.16027088	0.065906971	437	383	20568	1.720441415	1
KEGG_PATHWAY	hsa00520:Amino sugar and nucleotide sugar metabolism	5	1.128668172	0.066358365	222	48	6910	3.242304805	0.99999992
GOTERM_BP_DIRECT	GO:0007275~multicellular organism development	20	4.514672686	0.066403657	418	526	16787	1.527007113	1
UP_SEQ_FEATURE	topological domain:Lumenal	16	3.611738149	0.066986881	435	450	20063	1.639887612	1
GOTERM_MF_DIRECT	GO:0030165~PDZ domain binding	6	1.354401806	0.067066054	414	86	16313	2.749073138	1
GOTERM_CC_DIRECT	GO:0031982~vesicle	7	1.58013544	0.067071352	427	122	18202	2.44584789	1
UP_KEYWORDS	EGF-like domain	10	2.257336343	0.067574963	437	238	20568	1.977578217	1
INTERPRO	IPR022308:Synaptic vesicle protein SV2	2	0.451467269	0.067638318	430	3	18593	28.82635659	1
INTERPRO	IPR018121:Seven-in-absentia protein, TRAF-like domain	2	0.451467269	0.067638318	430	3	18593	28.82635659	1
GOTERM_BP_DIRECT	GO:0007162~negative regulation of cell adhesion	4	0.902934537	0.067751622	418	38	16787	4.22739864	1
GOTERM_BP_DIRECT	GO:0060395~SMAD protein signal transduction	5	1.128668172	0.068017552	418	62	16787	3.238732829	1
GOTERM_CC_DIRECT	GO:1902495~transmembrane transporter complex	2	0.451467269	0.068585319	427	3	18202	28.41842311	1
GOTERM_CC_DIRECT	GO:0005967~mitochondrial pyruvate dehydrogenase complex	2	0.451467269	0.068585319	427	3	18202	28.41842311	1
GOTERM_BP_DIRECT	GO:0016925~protein sumoylation	7	1.58013544	0.069293219	418	116	16787	2.4234656	1
KEGG_PATHWAY	hsa00510:N-Glycan biosynthesis	5	1.128668172	0.070528553	222	49	6910	3.176135319	0.999999972
GOTERM_BP_DIRECT	GO:0006886~intracellular protein transport	11	2.483069977	0.07072985	418	236	16787	1.871877788	1
UP_KEYWORDS	Cytoplasm	116	26.18510158	0.071628566	437	4794	20568	1.138860647	1
GOTERM_MF_DIRECT	GO:0046934~phosphatidylinositol-4,5-bisphosphate 3-kinase activity	5	1.128668172	0.071848711	414	62	16313	3.177692068	1
SMART	SM00282:LamG	4	0.902934537	0.07187991	233	42	10071	4.116492949	0.999999772
INTERPRO	IPR011701:Major facilitator superfamily	5	1.128668172	0.07199331	430	68	18593	3.179377565	1
UP_KEYWORDS	Cell junction	21	4.740406321	0.07202988	437	664	20568	1.488544567	1
UP_KEYWORDS	Acyltransferase	8	1.805869074	0.072376649	437	171	20568	2.201935044	1
GOTERM_BP_DIRECT	GO:0008053~mitochondrial fusion	3	0.677200903	0.072498755	418	18	16787	6.69338118	1
GOTERM_BP_DIRECT	GO:0006796~phosphate-containing compound metabolic process	3	0.677200903	0.072498755	418	18	16787	6.69338118	1
GOTERM_BP_DIRECT	GO:0030033~microvillus assembly	3	0.677200903	0.072498755	418	18	16787	6.69338118	1
GOTERM_BP_DIRECT	GO:0097116~gephyrin clustering involved in postsynaptic density assembly	2	0.451467269	0.072690328	418	3	16787	26.77352472	1
UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	6	1.354401806	0.072914678	435	103	20063	2.686709073	1
KEGG_PATHWAY	hsa04310:Wnt signaling pathway	9	2.031602709	0.074312782	222	138	6910	2.029964747	0.99999999
GOTERM_MF_DIRECT	GO:0015269~calcium-activated potassium channel activity	3	0.677200903	0.074932455	414	18	16313	6.567230274	1
GOTERM_MF_DIRECT	GO:0004842~ubiquitin-protein transferase activity	14	3.16027088	0.075920086	414	329	16313	1.676739644	1
GOTERM_CC_DIRECT	GO:0043209~myelin sheath	8	1.805869074	0.076313808	427	157	18202	2.172108773	1
GOTERM_BP_DIRECT	GO:0045184~establishment of protein localization	4	0.902934537	0.076573508	418	40	16787	4.016028708	1
GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	10	2.257336343	0.076732753	414	205	16313	1.922116178	1
UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	20	4.514672686	0.077468767	435	615	20063	1.499897206	1
GOTERM_BP_DIRECT	GO:0007584~response to nutrient	6	1.354401806	0.078997043	418	92	16787	2.619149157	1
GOTERM_BP_DIRECT	GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	6	1.354401806	0.078997043	418	92	16787	2.619149157	1
GOTERM_BP_DIRECT	GO:0006357~regulation of transcription from RNA polymerase II promoter	17	3.837471783	0.079481596	418	437	16787	1.562299497	1
GOTERM_BP_DIRECT	GO:0045879~negative regulation of smoothened signaling pathway	3	0.677200903	0.079737396	418	19	16787	6.34109796	1
UP_KEYWORDS	Magnesium	18	4.063205418	0.080045167	437	551	20568	1.537558091	1
GOTERM_BP_DIRECT	GO:0043408~regulation of MAPK cascade	4	0.902934537	0.081164342	418	41	16787	3.918076788	1
UP_KEYWORDS	Mitochondrion outer membrane	6	1.354401806	0.08232214	437	109	20568	2.590808893	1
UP_SEQ_FEATURE	domain:EGF-like 3	5	1.128668172	0.082492944	435	76	20063	3.034331518	1
UP_KEYWORDS	Postsynaptic cell membrane	8	1.805869074	0.083391464	437	177	20568	2.127293178	1
KEGG_PATHWAY	hsa04022:cGMP-PKG signaling pathway	10	2.257336343	0.084233331	222	166	6910	1.875067839	0.999999999
GOTERM_BP_DIRECT	GO:0046854~phosphatidylinositol phosphorylation	6	1.354401806	0.084812395	418	94	16787	2.56342258	1
INTERPRO	IPR011162:MHC classes I/II-like antigen recognition protein	4	0.902934537	0.085088556	430	45	18593	3.843514212	1

Supplementary Table S2 (continued)

GOTERM_CC_DIRECT	GO:0030496~midbody	7	1.58013544	0.085127349	427	130	18202	2.295334174	1
UP_KEYWORDS	Allosteric enzyme	4	0.902934537	0.085349517	437	49	20568	3.842151964	1
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	40	9.029345372	0.085860351	427	1331	18202	1.281070914	1
GOTERM_BP_DIRECT	GO:0006024~glycosaminoglycan biosynthetic process	4	0.902934537	0.085871287	418	42	16787	3.824789246	1
GOTERM_BP_DIRECT	GO:0006289~nucleotide-excision repair	4	0.902934537	0.085871287	418	42	16787	3.824789246	1
GOTERM_BP_DIRECT	GO:0042326~negative regulation of phosphorylation	3	0.677200903	0.087189077	418	20	16787	6.024043062	1
GOTERM_BP_DIRECT	GO:0001892~embryonic placenta development	3	0.677200903	0.087189077	418	20	16787	6.024043062	1
KEGG_PATHWAY	hsa00500:Starch and sucrose metabolism	4	0.902934537	0.087306651	222	33	6910	3.772863773	1
UP_KEYWORDS	Cell adhesion	16	3.611738149	0.087465519	437	479	20568	1.572154039	1
INTERPRO	IPR000742:Epidermal growth factor-like domain	10	2.257336343	0.0879995	430	231	18593	1.871841337	1
INTERPRO	IPR004162:Seven-in-absentia protein, sina	2	0.451467269	0.089154357	430	4	18593	21.61976744	1
INTERPRO	IPR023213:Chloramphenicol acetyltransferase-like domain	2	0.451467269	0.089154357	430	4	18593	21.61976744	1
INTERPRO	IPR001646:Pentapeptide repeat	2	0.451467269	0.089154357	430	4	18593	21.61976744	1
INTERPRO	IPR013010:Zinc finger, SIAH-type	2	0.451467269	0.089154357	430	4	18593	21.61976744	1
INTERPRO	IPR002355:Multicopper oxidase, copper-binding site	2	0.451467269	0.089154357	430	4	18593	21.61976744	1
INTERPRO	IPR001078:2-oxoacid dehydrogenase acyltransferase, catalytic domain	2	0.451467269	0.089154357	430	4	18593	21.61976744	1
INTERPRO	IPR018000:Neurotransmitter-gated ion-channel, conserved site	4	0.902934537	0.089540715	430	46	18593	3.759959555	1
GOTERM_MF_DIRECT	GO:0005160~transforming growth factor beta receptor binding	4	0.902934537	0.08969848	414	42	16313	3.752703014	1
GOTERM_BP_DIRECT	GO:0018108~peptidyl-tyrosine phosphorylation	8	1.805869074	0.089735975	418	154	16787	2.08624868	1
INTERPRO	IPR002464:DNA/RNA helicase, ATP-dependent, DEAH-box type, conserved site	3	0.677200903	0.090635704	430	22	18593	5.896300211	1
GOTERM_BP_DIRECT	GO:0051290~protein heterotetramerization	4	0.902934537	0.090691388	418	43	16787	3.735840659	1
UP_KEYWORDS	Transmembrane helix	133	30.02257336	0.090896043	437	5621	20568	1.1136499	1
UP_KEYWORDS	Tricarboxylic acid cycle	3	0.677200903	0.091138165	437	24	20568	5.883295195	1
GOTERM_BP_DIRECT	GO:0031954~positive regulation of protein autophosphorylation	3	0.677200903	0.094838808	418	21	16787	5.737183869	1
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	11	2.483069977	0.094958425	418	250	16787	1.767052632	1
GOTERM_BP_DIRECT	GO:0051882~mitochondrial depolarization	2	0.451467269	0.095729421	418	4	16787	20.08014354	1
GOTERM_BP_DIRECT	GO:0038094~Fc-gamma receptor signaling pathway	2	0.451467269	0.095729421	418	4	16787	20.08014354	1
GOTERM_BP_DIRECT	GO:0006933~negative regulation of cell adhesion involved in substrate-bound cell migration	2	0.451467269	0.095729421	418	4	16787	20.08014354	1
GOTERM_BP_DIRECT	GO:0097118~neuroligin clustering involved in postsynaptic membrane assembly	2	0.451467269	0.095729421	418	4	16787	20.08014354	1
GOTERM_BP_DIRECT	GO:0002283~neutrophil activation involved in immune response	2	0.451467269	0.095729421	418	4	16787	20.08014354	1
GOTERM_BP_DIRECT	GO:1990182~exosomal secretion	2	0.451467269	0.095729421	418	4	16787	20.08014354	1
BIOCARTA	h_g1Pathway:Cell Cycle: G1/S Check Point	4	0.902934537	0.095927216	61	30	1625	3.551912568	0.999999332
GOTERM_MF_DIRECT	GO:0003712~transcription cofactor activity	5	1.128668172	0.097403141	414	69	16313	2.85531751	1
GOTERM_MF_DIRECT	GO:0005221~intracellular cyclic nucleotide activated cation channel activity	2	0.451467269	0.097496276	414	4	16313	19.70169082	1
GOTERM_MF_DIRECT	GO:0019834~phospholipase A2 inhibitor activity	2	0.451467269	0.097496276	414	4	16313	19.70169082	1
INTERPRO	IPR001111:Transforming growth factor-beta, N-terminal	3	0.677200903	0.097807309	430	23	18593	5.639939333	1
GOTERM_MF_DIRECT	GO:0015297~antiporter activity	3	0.677200903	0.097935121	414	21	16313	5.62905452	1
UP_KEYWORDS	Transmembrane	133	30.02257336	0.097942165	437	5639	20568	1.110095068	1
UP_SEQ_FEATURE	topological domain:Mitochondrial intermembrane	4	0.902934537	0.097998806	435	51	20063	3.617399144	1
INTERPRO	IPR006029:Neurotransmitter-gated ion-channel transmembrane domain	4	0.902934537	0.098728975	430	48	18593	3.603294574	1
INTERPRO	IPR006201:Neurotransmitter-gated ion-channel	4	0.902934537	0.098728975	430	48	18593	3.603294574	1
INTERPRO	IPR006202:Neurotransmitter-gated ion-channel ligand-binding	4	0.902934537	0.098728975	430	48	18593	3.603294574	1
UP_KEYWORDS	Mitosis	10	2.257336343	0.099685582	437	258	20568	1.82427758	1
UP_KEYWORDS	Retinitis pigmentosa	5	1.128668172	0.099791948	437	83	20568	2.835322985	1